

Shears, Beverly

From: Devi, Sarvamangala
 Sent: Wednesday, July 06, 2005 8:49 AM
 To: Shears, Beverly
 Subject: 10/606,618

Beverly:

In application 10/606,618, please perform a search for SEQ ID NO: 4 and an at least eight amino acid-long fragment thereof; a polypeptide comprising amino acids 1-178 of SEQ ID NO: 4; and a polypeptide comprising amino acids 720 to 745 of SEQ ID NO: 4 in commercial and pending databases.

Please include an inventors' name search for: Ralph C. Judd and Scott D. Manning.

Thanx.

S. DEVI, Ph.D.
 AU 1645
 Rems - 3C18

1

Date completed: _____

Searcher: Beverly e 2523

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

____ STIC

____ CM-1

____ Pre-S

Type of Search

____ N.A. Sequence

____ A.A. Sequence

____ Structure

____ Bibliographic

Vendors

____ IG

____ STN

____ Dialog

____ APS

____ Geninfo

____ SDC

____ DARC/Questel

____ Other CGN

THIS PAGE BLANK (USPTO)



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 158556

TO: Sarvamangala Devi
Art Unit: 1645
Location: REM 3C18
Serial Number: 10/606618

Monday, July 11, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:37:49 ; Search time 175 Seconds
(without alignments)
2332.155 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMMLGISPLAF.....LKKKPEDEIQRFQGLGTTF 797

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	2	O30912
2	752	94.4	797	2	Q9JX31
3	752	94.4	797	2	Q9KIH0
4	157	19.7	792	2	P95359
5	13	1.6	771	2	Q7NVY6
6	13	1.6	786	2	Q88MH2
7	13	1.6	787	2	Q88H14
8	10	1.3	765	2	Q8XZL3
9	9	1.1	328	2	Q9SMN7
10	9	1.1	361	2	Q6LS43
11	9	1.1	435	2	Q9LXP7
12	9	1.1	713	2	Q9ZAE1
13	9	1.1	713	2	Q72J38
14	9	1.1	769	2	Q62JD2
15	9	1.1	769	2	Q63T20
16	9	1.1	778	2	Q7VYC2
17	9	1.1	778	2	Q7WA52
18	9	1.1	778	2	Q7WJ86
19	9	1.1	797	2	Q9S341
20	9	1.1	797	2	Q7N8N9
21	9	1.1	952	2	Q8C0X4
22	9	1.1	1035	2	Q9M7J0
23	8	1.0	55	2	Q8MT28
24	8	1.0	82	1	VIM3
25	8	1.0	129	2	Q97L79
26	8	1.0	186	2	Q9ATW3
27	8	1.0	225	2	Q6B441
28	8	1.0	225	2	Q9ZU33
29	8	1.0	241	2	Q8H308
30	8	1.0	277	2	Q87R36
31	8	1.0	290	2	Q6FRt4

32	8	1.0	299	2	Q8NSK6	Q8nsk6 corynebacte
33	8	1.0	321	2	Q86GZ0	Q86gz0 rhipicephal
34	8	1.0	334	1	GYAR_PYRHO	O58320 pyrococcus
35	8	1.0	334	2	Q8MTY1	O8mty1 rhipicephal
36	8	1.0	335	1	GYAR_PYRAB	Q9uyr1 pyrococcus
37	8	1.0	337	2	Q9KRW5	Q9krw5 vibrio chol
38	8	1.0	341	2	Q9SE52	Q9se52 eriosema ps
39	8	1.0	426	2	O81885	O81885 arabidopsis
40	8	1.0	428	2	Q75JR2	Q75jr2 dictyosteli
41	8	1.0	429	1	FLIK_BACSU	P23451 bacillus su
42	8	1.0	439	2	Q8S7B4	Q8s7b4 oryza sativ
43	8	1.0	439	2	Q7XFL9	Q7xfl9 oryza sativ
44	8	1.0	447	2	Q6SEY9	Q6set9 bacillus li
45	8	1.0	461	2	Q93ZN9	Q93zn9 arabidopsis
46	8	1.0	474	2	Q9T200	Q9t200 bacterioph
47	8	1.0	529	2	Q6TNE9	Q6tne9 symbiobacte
48	8	1.0	558	2	Q7F9Z5	Q7f9z5 oryza sativ
49	8	1.0	558	2	Q7XK07	Q7xk07 oryza sativ
50	8	1.0	583	2	Q911V1	Q911v1 pseudomonas
51	8	1.0	758	2	Q82U03	Q82u03 nitrosomona
52	8	1.0	825	2	Q6FCG7	Q6fcg7 acinetobact
53	8	1.0	826	2	Q8EGG7	Q8egg7 shewanella
54	8	1.0	903	1	MSPI_SCHPO	P87320 schizosacch
55	8	1.0	1066	2	Q6NP12	Q6np12 drosophila
56	8	1.0	1085	2	Q8FQ00	Q8fq00 corynebacte
57	8	1.0	1363	1	ILPR_BRALA	O02466 branchiosto
58	8	1.0	1459	2	Q75G47	Q75g47 oryza sativ
59	8	1.0	1475	2	Q9LQU6	Q9lqu6 arabidopsis
60	8	1.0	1577	1	HLVA_PROMI	P16466 proteus mir
61	8	1.0	2408	2	Q9V549	Q9v549 drosophila
62	8	1.0	2903	2	Q9N8R7	Q9n8r7 trypanosoma
63	8	1.0	4919	2	Q9ZHL0	Q9zhl0 haemophilus
64	8	1.0	6199	2	Q6JAN0	Q6jan0 brachydanio
65	7	0.9	63	2	Q8TE37	Q8te37 homo sapien
66	7	0.9	65	2	Q82UE9	Q82ue9 nitrosomona
67	7	0.9	67	2	Q6TMQ2	Q6tmq2 streptomyce
68	7	0.9	71	2	Q8XWZ3	Q8xmz3 clostridium
69	7	0.9	75	2	Q8X5D6	Q8x5d6 escherichia
70	7	0.9	75	2	Q83LQ3	Q83lq3 shigella fl
71	7	0.9	76	1	DICC_ECOLI	P06965 escherichia
72	7	0.9	85	2	Q6D0U7	Q6d0u7 erwinia car
73	7	0.9	93	2	Q726R5	Q726r5 desulfovibr
74	7	0.9	95	2	Q9XXG0	Q9xxg0 caenorhabdi
75	7	0.9	98	2	Q6G599	Q6g599 bartonella
76	7	0.9	101	1	PHS_STRCO	O86722 streptomyce
77	7	0.9	102	1	Q76445	O76445 caenorhabdi
78	7	0.9	104	2	RL21_METKA	Q8tuu3 methanopyru
79	7	0.9	104	2	Q9IN54	Q9in54 citrus psor
80	7	0.9	104	2	Q9IN56	Q9in56 citrus psor
81	7	0.9	104	2	Q9IN57	Q9in57 citrus psor
82	7	0.9	104	2	Q9IN58	Q9in58 citrus psor
83	7	0.9	104	2	Q9IN59	Q9in59 citrus psor
84	7	0.9	104	2	Q9IN60	Q9in60 citrus psor
85	7	0.9	109	2	Q9Y9U5	Q9y9u5 aeropyrum p
86	7	0.9	115	2	Q7S7S3	Q7s7s3 neurospora
87	7	0.9	115	2	Q8RSN6	Q8rsn6 uncultured
88	7	0.9	120	2	Q6CQL2	Q6cql2 kluyveromyc
89	7	0.9	123	1	KNG_GADMO	P83856 gadus morhu
90	7	0.9	124	1	CRCB_PHOLL	Q7n768 photorhabdu
91	7	0.9	126	2	Q9VM79	Q9vm79 drosophila
92	7	0.9	127	2	Q0C096	O0C096 methanococc
93	7	0.9	128	2	Q0C266	Q0c266 neurospora
94	7	0.9	130	2	Q76CY7	Q76cy7 conger myri
95	7	0.9	130	2	Q9PV14	Q9pv14 mola mola (
96	7	0.9	131	2	Q93773	Q93773 uncultured
97	7	0.9	131	2	Q9A7L3	Q9a7l3 caulobacter
98	7	0.9	134	2	Q8PN27	O8pn27 xanthomonas
99	7	0.9	135	2	Q45783	O45783 caenorhabdi
100	7	0.9	138	2	Q7X116	Q7x116 leptospiril
101	7	0.9	139	2	Q7RZ14	Q7rz14 arabidopsis
102	7	0.9	140	2	Q9EMS9	Q9ems9 amacta moo
103	7	0.9	145	2	Q91110	Q91110 morone saxa
104	7	0.9	148	2	O50574	O50574 bacillus ps

105	7	0.9	150	1	SSRP_CAMJE	Q9pni9 campylobact	178	7	0.9	243	2	Q89DF6	Q89df6 bradyrhizob
106	7	0.9	150	2	Q6D5B1	Q6d5b1 erwinia car	179	7	0.9	246	2	Q98FG4	Q98fg4 rhizobium l
107	7	0.9	156	2	Q70T64	Q70t64 ciona intes	180	7	0.9	248	2	Q8PUT8	Q8put8 methanosarc
108	7	0.9	157	2	Q8ETJ7	Q8etj7 oceanobacil	181	7	0.9	249	2	Q98K42	Q98k42 rhizobium l
109	7	0.9	163	2	Q8GV17	Q8gv17 arabidopsis	182	7	0.9	248	2	Q8TJK1	Q8tjk1 methanosarc
110	7	0.9	164	2	Q7R6G1	Q7r6g1 giardia lam	183	7	0.9	249	2	Q81AW6	Q81aw6 bacillus ce
111	7	0.9	168	2	Q6EPF5	Q6epf5 oryza sativ	184	7	0.9	254	2	Q7SAF5	Q7saf5 neurospora
112	7	0.9	168	2	Q9DKM2	Q9dkm2 spodoptera	185	7	0.9	254	2	Q946T1	Q946t1 sorghum bic
113	7	0.9	169	1	YLZ6_CABEL	P34419 caenorhabdi	186	7	0.9	255	2	Q97NR2	Q97nr2 streptococc
114	7	0.9	171	2	Q9ZAL7	Q9zal7 listeria iv	187	7	0.9	255	2	Q8CV97	Q8cv97 streptococc
115	7	0.9	171	2	Q97OH7	Q97oh7 streptococc	188	7	0.9	257	1	HADD_RHISP	Q8kls9 rhizobium s
116	7	0.9	172	2	Q9JGT9	Q9jgt9 northern ce	189	7	0.9	260	2	Q8VST1	Q8vst1 vibrio para
117	7	0.9	173	2	Q9SVE4	Q9sve4 arabidopsis	190	7	0.9	264	2	Q8MSS7	Q8ms7 drosophila
118	7	0.9	176	2	Q8SRN5	Q8srn5 encephalito	191	7	0.9	264	2	Q84478	Q84478 chlamydia t
119	7	0.9	177	2	Q676Z8	Q676z8 hyacinthus	192	7	0.9	264	2	Q824J5	Q824j5 chlamydophi
120	7	0.9	177	2	Q9R8W8	Q9r8w8 rhizobium s	193	7	0.9	264	2	Q9PJS1	Q9pjs1 chlamydia m
121	7	0.9	177	2	Q9R8X0	Q9r8x0 rhizobium s	194	7	0.9	266	2	Q8CES7	Q8ces7 mus muscula
122	7	0.9	177	2	Q9R8X1	Q9r8x1 rhizobium s	195	7	0.9	267	2	Q61I73	Q61i73 drosophila
123	7	0.9	177	2	Q9R8X2	Q9r8x2 rhizobium s	196	7	0.9	267	2	Q74C45	Q74c45 geobacter s
124	7	0.9	177	2	Q9Z3N0	Q9z3n0 rhizobium s	197	7	0.9	267	2	Q7NGC2	Q7ngc2 geobacter s
125	7	0.9	178	2	Q9Z3N4	Q9z3n4 rhizobium s	198	7	0.9	267	2	Q893R1	Q893r1 clostridium
126	7	0.9	179	2	Q6H0X9	Q6h0x9 sulfolobus	199	7	0.9	268	1	AROX_THEAC	Q9h1e5 thermoplasm
127	7	0.9	180	2	Q84IV2	Q84iv2 mycobacteri	200	7	0.9	268	2	Q86780	Q86780 streptomyc
128	7	0.9	184	2	Q264Z9	Q264z9 methanobact	201	7	0.9	269	2	Q81IU2	Q81iu2 plasmodium
129	7	0.9	184	2	Q6NE26	Q6ne26 leptospira	202	7	0.9	269	2	Q9XAC7	Q9xac7 streptomyc
130	7	0.9	184	2	Q6FCT9	Q6fct9 acinetobact	203	7	0.9	270	2	Q6BTI8	Q6bti8 debaryomyc
131	7	0.9	185	2	Q62LFF2	Q62lff2 burkholderi	204	7	0.9	272	2	Q64ZK6	Q64zk6 bacteroides
132	7	0.9	185	2	Q63WA2	Q63wa2 burkholderi	205	7	0.9	273	2	Q6Z0W7	Q6z0w7 oryza sativ
133	7	0.9	187	2	Q83NG0	Q83ng0 tropheryma	206	7	0.9	274	2	Q87KK2	Q87kk2 vibrio para
134	7	0.9	190	2	Q78ZU6	Q78zu6 gallid herp	207	7	0.9	277	2	Q7IZT2	Q7izt2 trypanosoma
135	7	0.9	190	2	Q9QTE3	Q9qte3 marek's dis	208	7	0.9	279	2	Q758X7	Q758x7 ashbya goss
136	7	0.9	193	2	Q8VUA8	Q8vua8 lactococcus	209	7	0.9	279	2	Q6F3A1	Q6f3a1 mus musculu
137	7	0.9	194	2	Q6CY336	Q6cy36 kluyveromyc	210	7	0.9	280	2	Q99X12	Q99xi2 streptococc
138	7	0.9	194	2	Q7XVA3	Q7xva3 griffithsia	211	7	0.9	280	2	Q7CMM8	Q7cm8 streptococc
139	7	0.9	196	2	Q8LMY9	Q8lmy9 oryza sativ	212	7	0.9	280	2	Q9A8A2	Q9a8a2 caulobacter
140	7	0.9	196	2	Q7THD4	Q7thd4 aichi virus	213	7	0.9	280	2	Q8KSH2	Q8ksh2 streptococc
141	7	0.9	196	2	Q7THD5	Q7thd5 aichi virus	214	7	0.9	281	2	Q8DUM0	Q8dum0 streptococc
142	7	0.9	196	2	Q7THD6	Q7thd6 aichi virus	215	7	0.9	282	2	Q96NE7	Q96ne7 homo sapien
143	7	0.9	197	2	Q83N11	Q83n11 tropheryma	216	7	0.9	283	2	Q9RJF9	Q9rjf9 streptomyc
144	7	0.9	199	2	Q62M56	Q62m56 burkholderi	217	7	0.9	287	1	PSA3_YEAST	P21242 saccharomyc
145	7	0.9	202	1	HIS7_RHIME	Q92tb0 rhizobium m	218	7	0.9	288	2	Q8W190	Q8w190 euglena gra
146	7	0.9	205	2	Q6CVD5	Q6cvd5 kluyveromyc	219	7	0.9	288	2	Q823B6	Q823b6 chlamydophi
147	7	0.9	207	1	THIE_CHRVO	Q7plr3 chromobacte	220	7	0.9	289	2	Q743L1	Q743l1 mycobacteri
148	7	0.9	207	1	Q7PXX3	Q7pxh3 anopheles g	221	7	0.9	290	2	Q749Y5	Q749y5 geobacter s
149	7	0.9	214	1	NODB_RHIGA	P50354 rhizobium g	222	7	0.9	291	2	Q30441	O30441 bordetella
150	7	0.9	214	2	Q9CD65	Q9cd65 mycobacteri	223	7	0.9	291	2	Q7W3M9	Q7w3m9 bordetella
151	7	0.9	216	2	Q6FXH5	Q6fxh5 candida gla	224	7	0.9	291	2	Q7WF05	Q7wf05 bordetella
152	7	0.9	216	2	Q7NFC9	Q7nfc9 geobacter	225	7	0.9	292	2	Q9REA4	Q9rea4 enterococcu
153	7	0.9	218	2	Q9Z5F9	Q9z5f9 mycobacteri	226	7	0.9	292	2	Q9GL75	Q9gl75 bos taurus
154	7	0.9	218	2	Q6ZEU7	Q6zeu7 burkholderi	227	7	0.9	295	2	Q9ERF5	Q9erf5 mesocricetu
155	7	0.9	218	2	Q63YC9	Q63yc9 burkholderi	228	7	0.9	297	2	Q7SG71	Q7sg71 neurospora
156	7	0.9	221	2	Q8KK26	Q8kk26 proteus vul	229	7	0.9	298	2	Q9GL74	Q9gl74 cercopithe
157	7	0.9	221	2	Q6DAJ2	Q6daj2 erwinia car	230	7	0.9	298	2	Q7M9T0	Q7m9t0 wolinella s
158	7	0.9	223	2	Q82ID5	Q82td5 nitrosomona	231	7	0.9	299	2	Q7QPM1	Q7qpm1 giardia lam
159	7	0.9	225	2	Q8KT67	Q8kt67 photorhabdu	232	7	0.9	299	2	Q7MGD6	Q7mgd6 vibrio vuln
160	7	0.9	225	2	Q7N025	Q7n025 photorhabdu	233	7	0.9	299	2	Q8D4T3	Q8d4t3 vibrio vuln
161	7	0.9	226	2	Q965W3	Q965w3 caenorhabdi	234	7	0.9	301	2	Q8PXU9	Q8pxu9 methanosarc
162	7	0.9	226	2	Q9VLK7	Q9vlk7 drosophila	235	7	0.9	301	2	Q82B65	Q82b65 streptomyc
163	7	0.9	227	2	Q63S36	Q63s36 burkholderi	236	7	0.9	304	2	Q8FRS6	Q8frs6 corynebacte
164	7	0.9	228	2	Q9EMK6	Q9emk6 ansacta moo	237	7	0.9	305	2	P90872	P90872 caenorhabdi
165	7	0.9	232	2	Q7QBH1	Q7qbh1 anopheles g	238	7	0.9	305	2	Q9RT24	Q9rt24 deinococcus
166	7	0.9	233	2	Q7USM9	Q7usm9 synchococc	239	7	0.9	305	2	Q6APE9	Q6ape9 desulfotale
167	7	0.9	233	2	Q9RJP1	Q9rjp1 streptomyc	240	7	0.9	306	2	Q7RUI7	Q7ru17 neurospora
168	7	0.9	234	2	Q25327	Q25327 helicobacte	241	7	0.9	306	2	Q8UCH5	Q8uch5 agrobacteri
169	7	0.9	234	2	Q9Z1M6	Q9z1m6 helicobacte	242	7	0.9	307	2	Q8LCA2	Q8lca2 arabidopsis
170	7	0.9	235	2	Q7NMY8	Q7nmy8 chromobacte	243	7	0.9	308	2	Q84L58	Q84l58 cicier ariet
171	7	0.9	238	2	Q7XBL0	Q7xb10 pachysandra	244	7	0.9	308	2	Q828C9	Q828c9 streptomyc
172	7	0.9	238	2	Q882R1	Q882r1 pseudomonas	245	7	0.9	308	2	Q8FCP5	Q8fcp5 escherichia
173	7	0.9	238	2	Q9HYM6	Q9hym6 pseudomonas	246	7	0.9	311	2	Q8U9T2	Q8u9t2 agrobacteri
174	7	0.9	241	2	Q68961	Q68961 helicobacte	247	7	0.9	314	2	Q8LG78	Q8lg78 arabidopsis
175	7	0.9	242	2	Q6GMV5	Q6gmv5 akebia trif	248	7	0.9	314	2	Q9LPG2	Q9lpg2 arabidopsis
176	7	0.9	242	2	Q7U774	Q7u774 synchococc	249	7	0.9	315	2	Q9FXV5	Q9fxv5 arabidopsis
177	7	0.9	243	2	Q7N9U3	Q7n9u3 photorhabdu	250	7	0.9	316	2	Q82W49	Q82w49 nitrosomona

251	7	0.9	316	2	065566	Q65566 bovine herp	324	7	0.9	361	2	082WK0	Q82wk0 nitrosomona
252	7	0.9	316	2	Q77CC0	Q77cc0 bovine herp	325	7	0.9	362	1	LDOX_VITVI	P51093 vitis vinif
253	7	0.9	317	2	Q6N9N0	Q6n9n0 rhodospseudo	326	7	0.9	362	1	RECA_BRAJA	Q89184 bradyrhizob
254	7	0.9	317	2	Q7N4V6	Q7n4v6 photorhabdu	327	7	0.9	362	2	Q8T114	Q8t114 physarum po
255	7	0.9	320	1	FLAI_TREHY	P32520 treponema h	328	7	0.9	362	2	Q9AX57	Q9ax57 oryza sativ
256	7	0.9	322	2	Q6H4W3	Q6h4w3 oryza sativ	329	7	0.9	362	2	Q73V31	Q73v31 mycobacteri
257	7	0.9	324	2	Q8XGHO	Q8xgh0 salmonella	330	7	0.9	362	2	Q6GN23	Q6gn23 xenopus lae
258	7	0.9	324	2	Q7CR48	Q7cr48 salmonella	331	7	0.9	363	1	LE3A_ASPNG	P87256 aspergillus
259	7	0.9	325	2	Q9P753	Q9p753 neurospora	332	7	0.9	363	2	Q877A9	Q877a9 aspergillus
260	7	0.9	325	2	Q9FAA4	Q9faa4 brevibacter	333	7	0.9	364	2	Q98G12	Q98g12 rhizobium l
261	7	0.9	325	2	Q6NHT0	Q6nht0 corynebacte	334	7	0.9	364	2	Q7ZWM8	Q7zwm8 xenopus lae
262	7	0.9	325	2	Q79VG6	Q79vg6 corynebacte	335	7	0.9	369	2	Q27855	Q27855 tetrahymena
263	7	0.9	326	2	Q8FQ21	Q8fq21 corynebacte	336	7	0.9	371	2	Q73RV5	Q73rv5 mycobacteri
264	7	0.9	328	2	Q6NQC3	Q6nqc3 arabidopsis	337	7	0.9	371	2	Q8FR78	Q8fr78 corynebacte
265	7	0.9	328	2	Q9RB11	Q9rb11 pectobacter	338	7	0.9	371	2	Q6R796	Q6r796 ostrleid her
266	7	0.9	328	2	Q7USN3	Q7usn3 rhodopirell	339	7	0.9	373	1	SECU_YEARST	P40316 saccharomyce
267	7	0.9	330	2	Q7U9S8	Q7u9s8 synechococc	340	7	0.9	373	1	RECA_RHOBA	Q7u9j0 rhodopirell
268	7	0.9	331	2	Q71118	Q71118 human immun	341	7	0.9	375	2	Q708L2	Q708l2 bacterioph
269	7	0.9	333	2	Q88VL6	Q88vl6 lactobacill	342	7	0.9	376	2	Q76L01	Q76l01 dileptus ma
270	7	0.9	335	2	Q9ZPW3	Q9zpw3 arabidopsis	343	7	0.9	376	2	Q7WZC5	Q7wzc5 lactobacill
271	7	0.9	335	2	Q71115	Q71115 human immun	344	7	0.9	376	2	Q74LB2	Q74lb2 lactobacill
272	7	0.9	335	2	Q71116	Q71116 human immun	345	7	0.9	377	1	RNG1_HUMAN	Q06587 homo sapien
273	7	0.9	335	2	Q71117	Q71117 human immun	346	7	0.9	377	2	Q35730	Q35730 mus musculu
274	7	0.9	335	2	Q71120	Q71120 human immun	347	7	0.9	377	2	Q6MGB6	Q6mgb6 rattus norv
275	7	0.9	335	2	Q71320	Q71320 human immun	348	7	0.9	377	2	Q621Z8	Q621z8 mus musculu
276	7	0.9	336	1	C1M1_MOUSE	Q08581 mus musculu	349	7	0.9	377	2	Q8AVZ7	Q8avz7 gallus gall
277	7	0.9	336	1	OTCC_STRP3	P65609 streptococc	350	7	0.9	377	2	Q8YBE1	Q8y3e1 brucella su
278	7	0.9	336	1	OTCC_STRP8	P65610 streptococc	351	7	0.9	379	2	Q8YBE1	Q8y3e1 brucella su
279	7	0.9	336	1	OTCC_STRPY	P16964 streptococc	352	7	0.9	380	2	Q9KVV7	Q9kyw7 streptomyce
280	7	0.9	336	2	Q99199	Q99199 mus musculu	353	7	0.9	380	2	Q96Q15	Q96q15 homo sapien
281	7	0.9	337	1	IMP2_HUMAN	Q9ug22 homo sapien	354	7	0.9	381	2	Q7MT14	Q7mt14 porphyronon
282	7	0.9	337	1	OTC2_STRA3	P65605 streptococc	355	7	0.9	382	2	Q6NWD4	Q6nwd4 brachydanio
283	7	0.9	337	1	OTC2_STRAS	P65606 streptococc	356	7	0.9	382	2	Q8KWF1	Q8kfw1 bacillus st
284	7	0.9	337	1	OTCC_STRAG	Q8rp83 streptococc	357	7	0.9	383	2	Q6UD24	Q6ud24 uncultured
285	7	0.9	339	2	Q8C9Y2	Q8c9y2 mus musculu	358	7	0.9	383	2	Q6UD50	Q6ud50 uncultured
286	7	0.9	340	2	Q9G644	Q9g644 calotes cal	359	7	0.9	383	2	Q63IN7	Q63in7 burkholderi
287	7	0.9	341	2	Q98CD7	Q98cd7 rhizobium l	360	7	0.9	383	2	Q8NR26	Q8nr26 corynebacte
288	7	0.9	341	2	Q7UJB2	Q7ujb2 rhodopirell	361	7	0.9	384	2	Q40492	Q40492 nicotiana t
289	7	0.9	344	2	Q9XG06	Q9xg06 actinobacil	362	7	0.9	384	2	Q9FSQ3	Q9fsq3 oryza sativ
290	7	0.9	344	2	Q630X0	Q630x0 bacillus ce	363	7	0.9	384	2	Q92LJ4	Q92lj4 rhizobium m
291	7	0.9	344	2	Q66J69	Q66j69 xenopus lae	364	7	0.9	385	2	Q8TRZ1	Q8trz1 methanosarc
292	7	0.9	345	2	Q6P164	Q6p164 homo sapien	365	7	0.9	385	2	Q7VS16	Q7vs16 bordetella
293	7	0.9	346	2	Q8JOW1	Q8jow1 cryptococcu	366	7	0.9	386	2	Q7WEB8	Q7web8 bordetella
294	7	0.9	346	2	Q8JUX2	Q8jux2 cryptococcu	367	7	0.9	386	2	RECA_LEPBI	P48290 leptospira
295	7	0.9	347	2	Q7PGU5	Q7pgus anopheles g	368	7	0.9	387	1	RECA_LEPBI	P48290 leptospira
296	7	0.9	347	2	Q8SH97	Q8sh97 brookesia p	369	7	0.9	387	2	Q6PFK0	Q6pfk0 brachydanio
297	7	0.9	347	2	Q8SHA3	Q8sha3 brookesia b	370	7	0.9	388	1	XYLA_STRCK	Q9s3z4 streptomyce
298	7	0.9	347	2	Q9SU74	Q9su74 arabidopsis	371	7	0.9	390	2	Q9LV7	Q9lv7 arabidopsis
299	7	0.9	348	2	Q6REG8	Q6reg8 rhodococcus	372	7	0.9	390	2	Q8T3J1	Q8t3j1 drosophila
300	7	0.9	348	2	Q70PA6	Q70pa6 mellittangiu	373	7	0.9	391	2	Q7RST8	Q7rst8 plasmodium
301	7	0.9	348	2	Q64RZ1	Q64rz1 bacteroides	374	7	0.9	393	2	Q65FQ4	Q65fq4 bacillus li
302	7	0.9	349	1	ISPG_CLOAB	Q97156 clostridium	375	7	0.9	393	2	Q8IK92	Q8ik92 plasmodium
303	7	0.9	349	2	Q8CFE7	Q8cf7 mus musculu	376	7	0.9	394	2	Q6HKK4	Q6hkk4 bacillus an
304	7	0.9	351	2	Q66K46	Q66k46 homo sapien	377	7	0.9	394	2	Q9R6T2	Q9r6t2 synechococc
305	7	0.9	351	2	Q70AX1	Q70ax1 actinoplane	378	7	0.9	398	2	Q89E17	Q89e17 bradyrhizob
306	7	0.9	351	2	Q6AL26	Q6al26 desulfotale	379	7	0.9	398	2	ENO_ARCFU	Q29133 archaeoglob
307	7	0.9	351	2	Q6NSS5	Q6nss5 mus musculu	380	7	0.9	399	1	ENO_ARCFU	Q29133 archaeoglob
308	7	0.9	353	2	Q6ZZG5	Q6zzg5 actinoplane	381	7	0.9	401	2	Q911P8	Q91lp8 pseudomonas
309	7	0.9	354	2	Q99XC6	Q99xc6 staphylococ	382	7	0.9	402	2	Q8ET06	Q8et06 oceanobacil
310	7	0.9	355	1	PHBC_CHRVI	P45370 c poly-beta	383	7	0.9	404	2	Q6BG17	Q6bg17 paramecium
311	7	0.9	355	2	Q9C778	Q9c778 arabidopsis	384	7	0.9	404	2	Q6SH30	Q6sh30 uncultured
312	7	0.9	355	2	Q31252	Q31252 anabaena sp	385	7	0.9	405	2	Q9NV04	Q9nv04 homo sapien
313	7	0.9	355	2	Q8NVY5	Q8nyv5 staphylococ	386	7	0.9	405	2	Q7PNQ3	Q7pnq3 anopheles g
314	7	0.9	355	2	Q8YYA1	Q8yya1 anabaena sp	387	7	0.9	406	2	Q86VPE8	Q86vl9 homo sapien
315	7	0.9	355	2	Q7NK07	Q7nk07 gloeobacter	388	7	0.9	407	2	Q6YPE8	Q6ype8 oryza sativ
316	7	0.9	355	2	Q6GD41	Q6gd41 staphylococ	389	7	0.9	408	2	Q6CMJ5	Q6cmj5 kluyveromyc
317	7	0.9	357	2	Q7NZU9	Q7nzu9 chromobacte	390	7	0.9	409	1	P6XC_PICPA	Q01961 picchia past
318	7	0.9	358	1	REC2_MYXXA	P48292 myxococcus	391	7	0.9	410	2	Q6AB18	Q6ab18 propionibac
319	7	0.9	358	2	Q81PE1	Q81pe1 bacillus an	392	7	0.9	410	2	Q8E2R6	Q8e2r6 streptococc
320	7	0.9	358	2	Q7S255	Q7s255 brachydanio	393	7	0.9	412	2	Q925T5	Q925t5 zymomonas m
321	7	0.9	360	2	Q7MEZ5	Q7mez5 vibrio vuln	394	7	0.9	413	2	Q96IZ5	Q96iz5 homo sapien
322	7	0.9	360	2	Q8D7X9	Q8d7x9 vibrio vuln	395	7	0.9	413	2	Q7QBV1	Q7qbv1 anopheles g
323	7	0.9	361	2	Q6L1J2	Q6l1j2 picrophillus	396	7	0.9	413	2	Q7QBV2	Q7qbv2 anopheles g

397	7	0.9	413	2	Q8JZV4	Q8jzv4 m riken cdn	470	7	0.9	476	2	Q8U552	Q8u552 agrobacteri
398	7	0.9	414	1	CD61_METAC	Q8tur2 methanosarc	471	7	0.9	476	2	Q7V9V6	Q7v9v6 prochloroco
399	7	0.9	414	1	CD61_METAC	Q8pxa8 methanosarc	472	7	0.9	477	2	Q87HT2	Q87ht2 vibrio para
400	7	0.9	415	1	PGK_ASHGO	Q757G0 ashbya goss	473	7	0.9	480	2	Q6R2R8	Q6r2r8 hyposoter d
401	7	0.9	416	2	Q99X43	Q99x43 staphylococ	474	7	0.9	482	2	Q892C7	Q892c7 clostridium
402	7	0.9	416	2	Q7AIY3	Q7aly3 staphylococ	475	7	0.9	485	2	Q6W1U7	Q6w1u7 rhizobium s
403	7	0.9	416	2	Q7AB14	Q7ab14 staphylococ	476	7	0.9	485	2	Q73LL4	Q73ll4 treponema d
404	7	0.9	416	2	Q6GCU8	Q6gcu8 staphylococ	477	7	0.9	486	2	Q6ZP84	Q6zpb4 homo sapien
405	7	0.9	416	2	Q6GKC8	Q6gkc8 staphylococ	478	7	0.9	487	2	Q8UOH5	Q8uoh5 pyrococcus
406	7	0.9	417	1	PGK_CANNA	P41757 candida mal	479	7	0.9	487	2	Q7SXF3	Q7sxf3 brachydanio
407	7	0.9	418	2	Q8DW5	Q8dww5 streptococc	480	7	0.9	488	2	Q6PIJ6	Q6pij6 homo sapien
408	7	0.9	419	1	Y4ML_RHLSN	P55571 rhizobium s	481	7	0.9	488	2	Q8SB18	Q8sb18 oryza sativ
409	7	0.9	420	1	CDC6_PYRFU	P81413 pyrococcus	482	7	0.9	488	2	Q89H76	Q89h76 bradyrhizob
410	7	0.9	420	1	YF41_METJA	Q58936 methanococc	483	7	0.9	489	1	C128_MYCBO	P63714 mycobacteri
411	7	0.9	420	2	Q9RJQ6	Q9rjq6 streptomyc	484	7	0.9	489	1	C128_MYCTU	P63713 mycobacteri
412	7	0.9	421	2	Q95V69	Q95v69 tetrahymena	485	7	0.9	489	1	QCLN_POTTR	Q28793 potorous tr
413	7	0.9	422	1	LACE_AGRRD	P29822 agrobacteri	486	7	0.9	493	2	Q761Y0	Q761y0 oryza sativ
414	7	0.9	422	2	Q8ZNC0	Q8znc0 salmonella	487	7	0.9	497	2	Q97RD6	Q97rd6 streptococc
415	7	0.9	423	2	Q93256	Q93256 gallus gall	488	7	0.9	497	2	Q8DQ91	Q8dq91 streptococc
416	7	0.9	424	2	Q89R42	Q89r42 bradyrhizob	489	7	0.9	498	2	Q97V40	Q97v40 sulfolobus
417	7	0.9	427	2	Q7Q6T1	Q7q6t1 anopheles g	490	7	0.9	498	2	Q6X195	Q6x195 bacterioph
418	7	0.9	428	2	Q6O947	Q6o947 trypanosoma	491	7	0.9	499	2	Q6X1A1	Q6x1a1 bacterioph
419	7	0.9	428	2	P74349	P74349 synecocyst	492	7	0.9	500	2	Q6X1A2	Q6x1a2 bacterioph
420	7	0.9	428	2	Q747R9	Q747r9 geobacter s	493	7	0.9	501	2	Q6X1A3	Q6x1a3 bacterioph
421	7	0.9	429	1	SYS_PHOLL	Q7n6e7 photorhabdu	494	7	0.9	502	1	DNAA_MYCLE	P46388 mycobacteri
422	7	0.9	429	2	Q8YCL3	Q8ycl3 brucella me	495	7	0.9	503	2	Q8MQF7	Q8mqf7 caenorhabdi
423	7	0.9	430	2	Q7RAW2	Q7raw2 plasmodium	496	7	0.9	503	2	Q8EK00	Q8ek00 shewanella
424	7	0.9	431	2	Q21194	Q21194 caenorhabdi	497	7	0.9	506	2	Q17537	Q17537 caenorhabdi
425	7	0.9	431	2	Q8HT85	Q8ht85 selaginella	498	7	0.9	507	2	Q6C8B4	Q6c8b4 varrowia li
426	7	0.9	431	2	Q73M29	Q73m29 treponema d	499	7	0.9	508	2	P90790	P90790 caenorhabdi
427	7	0.9	432	2	Q66H32	Q66h32 rattus norv	500	7	0.9	509	2	Q9VBP7	Q9vbp7 drosophila
428	7	0.9	432	1	CDC6_PYRAB	Q9v2f2 pyrococcus	501	7	0.9	509	2	Q8D0L7	Q8d0l7 yersinia pe
429	7	0.9	432	2	Q6NWF0	Q6nwf0 brachydanio	502	7	0.9	514	2	Q9DF59	Q9df59 brachydanio
430	7	0.9	435	2	Q9TXJ4	Q9txj4 leishmania	503	7	0.9	515	1	PVR1_MOUSE	Q9jkt6 mus musculu
431	7	0.9	435	2	Q6G2S5	Q6g2s5 bartonella	504	7	0.9	515	1	PVR1_PIG	Q9gl76 sus scrofa
432	7	0.9	436	2	Q836C0	Q836c0 enterococcu	505	7	0.9	515	2	Q97Y93	Q97y93 sulfolobus
433	7	0.9	437	1	CDC6_PYRHO	O57864 pyrococcus	506	7	0.9	515	2	Q6P9M9	Q6p9m9 mus musculu
434	7	0.9	437	2	Q7NHM7	Q7nhm7 glieobacter	507	7	0.9	516	2	Q7MQB5	Q7mqb5 vibrio vuln
435	7	0.9	437	2	Q6D216	Q6d216 erwinia car	508	7	0.9	517	1	PVR1_HUMAN	Q12223 homo sapien
436	7	0.9	438	2	Q6BC08	Q6bc08 edwardsiell	509	7	0.9	518	1	CD63_HALN1	Q9hms3 halobacteri
437	7	0.9	444	2	Q23497	Q23497 caenorhabdi	510	7	0.9	518	2	Q747N5	Q747n5 geobacter s
438	7	0.9	444	2	Q89M95	Q89m95 bradyrhizob	511	7	0.9	519	2	Q7S8P0	Q7s8p0 neurospora
439	7	0.9	444	2	Q89NM0	Q89nm0 bradyrhizob	512	7	0.9	526	1	K1CJ3_BOVIN	P06394 bos taurus
440	7	0.9	445	2	Q6N715	Q6n715 rhodopseudo	513	7	0.9	526	2	Q8RME3	Q8rme3 alcaligenes
441	7	0.9	446	2	Q6BU59	Q6bu59 debaryomyce	514	7	0.9	527	2	Q63A80	Q63a80 bacillus ce
442	7	0.9	446	2	Q7SB26	Q7sb26 neurospora	515	7	0.9	527	2	Q6HHM4	Q6hhm4 bacillus th
443	7	0.9	447	2	Q7QKE9	Q7qke9 anopheles g	516	7	0.9	529	2	Q9FD13	Q9fdi3 brevibacter
444	7	0.9	448	2	Q8Y1V0	Q8y1v0 ralstonia s	517	7	0.9	532	2	Q7NYE6	Q7nye6 chromobacte
445	7	0.9	451	1	VPS9_YEAST	P54787 saccharomyc	518	7	0.9	532	1	YDU2_SCHPO	O13863 schizosacch
446	7	0.9	453	2	Q6A855	Q6a855 propionibac	519	7	0.9	537	2	Q6MD44	Q6md44 parachlamyd
447	7	0.9	456	2	O57794	O57794 pyrococcus	520	7	0.9	537	2	Q8QQ94	Q8qq94 avian infec
448	7	0.9	456	2	Q8R9H8	Q8r9h8 thermoanaer	521	7	0.9	543	2	Q6D418	Q6d418 erwinia car
449	7	0.9	459	2	Q881M9	Q881m9 pseudomonas	522	7	0.9	545	2	Q7QY12	Q7qy12 giardia lam
450	7	0.9	460	2	Q98R23	Q98r23 guillardia	523	7	0.9	545	2	Q66A41	Q66a41 yersinia ps
451	7	0.9	460	2	Q74GQ7	Q74gq7 geobacter s	524	7	0.9	545	2	Q8ZE13	Q8zel3 yersinia pe
452	7	0.9	461	2	Q6JKE9	Q6jke9 neodiprion	525	7	0.9	545	2	O6NJCS	O6njcs corynebacte
453	7	0.9	463	2	Q6SY98	Q6sy98 photorhabdu	526	7	0.9	546	2	Q7UT65	Q7ut65 rhodopirell
454	7	0.9	464	2	Q7Z3V7	Q7z3v7 homo sapien	527	7	0.9	547	2	Q75AW8	Q75aw8 ashbya goss
455	7	0.9	464	2	Q7ACN3	Q7acn3 escherichia	528	7	0.9	547	2	Q73J78	Q73j78 treponema d
456	7	0.9	464	2	Q8X7J5	Q8x7j5 escherichia	529	7	0.9	547	2	Q8ALJ6	Q8alj6 bacteroides
457	7	0.9	464	2	Q8CVA8	Q8cvx8 escherichia	530	7	0.9	550	2	Q9RBI1	Q9rb11 acinetobact
458	7	0.9	466	2	Q8FVD7	Q8fvd7 brucella su	531	7	0.9	550	2	Q6FCC3	Q6fc3 acinetobact
459	7	0.9	469	2	O51997	O51997 halobacteri	532	7	0.9	551	2	Q6J9V5	Q6j9v5 zea mays (m
460	7	0.9	469	2	Q6CSM6	Q6csm6 kluyveromyc	533	7	0.9	556	2	Q810A1	Q810a1 mus musculu
461	7	0.9	470	2	Q6AF02	Q6af02 leifsonia x	534	7	0.9	556	2	Q9D972	Q9d972 mus musculu
462	7	0.9	471	2	Q9EZF8	Q9ezf8 streptococc	535	7	0.9	562	1	CH60_TRYCR	Q95046 trypanosoma
463	7	0.9	471	2	Q9RCK6	Q9rck6 streptomyc	536	7	0.9	562	2	Q8NK91	Q8nk91 aspergillus
464	7	0.9	471	2	Q92CE1	Q92ce1 listeria in	537	7	0.9	562	2	Q75AY9	Q75ay9 ashbya goss
465	7	0.9	472	2	Q9F2B6	Q9f2b6 thauera aro	538	7	0.9	562	2	Q9V725	Q9v725 drosophila
466	7	0.9	473	2	Q712I1	Q712i1 streptomyc	539	7	0.9	564	2	Q9POT6	Q9pt6 ureaplasma
467	7	0.9	473	2	Q84I42	Q84i42 streptomyc	540	7	0.9	567	2	Q9HGH9	Q9hgh9 aspergillus
468	7	0.9	473	2	Q7MXZ1	Q7mxz1 porphyronon	541	7	0.9	572	2	Q6ZH86	Q6zh86 oryza sativ
469	7	0.9	475	2	Q6Y636	Q6y636 mus musculu	542	7	0.9	573	2	Q9VDS0	Q9vds0 drosophila

543	7	0.9	575	2	065IP7	Q65ip7 bacillus li	616	7	0.9	728	1	KDGL ARATH	Q39017 arabidopsis
544	7	0.9	580	2	Q89YL8	Q89yl8 bacteroides	617	7	0.9	728	2	Q9YQY0	Q9yqy0 ranid herpe
545	7	0.9	581	2	Q6TBO7	Q6tbo7 manheimia	618	7	0.9	733	2	Q9UBZ1	Q9ubz1 homo sapien
546	7	0.9	583	1	ARSA_ECOLI	P52145 escherichia	619	7	0.9	733	2	Q8PIV9	Q8piv9 xanthomonas
547	7	0.9	583	1	ARSA_ACIMU	O50593 acidiphiliiu	620	7	0.9	734	2	Q7NP44	Q7np44 gloeobacter
548	7	0.9	584	2	Q79SA6	Q79sa6 incn plasmi	621	7	0.9	741	2	Q87UF7	Q87uf7 pseudomonas
549	7	0.9	584	2	Q98N7	Q98nt7 rhizobium 1	622	7	0.9	745	1	HGL2 ARATH	P46607 arabidopsis
550	7	0.9	585	2	Q9KJ13	Q9kji3 klebsiella	623	7	0.9	747	2	Q9CSF1	Q9csf1 arabidopsis
551	7	0.9	587	1	RGPI_HUMAN	P46050 homo sapien	624	7	0.9	747	2	Q7P2X4	Q7p2x4 fusobacteri
552	7	0.9	588	2	Q6LLI2	Q6lll2 pictrophilus	625	7	0.9	750	2	Q8PHT0	Q8pht0 xanthomon
553	7	0.9	589	1	RGPI_MOUSE	P46061 mus musculu	626	7	0.9	755	2	Q6KG24	Q6kg24 oryza sativ
554	7	0.9	589	2	Q91YS2	Q91ys2 mus musculu	627	7	0.9	756	2	Q751Y0	Q751y0 ashbya goss
555	7	0.9	589	2	Q7TWM1	Q7tmw1 mus musculu	628	7	0.9	758	2	Q6RSM0	Q6fsw0 candida gla
556	7	0.9	589	2	Q8C2E3	Q8c2e3 mus musculu	629	7	0.9	761	2	Q9H2G6	Q9h2g6 homo sapien
557	7	0.9	589	2	Q6NZB5	Q6nzb5 mus musculu	630	7	0.9	763	2	Q64Z23	Q64z23 bacteroides
558	7	0.9	594	2	Q86JK0	Q86jk0 dictyosteli	631	7	0.9	771	2	Q81Z98	Q81z98 arabidopsis
559	7	0.9	596	2	Q6X194	Q6x194 bacterioph	632	7	0.9	773	2	Q33541	O33541 endosymbion
560	7	0.9	596	2	Q6X197	Q6x197 bacterioph	633	7	0.9	774	2	Q6FN99	Q6fn99 candida gla
561	7	0.9	596	2	Q6X198	Q6x198 bacterioph	634	7	0.9	778	2	Q73G77	Q73g77 wolbachia p
562	7	0.9	596	2	Q6X199	Q6x199 bacterioph	635	7	0.9	784	2	Q87E11	Q87e11 xylella fas
563	7	0.9	596	2	Q6X1A0	Q6x1a0 bacterioph	636	7	0.9	784	2	Q9PEI2	Q9pei2 xylella fas
564	7	0.9	596	2	Q6X1A4	Q6x1a4 bacterioph	637	7	0.9	786	2	Q86L03	Q86l03 dictyosteli
565	7	0.9	596	2	Q6T811	Q6t811 manheimia	638	7	0.9	788	2	Q8PML3	Q8pml3 xanthomonas
566	7	0.9	604	2	O04098	O04098 arabidopsis	639	7	0.9	794	2	Q8P569	Q8p569 xanthomonas
567	7	0.9	605	1	NRDD_BPT4	P07071 bacterioph	640	7	0.9	795	2	Q886N5	Q886n5 pseudomonas
568	7	0.9	605	2	Q6BB07	Q6bp07 debaryomyce	641	7	0.9	796	2	Q8PEN2	Q8ppn2 xanthomonas
569	7	0.9	605	2	Q7Y558	Q7y558 bacterioph	642	7	0.9	797	2	Q9HXI4	Q9hxy4 pseudomonas
570	7	0.9	610	2	Q8W6J7	Q8w6j7 sinorhizobi	643	7	0.9	798	2	Q7PMI8	Q7pmi8 anopheles g
571	7	0.9	610	2	Q62J44	Q62j44 burkholderi	644	7	0.9	799	1	Y231_BUCAP	Q8k9s5 buchnera ap
572	7	0.9	610	2	Q63ST4	Q63st4 burkholderi	645	7	0.9	807	2	Q94HV9	Q94hv9 arabidopsis
573	7	0.9	612	2	Q912F4	Q91zf4 cereal yell	646	7	0.9	808	2	Q8B1B8	Q8bh8 mus musculu
574	7	0.9	614	2	Q7Q2A3	Q7q2a3 anopheles g	647	7	0.9	809	2	Q96JS3	Q96js3 homo sapien
575	7	0.9	616	1	GLMS_AERPE	Q9ycq6 a glucosami	648	7	0.9	811	2	Q6K7R9	Q6k7r9 oryza sativ
576	7	0.9	619	1	CALX_CABEL	P34652 caenorhabdi	649	7	0.9	811	2	Q80T97	Q80t97 mus musculu
577	7	0.9	620	1	ORC2_YEAST	P32833 saccharomyc	650	7	0.9	812	2	Q8XF68	Q8xf68 salmonella
578	7	0.9	623	2	Q96J32	Q96jj2 homo sapien	651	7	0.9	812	2	Q7CP94	Q7cp94 salmonella
579	7	0.9	623	2	Q8YQ88	Q8yq88 anabaena sp	652	7	0.9	813	1	RNR_ECOLI	P21499 escherichia
580	7	0.9	626	2	Q65N18	Q65n18 bacillus li	653	7	0.9	813	1	RNR_SHIFL	P30851 shigella fl
581	7	0.9	628	2	Q82HQ5	Q82hd5 streptomyce	654	7	0.9	818	2	Q8NM59	Q8nm59 corynebacte
582	7	0.9	632	1	H114_HUMAN	Q81uh5 homo sapien	655	7	0.9	818	2	Q8PAW1	Q8paw1 xanthomonas
583	7	0.9	632	1	H114_MOUSE	Q80tn5 mus musculu	656	7	0.9	821	2	Q69DS5	Q69ds5 oryza sativ
584	7	0.9	632	2	Q7U778	Q7u778 synechococc	657	7	0.9	822	2	Q6H6R9	Q6h6r9 oryza sativ
585	7	0.9	641	2	Q9KWU1	Q9kwu1 synechomona	658	7	0.9	823	2	Q9S7P3	Q9s7p3 arabidopsis
586	7	0.9	646	2	Q6ZPH4	Q6zph4 mus musculu	659	7	0.9	827	2	Q8FAK5	Q8fak5 escherichia
587	7	0.9	647	2	Q73NK7	Q73nk7 treponema d	660	7	0.9	827	2	Q8XDL9	Q8xdl9 escherichia
588	7	0.9	649	1	LONH_METJA	Q58812 methanococc	661	7	0.9	838	2	Q7QNU7	Q7qnu7 giardia lam
589	7	0.9	651	2	Q6TKP9	Q6tkp9 homo sapien	662	7	0.9	841	2	Q7NMS8	Q7nms8 gloeobacter
590	7	0.9	654	2	Q62L07	Q62l07 burkholderi	663	7	0.9	845	2	Q6VAL8	Q6val8 arsenite-ox
591	7	0.9	656	2	Q9SLA7	Q9sla7 arabidopsis	664	7	0.9	849	2	Q6DB45	Q6db45 erwinia car
592	7	0.9	659	2	Q6LLS1	Q6lls1 photobacter	665	7	0.9	850	2	Q8FC25	Q8fc25 escherichia
593	7	0.9	661	2	Q7MC29	Q7mc29 vibrio vuln	666	7	0.9	856	2	Q97KW5	Q97kw5 clostridium
594	7	0.9	661	2	Q8D582	Q8d582 vibrio vuln	667	7	0.9	857	2	Q6AJQ8	Q6ajq8 desulfotale
595	7	0.9	662	2	Q6XB70	Q6xbj0 mycobacteri	668	7	0.9	859	2	Q6UDK3	Q6udk3 psittacid h
596	7	0.9	663	2	Q6BNA8	Q6bna8 debaryomyce	669	7	0.9	868	2	Q75BV7	Q75bv7 ashbya goss
597	7	0.9	663	2	Q8RWP2	Q8rwp2 arabidopsis	670	7	0.9	870	2	Q6ATA6	Q6ata6 oryza sativ
598	7	0.9	663	2	Q94OB9	Q94ob9 arabidopsis	671	7	0.9	873	2	Q74A79	Q74a79 geobacter s
599	7	0.9	663	2	Q67ZT9	Q67zt9 arabidopsis	672	7	0.9	883	2	Q6CRS9	Q6crs9 kluyveromyc
600	7	0.9	665	1	MTR1_HUMAN	Q13613 homo sapien	673	7	0.9	885	2	Q8A1E1	Q8a1e1 bacteroides
601	7	0.9	666	2	Q89DT9	Q89dt9 bradyrhizob	674	7	0.9	887	2	Q8XV49	Q8xv49 ralaetonia s
602	7	0.9	666	2	Q9KKR7	Q9kk7 vibrio chol	675	7	0.9	888	2	Q9LQ62	Q9lq62 arabidopsis
603	7	0.9	674	2	Q7QB46	Q7qb46 anopheles g	676	7	0.9	893	2	Q6C3K8	Q6c3k8 yarrowia li
604	7	0.9	680	2	Q8IMW5	Q8imes drosophila	677	7	0.9	897	2	Q7KN84	Q7kn84 drosophila
605	7	0.9	684	2	Q7S840	Q7s840 neurospora	678	7	0.9	897	2	Q9VQZ6	Q9vgz6 drosophila
606	7	0.9	684	2	Q7X7M2	Q7x7m2 oryza sativ	679	7	0.9	897	2	Q9W354	Q9w354 drosophila
607	7	0.9	685	2	Q6S001	Q6s001 dictyosteli	680	7	0.9	916	2	Q9V354	Q9v354 drosophila
608	7	0.9	693	2	Q63TE4	Q63te4 burkholderi	681	7	0.9	942	2	Q18298	Q18298 caenorhabdi
609	7	0.9	695	2	Q88PS4	Q88ps4 pseudomonas	682	7	0.9	944	2	Q7Q0U5	Q7q0u5 anopheles g
610	7	0.9	697	2	Q7QPS2	Q7qps2 giardia lam	683	7	0.9	946	2	Q9EV24	Q9ev24 manheimia
611	7	0.9	697	2	Q9VEP8	Q9vep8 drosophila	684	7	0.9	946	2	Q89GU0	Q89gu0 bradyrhizob
612	7	0.9	699	2	Q82E12	Q82e12 streptomyce	685	7	0.9	946	2	Q89XV1	Q89xv1 bradyrhizob
613	7	0.9	702	2	Q8G6C8	Q8g6c8 bifidobacte	686	7	0.9	947	1	LKTA_PASSP	P55123 pasteurella
614	7	0.9	717	2	Q9VAY0	Q9vay0 drosophila	687	7	0.9	947	2	Q6FKI5	Q6fki5 candida gla
615	7	0.9	718	2	Q7RPJ6	Q7rpj6 plasmodium	688	7	0.9	948	2	Q7XTP3	Q7xtp3 oryza sativ

689	7	0.9	949	2	057149	057149 human herpe	762	7	0.9	1187	2	Q94CJ9	Q94cj9 arabidopsis
690	7	0.9	950	1	P4R1_HUMAN	Q8tf05 homo sapien	763	7	0.9	1222	2	Q868R4	Q868r4 anopheles g
691	7	0.9	951	1	P4R1_MOUSE	Q8k2v1 mus musculu	764	7	0.9	1222	2	Q98PR9	Q98pr9 mycoplasma
692	7	0.9	951	1	P4R1_RAT	Q8vio2 rattus norv	765	7	0.9	1239	2	Q9DEF4	Q9def4 xenopus lae
693	7	0.9	952	2	Q6BKU6	Q6bki6 debaryomyce	766	7	0.9	1259	2	Q44971	Q44971 caenorhabdi
694	7	0.9	952	2	Q6H911	Q6h9i1 botrytis ci	767	7	0.9	1260	2	Q804R3	Q804r3 brachydanio
695	7	0.9	953	1	LKAB_PASHA	P16535 pasteurella	768	7	0.9	1276	2	Q7UKG2	Q7ukg2 rhodopirell
696	7	0.9	953	1	LKAB_PASHA	P55118 pasteurella	769	7	0.9	1277	2	Q6BFB2	Q6bfb2 paramecium
697	7	0.9	953	2	Q6TB03	Q6tb03 manheimia	770	7	0.9	1285	2	Q6UNF4	Q6unf4 ictalurus p
698	7	0.9	953	2	Q9ETG5	Q9etg5 pasteurella	771	7	0.9	1301	2	Q7XB17	Q7xb17 drosophila
699	7	0.9	953	2	Q9ETX2	Q9etx2 manheimia	772	7	0.9	1301	2	Q9U982	Q9u982 drosophila
700	7	0.9	953	2	Q9EV23	Q9ev23 manheimia	773	7	0.9	1322	2	Q6CKZ5	Q6ckz5 kluyveromyc
701	7	0.9	953	2	Q9EV25	Q9ev25 manheimia	774	7	0.9	1336	2	Q73550	Q73550 semliki for
702	7	0.9	953	2	Q9EV26	Q9ev26 manheimia	775	7	0.9	1349	2	Q9LW06	Q9lwo6 streptomyce
703	7	0.9	953	2	Q9EV29	Q9ev29 pasteurella	776	7	0.9	1350	2	Q9VWB0	Q9vwb0 drosophila
704	7	0.9	953	2	Q9EV30	Q9ev30 pasteurella	777	7	0.9	1361	2	Q8QZ08	Q8qzg8 chilo iride
705	7	0.9	953	2	Q9EV31	Q9ev31 pasteurella	778	7	0.9	1366	2	Q8QZ08	Q8qzg8 chilo iride
706	7	0.9	953	2	Q9EV32	Q9ev32 pasteurella	779	7	0.9	1370	2	Q8ZFG3	Q8zpg3 arabidopsis
707	7	0.9	953	2	Q9EV33	Q9ev33 pasteurella	780	7	0.9	1382	2	Q6A078	Q6a078 mus musculu
708	7	0.9	953	2	Q9EV34	Q9ev34 pasteurella	781	7	0.9	1390	2	Q7P330	Q7p330 fusbacteri
709	7	0.9	953	2	Q9EV34	Q9ev34 pasteurella	782	7	0.9	1415	2	Q6PL18	Q6pl18 homo sapien
710	7	0.9	963	1	KINH_HUMAN	P33176 homo sapien	783	7	0.9	1415	2	Q6FV13	Q6fv13 candida gla
711	7	0.9	967	2	O8TDL2	Q8tdl2 homo sapien	784	7	0.9	1418	2	Q98SM6	Q98sw6 xenopus lae
712	7	0.9	976	2	Q8UI58	Q8uis8 leishmania	785	7	0.9	1422	2	Q8IBL9	Q8ibl9 plasmodium
713	7	0.9	978	2	Q8N890	Q8n890 homo sapien	786	7	0.9	1434	1	PTC1_MOUSE	Q6115 mus musculu
714	7	0.9	983	1	GCSP_ANASP	Q7ynf9 anabaena sp	787	7	0.9	1434	2	Q6UY90	Q6uy90 rattus norv
715	7	0.9	985	2	Q7Q8G8	Q7q8g8 anopheles g	788	7	0.9	1442	1	PTC1_CHICK	Q90693 gallus gall
716	7	0.9	988	2	Q63LC1	Q63lc1 burkholderi	789	7	0.9	1444	2	Q7WUL1	Q7wul1 neisseria m
717	7	0.9	988	2	Q63VP1	Q63vp1 burkholderi	790	7	0.9	1447	1	PTC1_HUMAN	Q13635 homo sapien
718	7	0.9	992	2	Q9UV08	Q9uv08 emericella	791	7	0.9	1449	2	Q9F3Z5	Q9f3z5 neisseria m
719	7	0.9	996	2	Q924M9	Q924m9 rattus norv	792	7	0.9	1449	2	Q9JWB4	Q9jwb4 neisseria m
720	7	0.9	996	2	Q6JTV1	Q6jtv1 mus musculu	793	7	0.9	1453	1	CE29_BOVIN	Q9f3z4 bos taurus
721	7	0.9	996	2	Q6P730	Q6p730 rattus norv	794	7	0.9	1454	2	Q9F3Z4	Q9f3z4 neisseria m
722	7	0.9	997	2	Q76BA8	Q76ba8 callorhinch	795	7	0.9	1457	2	Q8GKS4	Q8gks4 neisseria m
723	7	0.9	997	2	Q76BB4	Q76bb4 potamotrygo	796	7	0.9	1457	2	Q9X7H1	Q9x7h1 neisseria m
724	7	0.9	1004	2	Q8TUS3	Q8tjs3 methanosarc	797	7	0.9	1463	2	Q9JXL6	Q9jxl6 neisseria m
725	7	0.9	1014	2	Q96PY4	Q96py4 homo sapien	798	7	0.9	1468	2	Q62998	Q62998 gallid herp
726	7	0.9	1016	2	Q8NSA4	Q8nsa4 corynebacte	799	7	0.9	1479	2	Q6SLD4	Q6slid4 cochllobolu
727	7	0.9	1016	2	Q888X2	Q888x2 pseudomonas	800	7	0.9	1479	2	Q7KQT5	Q7kqt5 drosophila
728	7	0.9	1018	2	Q7RRF9	Q7rrf9 plasmodium	801	7	0.9	1482	2	Q9V4Y0	Q9v4y0 drosophila
729	7	0.9	1021	2	Q6FS37	Q6fs37 candida gla	802	7	0.9	1487	2	Q8RHT9	Q8rht9 fusbacteri
730	7	0.9	1025	2	Q7R6E6	Q7r6e6 giardia lam	803	7	0.9	1508	1	BCSC_XANAC	P58938 xanthomonas
731	7	0.9	1031	2	Q6Y293	Q6yz93 oryza sativ	804	7	0.9	1513	2	Q9WSZ8	Q9wsz8 human herpe
732	7	0.9	1036	2	Q9COC0	Q9coc0 homo sapien	805	7	0.9	1520	2	Q9QJ16	Q9qj16 human herpe
733	7	0.9	1045	2	Q6CQ79	Q6cq79 kluyveromyc	806	7	0.9	1539	1	CE29_HUMAN	Q15078 homo sapien
734	7	0.9	1054	2	Q67430	Q67430 aquifex aeo	807	7	0.9	1572	2	Q7SGQ7	Q7sgq7 neurospora
735	7	0.9	1057	2	Q9V9G1	Q9v9g1 drosophila	808	7	0.9	1584	2	Q8QOG8	Q8qog8 methanosarc
736	7	0.9	1065	2	Q96SE1	Q96se1 homo sapien	809	7	0.9	1608	2	Q6FX52	Q6fx52 candida gla
737	7	0.9	1071	2	Q9VBA3	Q9vba3 drosophila	810	7	0.9	1618	2	Q9KKB1	Q9kxb1 rickettsia
738	7	0.9	1087	2	Q6C117	Q6c117 yarrowia li	811	7	0.9	1632	2	Q8QHS2	Q8qhs2 human herpe
739	7	0.9	1088	1	DP2L_THEVO	Q97c+6 thermoplasm	812	7	0.9	1656	1	OMPB_RICJA	Q06653 r outer mem
740	7	0.9	1088	2	Q28333	Q28333 archaeoglob	813	7	0.9	1686	2	Q9RWI1	Q9rwi1 deinococcus
741	7	0.9	1092	2	Q6J4U7	Q6j4u7 drosophila	814	7	0.9	1686	2	O00443	Q00443 homo sapien
742	7	0.9	1095	2	Q6C4Q2	Q6c4q2 yarrowia li	815	7	0.9	1708	2	Q7XWZ9	Q7xwz9 oryza sativ
743	7	0.9	1098	2	Q6CPF5	Q6cpf5 kluyveromyc	816	7	0.9	1724	2	Q70TF5	Q70tf5 oncorhynch
744	7	0.9	1098	2	Q7QUN5	Q7qun5 giardia lam	817	7	0.9	1766	2	Q6XHA8	Q6xha8 dictyosteli
745	7	0.9	1107	2	Q7Q7N3	Q7q7n3 anopheles g	818	7	0.9	1804	2	Q809B7	Q809b7 semliki for
746	7	0.9	1107	2	Q7MK55	Q7mw55 porphyromon	819	7	0.9	1896	2	Q84MR5	Q84mr5 oryza sativ
747	7	0.9	1121	1	WDR6_HUMAN	Q9nnw5 homo sapien	820	7	0.9	1928	2	Q8D674	Q8d674 vibrio vuln
748	7	0.9	1125	2	Q6BM05	Q6bm05 debaryomyce	821	7	0.9	1943	2	O25331	O25331 helicobacte
749	7	0.9	1125	2	Q99ME2	Q99me2 mus musculu	822	7	0.9	1956	2	Q9Y2K3	Q9y2k3 homo sapien
750	7	0.9	1128	2	Q6AMN5	Q6amn5 desulfotale	823	7	0.9	1989	2	Q9ERT7	Q9ert7 mus musculu
751	7	0.9	1130	2	Q7PXL7	Q7pxl7 anopheles g	824	7	0.9	2134	2	Q7QAT6	Q7qat6 anopheles g
752	7	0.9	1132	2	Q6P0N0	Q6p0n0 homo sapien	825	7	0.9	2174	2	Q92UW8	Q92uw8 rhizobium m
753	7	0.9	1132	2	Q7RAI4	Q7rai4 plasmodium	826	7	0.9	2215	2	Q7WBN0	Q7wbn0 bordetella
754	7	0.9	1139	2	Q54073	Q54073 synecococc	827	7	0.9	2223	2	Q7WTF4	Q7wtf4 streptomyce
755	7	0.9	1139	2	Q8DGF2	Q8dgt2 synecococc	828	7	0.9	2274	2	Q9Z1K7	Q9z1k7 mus musculu
756	7	0.9	1156	2	Q93209	Q93209 feline foam	829	7	0.9	2303	2	O95996	O95996 homo sapien
757	7	0.9	1156	2	P90458	P90458 feline sync	830	7	0.9	2431	1	POLN_SFV	P08411 semliki for
758	7	0.9	1156	2	Q70LW4	Q70lw4 feline foam	831	7	0.9	2431	2	Q8JMP6	Q8jmp6 semliki for
759	7	0.9	1156	2	Q70LW8	Q70lw8 feline foam	832	7	0.9	2432	2	Q8I5I9	Q8i5i9 plasmodium
760	7	0.9	1156	2	Q6GM32	Q6gm32 xenopus lae	833	7	0.9	2432	2	Q9QBM1	Q9qbm1 semliki for
761	7	0.9	1165	2	Q7PKP8	Q7pkp8 anopheles g	834	7	0.9	2478	2	Q66G98	Q66g98 homo sapien

835	7	0.9	2838	2	08VHJ9	Q8vhi9 rattus norv	908	6	0.8	53	2	Q6PMW3	Q6pmw3 bos taurus
836	7	0.9	2909	2	Q8MV78	Q8my78 asterina pe	909	6	0.8	54	2	Q8RT38	Q8rt38 lactobacill
837	7	0.9	3122	2	R89459	R89459 human herpe	910	6	0.8	56	2	Q65VES	Q65ves manhelmia
838	7	0.9	3194	2	Q8ZLM3	Q8zlm3 helicobacte	911	6	0.8	57	2	Q8VJH5	Q8vjh5 mycobacteri
839	7	0.9	3216	2	Q8FKQ3	Q8fkq3 escherichia	912	6	0.8	57	2	Q7S794	Q7s794 neurospora
840	7	0.9	3242	2	Q8G9X9	Q8g9x9 escherichia	913	6	0.8	57	2	Q8S257	Q8s257 streptococc
841	7	0.9	3346	2	Q8WNS4	Q8wns4 bordetella	914	6	0.8	57	2	Q668F2	Q668f2 vercinia ps
842	7	0.9	3455	2	Q7WTD6	Q7wt66 streptomyc	915	6	0.8	57	2	Q64QM5	Q64qm5 bacteroides
843	7	0.9	3836	2	Q6TW53	Q6ty53 hirudo medi	916	6	0.8	57	2	Q8ZCC5	Q8zcc5 yersinia pe
844	7	0.9	3956	2	Q7WTF2	Q7wtf2 streptomyc	917	6	0.8	58	2	Q9S4C7	Q9s4c7 porphyromon
845	7	0.9	4106	2	Q846X2	Q846x2 streptomyc	918	6	0.8	58	2	Q7TL98	Q7tl98 tomato leaf
846	7	0.9	4485	1	DYHG CHLRE	Q39575 chlamydomon	919	6	0.8	58	2	Q88540	Q88540 tomato leaf
847	7	0.9	5369	2	Q9R9J0	Q9r9j0 bacillus su	920	6	0.8	58	2	Q88550	Q88550 tomato leaf
848	6	0.8	18	2	Q6LEN9	Q6len9 homo sapien	921	6	0.8	58	2	Q8B5S8	Q8b5s8 tomato leaf
849	6	0.8	23	2	Q96708	Q96708 ilyanassa o	922	6	0.8	58	2	Q8B5T2	Q8b5t2 tomato leaf
850	6	0.8	23	2	Q25138	Q25138 halictotis ru	923	6	0.8	58	2	Q9QD89	Q9qd89 human immun
851	6	0.8	23	2	Q25161	Q25161 halictotis s	924	6	0.8	59	2	Q6EB62	Q6eb62 campylobact
852	6	0.8	23	2	Q86MM9	Q86mm9 pecten maxi	925	6	0.8	59	2	Q8KCM6	Q8kcm6 chlorobium
853	6	0.8	25	1	GBX1 MOUSE	R82976 mus musculu	926	6	0.8	60	2	Q81TF7	Q81tf7 bacillus an
854	6	0.8	25	2	Q8MWT1	Q8mwt1 eisenia and	927	6	0.8	60	2	Q9RT52	Q9rt52 deinococcus
855	6	0.8	26	2	Q8NTR0	Q8ntr0 eupyrymna sc	928	6	0.8	62	2	Q81F77	Q81f77 trypanosoma
856	6	0.8	27	2	Q02601	Q02601 berce ovata	929	6	0.8	62	2	Q7P310	Q7p310 fusobacteri
857	6	0.8	27	2	Q97457	Q97457 tryptetes a	930	6	0.8	62	2	Q8G8G5	Q8g8g5 mycoplasma
858	6	0.8	27	2	Q17148	Q17148 branchiosto	931	6	0.8	62	2	Q72UB4	Q72ub4 leptospira
859	6	0.8	27	2	Q26396	Q26396 ctenodrilus	932	6	0.8	62	2	Q8F0R6	Q8f0r6 leptospira
860	6	0.8	27	2	Q26533	Q26533 saccoglossu	933	6	0.8	63	2	Q8GWT9	Q8gwt9 arabidopsis
861	6	0.8	27	2	Q7KQAS	Q7kqas tryptetes a	934	6	0.8	63	2	Q6T2C0	Q6t2c0 streptomyc
862	6	0.8	27	2	Q90299	Q90299 carassius a	935	6	0.8	63	2	Q71J91	Q71j91 lactobacill
863	6	0.8	27	2	Q91272	Q91272 petromyzon	936	6	0.8	63	2	Q9SW93	Q9sw93 streptomyc
864	6	0.8	27	2	Q91273	Q91273 petromyzon	937	6	0.8	63	2	Q8NQG0	Q8nqg0 corynebacte
865	6	0.8	28	2	Q17074	Q17074 antheraea p	938	6	0.8	63	2	Q73794	Q73794 xenopus lae
866	6	0.8	29	2	Q17073	Q17073 antheraea p	939	6	0.8	64	2	Q633Q4	Q633q4 bacillus ce
867	6	0.8	30	2	Q96707	Q96707 lithobius f	940	6	0.8	64	2	Q72V64	Q72v64 leptospira
868	6	0.8	31	2	Q86LM4	Q86lm4 lumbricus f	941	6	0.8	64	2	Q722K4	Q722k4 bacillus ce
869	6	0.8	32	2	Q86LM5	Q86lm5 urechis cau	942	6	0.8	64	2	Q817K2	Q817k2 bacillus an
870	6	0.8	32	2	Q86LM6	Q86lm6 loligo opal	943	6	0.8	64	2	Q81L53	Q81l53 bacillus an
871	6	0.8	32	2	Q65V69	Q65v69 manhelmia	944	6	0.8	64	2	Q8SZP2	Q8szp2 leptospira
872	6	0.8	33	2	Q9XS29	Q9xs29 sus scrofa	945	6	0.8	65	2	Q71714	Q71714 human immun
873	6	0.8	33	2	Q8V9C6	Q8v9c6 cotton leaf	946	6	0.8	65	2	Q7NAX6	Q7nxa6 chromobacte
874	6	0.8	33	2	Q91EV0	Q91ev0 cotton leaf	947	6	0.8	65	2	Q9PFF3	Q9pff3 xylella fas
875	6	0.8	34	2	Q7PD47	Q7pd47 giardia lam	948	6	0.8	66	2	Q9NQP6	Q9nqp6 homo sapien
876	6	0.8	35	2	Q79471	Q79471 human immun	949	6	0.8	66	2	P87463	P87463 hemidactylu
877	6	0.8	36	2	Q748T1	Q748t1 geobacter s	950	6	0.8	66	2	Q8U809	Q8u809 agrobacteri
878	6	0.8	36	2	Q91144	Q91144 notophthalm	951	6	0.8	66	2	Q9DQ45	Q9dq45 human immun
879	6	0.8	38	2	Q91XM7	Q91xm7 rattus norv	952	6	0.8	66	2	Q9DQ48	Q9dq48 human immun
880	6	0.8	38	2	Q9JL01	Q9j101 rattus norv	953	6	0.8	66	2	Q9DQ49	Q9dq49 human immun
881	6	0.8	39	2	Q9UD61	Q9ud61 homo sapien	954	6	0.8	66	2	Q9DQ50	Q9dq50 human immun
882	6	0.8	39	2	Q6SXQ4	Q6sxq4 eptaretus	955	6	0.8	66	2	Q9DQ51	Q9dq51 human immun
883	6	0.8	39	2	Q6M7D0	Q6m7d0 corynebacte	956	6	0.8	66	2	Q9DQ52	Q9dq52 human immun
884	6	0.8	40	2	Q25534	Q25534 mytilus tro	957	6	0.8	67	2	Q61698	Q61698 hydra atten
885	6	0.8	42	2	Q61336	Q61336 panulirus i	958	6	0.8	67	2	Q61X53	Q61x53 spiropasma
886	6	0.8	42	2	Q8F264	Q8f264 leptospira	959	6	0.8	67	2	Q7D2H8	Q7d2h8 agrobacteri
887	6	0.8	43	2	Q8EF80	Q8ef80 shewanella	960	6	0.8	67	2	Q8X443	Q8x443 escherichia
888	6	0.8	43	2	Q91F98	Q91f98 chilo iride	961	6	0.8	67	2	Q7UE29	Q7ue29 rhodopirell
889	6	0.8	44	2	Q7R8B6	Q7r8b6 plasmodium	962	6	0.8	67	2	Q8ZQ11	Q8zq11 streptomyc
890	6	0.8	44	2	Q87W23	Q87w23 pseudomonas	963	6	0.8	68	2	Q8FUD4	Q8fud4 methanosarc
891	6	0.8	45	2	Q7YJ33	Q7y733 nicotiana s	964	6	0.8	68	2	Q75M26	Q75m26 homo sapien
892	6	0.8	45	2	Q7XL87	Q7xl87 oryza sativ	965	6	0.8	68	2	Q98RX3	Q98rx3 quillaria
893	6	0.8	45	2	Q6UMM0	Q6umm0 hepatitis c	966	6	0.8	68	2	Q9K928	Q9k928 bacillus ha
894	6	0.8	45	2	Q6UMM1	Q6umm1 hepatitis c	967	6	0.8	68	2	Q11613	Q11613 human immun
895	6	0.8	47	2	Q7P7U7	Q7p7u7 anopheles g	968	6	0.8	69	1	RL38 LYCES	RL38 lyceiso
896	6	0.8	47	2	Q95W96	Q95w96 equus cabal	969	6	0.8	69	2	Q6KZ16	Q6kz16 picophilus
897	6	0.8	48	2	Q6F5J0	Q6f5j0 bovine vira	970	6	0.8	69	2	Q71HS8	Q71hs8 lactobacill
898	6	0.8	49	2	Q6CSL8	Q6cs18 kluyveromyc	971	6	0.8	69	2	Q9R3Q4	Q9r3q4 streptococc
899	6	0.8	49	2	Q7YUJ0	Q7yu10 trypanosoma	972	6	0.8	69	2	Q9RCM3	Q9rcm3 streptococc
900	6	0.8	50	2	Q6QW42	Q6qw42 azospirillu	973	6	0.8	69	2	Q9RCM7	Q9rcm7 streptococc
901	6	0.8	50	2	Q7YJ13	Q7y713 nicotiana t	974	6	0.8	69	2	Q65GZ4	Q65gz4 bacillus li
902	6	0.8	51	2	Q8NSN4	Q8nsn4 corynebacte	975	6	0.8	69	2	Q9WCQ3	Q9wcq3 human immun
903	6	0.8	51	2	Q73UMC2	Q73umc2 mycobacteri	976	6	0.8	70	1	RL31 ECOLI	RL31 escherichia
904	6	0.8	51	2	Q73UMC6	Q7umc6 rhodopirell	977	6	0.8	70	2	Q8TQ78	Q8tq78 methanosarc
905	6	0.8	52	2	Q8MRT2	Q8mrt2 drosophila	978	6	0.8	70	2	Q8H5L7	Q8h5l7 oryza sativ
906	6	0.8	52	2	Q8YNI7	Q8yn17 anabaena sp	979	6	0.8	70	2	Q83PD4	Q83pd4 shigella fl
907	6	0.8	52	2	Q87259	Q87259 chimpanzee	980	6	0.8	70	2	Q8BMZ8	Q8bmz8 mus musculu

981 6 0.8 71 1 RL31_PSEPK Q88cu3 pseudomonas
 982 6 0.8 71 1 RS28_ARCFU O29493 archaeoglob
 983 6 0.8 71 2 Q8WMH0 Q8wmh0 sus scrofa
 984 6 0.8 71 2 Q9GJ62 Q9gj62 salmo trutt
 985 6 0.8 71 2 Q9GJ63 Q9gj63 salmo trutt
 986 6 0.8 71 2 Q9GJ65 Q9gj65 salmo trutt
 987 6 0.8 71 2 Q9GJ66 Q9gj66 salmo trutt
 988 6 0.8 71 2 Q9GJ67 Q9gj67 salmo trutt
 989 6 0.8 71 2 Q9GJ68 Q9gj68 salmo trutt
 990 6 0.8 71 2 Q9GJ71 Q9gj71 salmo trutt
 991 6 0.8 71 2 Q9GJ72 Q9gj72 salmo trutt
 992 6 0.8 71 2 Q62C83 Q62c83 burkholderi
 993 6 0.8 71 2 Q7MYC6 Q7myc6 photorhabdu
 994 6 0.8 71 2 Q7VM76 Q7vm76 haemophilus
 995 6 0.8 72 2 O15172 O15172 homo sapien
 996 6 0.8 72 2 Q9WC08 Q9wc08 human immu
 997 6 0.8 73 1 P56613 P56613 aquifex ae
 998 6 0.8 73 1 P10571 P10571 bacillus me
 999 6 0.8 73 2 Q47834 Q47834 enterococcu
 1000 6 0.8 73 2 Q83AD2 Q83ad2 coxiella bu

ALIGNMENTS

RESULT 1

O30912 ID O30912 PRELIMINARY; PRT; 797 AA.
 AC O30912;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Outer membrane protein Omp85.
 GN Name=omp85;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HH;
 RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
 RT Manning D.S.; Reschke D.K.; Judd R.C.;
 RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
 RT are similar to Haemophilus influenzae D-15-Ag and Pasteurella
 RT multocida Oma87.";
 RL Microb. Pathog. 25:11-21(1998).
 DR EMBL; AF021245; AAC17599.1; -;
 DR InterPro; IPR000184; Bac_surfAg_D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac surface Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 SQ SEQUENCE 797 AA; 89539 MW; CF911B5F70B999CF CRC64;

Query Match 100.0%; Score 797; DB 2; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSA 60
 DB 1 MKLQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSA 60
 QY 61 IISLVTATGFDDVRVETADQGLLTIVERTPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
 DB 61 IISLVTATGFDDVRVETADQGLLTIVERTPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
 QY 121 SQYFNQATLNAQVAGLKEEYLGKGMNIQTTPKVKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLNAQVAGLKEEYLGKGMNIQTTPKVKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNOVYSDRLKRMQMSLTGGITWLTTRSNQFNQKFAQDMKVTDFYQNNGVDFPRIL 240
 DB 181 FEGNOVYSDRLKRMQMSLTGGITWLTTRSNQFNQKFAQDMKVTDFYQNNGVDFPRIL 240

241 DTDIQTNEKTKQTIKIVHEGGRFWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
 DB DTDIQTNEKTKQTIKIVHEGGRFWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
 QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIHPGRKIYVNEIHTGNKT 360
 DB 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIHPGRKIYVNEIHTGNKT 360
 QY 361 RDEVVRRELQMESAPYDTSKLQSKRVELLGYFDNVQFDVAVPLAGTDPKVDLNNSLTE 420
 DB 361 RDEVVRRELQMESAPYDTSKLQSKRVELLGYFDNVQFDVAVPLAGTDPKVDLNNSLTE 420
 QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSTDPYFTA 480
 DB 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSTDPYFTA 480
 QY 481 DGVSLGYDYVGAFAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 DB 481 DGVSLGYDYVGAFAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPKHYADFIKYGKTDGTSKPGWLYKGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
 DB 541 YNKAPKHYADFIKYGKTDGTSKPGWLYKGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
 QY 601 LPGSKLQYYSATHNQTFWFFLSKTFITMLGGEVGIAGGYGRTEKIEIPFFENFYGGGLGSRV 660
 DB 601 LPGSKLQYYSATHNQTFWFFLSKTFITMLGGEVGIAGGYGRTEKIEIPFFENFYGGGLGSRV 660
 QY 661 GYESGTLGPKVYDEYGEKISYGNKKANYSAELLFPMPCAKDARTVRLSLFADAGSVWDG 720
 DB 661 GYESGTLGPKVYDEYGEKISYGNKKANYSAELLFPMPCAKDARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSSATGGRVQNIYCGAGNTHKSTFTNELRYLSAGGAVTWLSPLGPMKFRYAYPLKK 780
 DB 721 KTYDDNSSSATGGRVQNIYCGAGNTHKSTFTNELRYLSAGGAVTWLSPLGPMKFRYAYPLKK 780
 QY 781 KPDEIQRFQFQGLGTTFF 797
 DB 781 KPDEIQRFQFQGLGTTFF 797
 RESULT 2
 Q9JX31 ID Q9JX31 PRELIMINARY; PRT; 797 AA.
 AC Q9JX31;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Outer membrane protein OMP85.
 GN Name=omp85; OrderedLocusNames=NMA0085;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis Z2491.";
 RL Nature 404:502-506(2000).
 DR EMBL; AL162752; CAB83401.1; -;
 DR PIR; D82000; D82000.
 DR InterPro; IPR000184; Bac_surfAg_D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac surface Ag; 1.


```
DR Pfam: PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88404 MW; 65DE47E00C9E1D1P CRC64;

Query Match
Best Local Similarity 94.4%; Score 752; DB 2; Length 797;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDVRVETAD 80
DB 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDVRVETAD 80
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOVFNQATLNOAVAGLKEEY 140
DB 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOVFNQATLNOAVAGLKEEY 140
QY 141 LGRGKLNIIQTPKVKTLARNRVDITIDEGSKAKITDIEFEGNQVYSRDKLRQMSLTE 200
DB 141 LGRGKLNIIQTPKVKTLARNRVDITIDEGSKAKITDIEFEGNQVYSRDKLRQMSLTE 200
QY 201 GGIWTLTRSNQFNEQKFAQDMKVTDFYQNGYDFRILDTDIQTNEDKTKQTIKTVH 260
DB 201 GGIWTLTRSNQFNEQKFAQDMKVTDFYQNGYDFRILDTDIQTNEDKTKQTIKTVH 260
QY 261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIONRMGSAGYAYS 320
DB 261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIONRMGSAGYAYS 320
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRELQMESAPYDTS 380
DB 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRELQMESAPYDTS 380
QY 381 KLQSKERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
DB 381 KLQSKERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
QY 441 SAGVSQDNLFSGTGSAAALRASRKTTLNGSLSPDTPYFTADGVSGLGVYVYKGFADPRKAS 500
DB 441 SAGVSQDNLFSGTGSAAALRASRKTTLNGSLSPDTPYFTADGVSGLGVYVYKGFADPRKAS 500
QY 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKPKHYADFIKKYGKTDG 560
DB 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKPKHYADFIKKYGKTDG 560
QY 561 TDGSGFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNNAEIALPGSKLOQYYSATHNQWTFPP 620
DB 561 TDGSGFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNNAEIALPGSKLOQYYSATHNQWTFPP 620
QY 621 LSKTFTMLGGEVGIAGGYGRTEIIPFPENFYGGGLSGVSGYSGTLGPKVYDEYGEKIS 680
DB 621 LSKTFTMLGGEVGIAGGYGRTEIIPFPENFYGGGLSGVSGYSGTLGPKVYDEYGEKIS 680
QY 681 YGNGKANVSAEALLFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
DB 681 YGNGKANVSAEALLFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
QY 741 AGNTHKSTFTNELRYSAGGAVTWSPLGPMKF 772
DB 741 AGNTHKSTFTNELRYSAGGAVTWSPLGPMKF 772

RESULT 3
Q9K1H0 PRELIMINARY; PRT; 797 AA.
AC Q9K1H0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein Omp85.
GN OrderedLocusNames=NM0182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
```

```
Db 621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENPYGGGLGSRGYESGTTGPKVYDYGSKIS 680
Qy 681 YGKNKANVASAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYG 740
Db 681 YGKNKANVASAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 4
P95359 PRELIMINARY; PRT; 792 AA.
AC P95359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN Name=omp85;
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=FA19;
RA MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
RT are similar to Haemophilus influenzae p-15-Ag and Pasteurella
RT multocida Oms87.";
RL Microb. Pathog. 25:11-21(1998).
RL ENBL; U81959; AAC17600.1; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 792 AA; 87868 MW; 90E32D24AA0513D8 CRC64;

Query Match 19.7%; Score 157; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.le-150;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Db 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Qy 392 LGYFDNVQFQDAVPLAGTPDKVDLNSLTERSTGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Db 392 LGYFDNVQFQDAVPLAGTPDKVDLNSLTERSTGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Qy 452 TGKSAALRASRSKTTLINGSLSFTDPYPTADGVSLGYD 488
Db 452 TGKSAALRASRSKTTLINGSLSFTDPYPTADGVSLGYD 488

RESULT 5
Q7NY6 PRELIMINARY; PRT; 771 AA.
AC Q7NY6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable outer membrane protein.
GN OrderedLocusNames=CV2204;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
```

```
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Pilho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunarez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR ENBL; AEO16917; AAQ59877.1; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 771 AA; 85250 MW; 272FA6D8B5F03BE8 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 771;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TVFNYPVVKVGD 52
Db 42 TVFNYPVVKVGD 54

RESULT 6
Q88MH2 PRELIMINARY; PRT; 786 AA.
AC Q88MH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein, bacterial surface antigen family.
GN OrderedLocusNames=PP1599;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzaz A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.W.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
```

```

RL Environ. Microbiol. 4:799-808 (2002).
DR ENBL; AE016779; AAN67220.1; -.
DR TIGR; PP1599; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 786 AA; 86513 MW; D88E288A938D9E98 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 DPVFTADGVSLGY 487
Db |||||
474 DPVFTADGVSLGY 486

RESULT 7
Q88H14 PRELIMINARY; PRT; 787 AA.
AC Q88H14;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bacterial surface antigen family protein.
GN OrderedLocusNames=PP3373;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2243060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Maazzeq A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808 (2002).
DR ENBL; AE016786; AAN68977.1; -.
DR TIGR; PP3373; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 787 AA; 86513 MW; 41FE0C4E311A6A97 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 DPVFTADGVSLGY 487
Db |||||
474 DPVFTADGVSLGY 486

RESULT 8
Q8XZ13 PRELIMINARY; PRT; 765 AA.
AC Q8XZ13;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.

```

```

GN Names=RS05280; OrderedLocusNames=RS01412;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangelot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum."
RT Nature 415:497-502 (2002).
DR EMBL; AL646064; CAD15114.1; -.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
DR PROSITE; PS00061; ADM_SHORT; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 1.3%; Score 10; DB 2; Length 765;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 KTRDEVVRR 368
Db |||||
365 KTRDEVVRR 374

RESULT 9
Q9SNM7 PRELIMINARY; PRT; 328 AA.
AC Q9SNM7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T8P19.130.
GN Names=T8P19.130;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choine N., Robert C., Brottier P., Wincker P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AL133315; CAB62351.1; -.
DR PIR; T46206; T46206.
DR InterPro; IPR007928; Antifreeze_CF.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 36233 MW; CDB4D2B1EA2530C6 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGVRGY 662
Db |||||
152 GGLGVRGY 160

RESULT 10

```

```
Q6L543
ID Q6L543 PRELIMINARY; PRT; 361 AA.
AC Q6L543;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein O61005_B11.2.
GN Name=O61005_B11.2;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsing Y.-I.-C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,
RA Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,
RA Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-F.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC108873; AAT44133.1; -
DR InterPro: IPR00184; Bac_surfAg_D15.
DR Pfam: PF01103; Bac_surface_Ag; 1.
KW Hypothetical protein.
SQ SEQUENCE 361 AA; 38699 MW; 2737C185F63779E CRC64;

Query Match 1.1%; Score 9; DB 2; Length 361;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGSRVGY 662
DB 255 GGLGSRVGY 263
|||||

RESULT 11
Q9LXP7 PRELIMINARY; PRT; 435 AA.
ID Q9LXP7
AC Q9LXP7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein F26G5_110.
GN Name=F26G5_110;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OC NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA D'Angelo M., Verzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,
RA Rudd S., Lencke K., Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL EMBL: AL353814; CAB88424.1; -
DR FIR: T49132; T49132.
DR InterPro: IPR00184; Bac_surfAg_D15.
DR Pfam: PF01103; Bac_surface_Ag; 1.
KW Hypothetical protein.
SQ SEQUENCE 435 AA; 47528 MW; C148B36074B49427 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGSRVGY 662
DB 255 GGLGSRVGY 263
|||||
```

```
Db 296 GGLGSRVGY 304

RESULT 12
Q9ZAE1 PRELIMINARY; PRT; 713 AA.
ID Q9ZAE1
AC Q9ZAE1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polynucleotide phosphorylase.
GN Name=pnp;
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OC NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=VK1;
RA Serganov A.A., Garber M.B., Portier C.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z84207; CAB06341.1; -
DR HSP: P05055; ISRO.
DR GO: GO:000175; F:3'-5'-exoribonuclease activity; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR GO: GO:0006396; P:RNA processing; IEA.
DR InterPro: IPR001247; 3 ExoRNase.
DR InterPro: IPR004087; KH.
DR InterPro: IPR004088; KH_type_1.
DR InterPro: IPR008994; Nucleic_acid_ob.
DR InterPro: IPR003029; S1.
DR Pfam: PF00013; KH_1; 1.
DR Pfam: PF03726; PNPase; 1.
DR Pfam: PF01138; RNase_PH; 2.
DR Pfam: PF03725; RNase_PH_C; 2.
DR Pfam: PF00575; S1; 1.
DR SMART: SM00322; KH; 1.
DR SMART: SM00316; S1; 1.
DR PROSITE: PS00084; KH_TYPE_1; 1.
DR PROSITE: PS0126; S1_1.
DR PROSITE: PS0126; S1_1.
SQ SEQUENCE 713 AA; 78192 MW; 2979859D9AC5EA82 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 DEVVRREL 370
DB 310 DEVVRREL 318
|||||

RESULT 13
Q72J38 PRELIMINARY; PRT; 713 AA.
ID Q72J38
AC Q72J38;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Polynucleotide phosphorylase.
GN OrderedLocusNames=TT0774;
OS Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSM 7039).
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OC NCBI_TaxID=262724;
RN [1]
RP SEQUENCE FROM N.A.
RA Henne A., Brueggemann H., Raasch C., Wierer A., Hartsch T.,
RA Liesegang H., Johann A., Lienard T., Gohl O., Martinez-Arias R.,
RA Jacobi C., Starkuviene V., Schlenczek S., Dencker S., Huber R.,
RA Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fritz H.-J.;
RL "The genome sequence of the extreme thermophile Thermus
thermophilus.";
```

```

RL  Nat. Biotechnol. 22:547-553(2004).
DR  EMBL: AE017303; AAS81120.1; -.
DR  GO: GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR  GO: GO:0003723; F:RNA binding; IEA.
DR  GO: GO:0006396; P:RNA processing; IEA.
DR  InterPro: IPR001247; 3 ExoRNase.
DR  InterPro: IPR004087; KH.
DR  InterPro: IPR004088; KH type 1.
DR  InterPro: IPR008994; Nucleic_acid_OB.
DR  InterPro: IPR003029; S1.
DR  Pfam: PF00013; KH_1; 1.
DR  Pfam: PF03726; PNPase; 1.
DR  Pfam: PF01138; RNase PH; 2.
DR  Pfam: PF01725; RNase PH_C; 2.
DR  Pfam: PF00575; S1; 1.
DR  SMART; SMO0322; KH; 1.
DR  SMART; SMO0316; S1; 1.
DR  PROSITE; PS0084; KH_TYPE_1; 1.
DR  PROSITE; PS0126; S1; 1.
DR  Complete proteome.
KW  Complete proteome.
SQ  SEQUENCE 713 AA; 78192 MW; 2979859DP9AC5EA82 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 362 DEVVRELR 370
DB 310 DEVVRELR 318
|||||

RESULT 14
Q62JD2 PRELIMINARY; PRT; 769 AA.
AC Q62JD2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 23-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Outer membrane protein, OMP85 family.
GN ORFNames=BMA1547;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Nieman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
RA Winn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
DR EMBL: CP000010; AAU4747.1; -.
SQ SEQUENCE 769 AA; 84848 MW; AADD3DE1446B20E0 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 769;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 TRDEVVRRE 368
DB 367 TRDEVVRRE 375
|||||

RESULT 15
Q63T20 PRELIMINARY; PRT; 769 AA.
ID Q63T20
AC Q63T20;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)

```

```

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative outer membrane protein.
GN ORFNames=BPSL2151;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagers K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL: BX571965; CAH36153.1; -.
SQ SEQUENCE 769 AA; 84906 MW; 9E0E33B0197B11B1 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 769;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 360 TRDEVVRRE 368
DB 367 TRDEVVRRE 375
|||||

Search completed: July 6, 2005, 15:50:38
Job time : 214 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:56:39 ; Search time 222.937 Seconds
(without alignments)
1830.683 Million cell updates/sec

Title: US-10-606-618-4
Perfect score: 4152
Sequence: 1 MKLKQIASALMLGIGISPLAF.....LKKKPEDEIQRFQGLGTF 797

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4152	100.0	797	2	O30912
2	4140	99.7	797	2	O30912
3	4136	99.6	797	2	O30912
4	3937.5	94.8	792	2	P95359
5	2052	49.4	771	2	O7NVY6
6	1555.5	37.5	758	2	O82U03
7	1497.5	36.1	765	2	O8X2I3
8	1477	35.6	769	2	O63T20
9	1476	35.5	769	2	O62JD2
10	1395.5	33.6	778	2	O7VYC2
11	1392.5	33.5	778	2	O7WJ86
12	1384.5	33.3	778	2	O7WA52
13	1320	31.8	795	2	O88GNS
14	1295	31.2	786	2	O88MH2
15	1279.5	30.8	797	2	O9HX4
16	1279	30.8	787	2	O88H14
17	1259.5	30.3	788	2	O8PML3
18	1254	30.2	784	2	O87E11
19	1252.5	30.2	825	2	O6FCG7
20	1249	30.1	818	2	O8PAW1
21	1241	29.9	784	2	O9PE12
22	1240	29.9	797	2	O7N8N9
23	1226	29.5	797	2	O9S341
24	1213.5	29.2	814	2	O6D8D5
25	1212	29.2	803	2	O8Z9A3
26	1206.5	29.1	826	2	O8EGG7
27	1201.5	28.9	804	2	O8ZRP0
28	1198	28.9	805	2	O6LN32
29	1197	28.8	795	2	O667J7
30	1197	28.8	795	2	O8ZHS8
31	1192.5	28.7	804	2	O87ME5

32 1180.5 28.4 804 2 Q7MIG8
33 1180.5 28.4 804 2 Q8DBF3
34 1178.5 28.4 810 1 UP05 ECOLI
35 1168.5 28.1 810 2 Q8KR34
36 1168 28.1 803 2 Q9KPW0
37 1161 28.0 785 2 Q9R2E3
38 1160 27.9 789 2 Q6SR79
39 1159 27.9 808 2 Q6Q8T1
40 1148 27.6 793 2 Q93PM2
41 1136 27.4 797 1 D151_HAEIN
42 1135 27.3 795 1 D152_HAEIN
43 1122.5 27.0 792 2 O32625
44 1116 26.9 793 1 D153_HAEIN
45 1113 26.8 803 2 Q83DT2

ALIGNMENTS

RESULT 1
O30912 ID O30912 PRELIMINARY; PRT; 797 AA.
AC O30912;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=HH;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Oma87.";
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF01245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B999CF CRC64;

Query Match 100.0%; Score 4152; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 5.3e-234;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGIQRTSPSTVFNYPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGIQRTSPSTVFNYPVKVGDYNDTHGSA 60
OY 61 ITKSLYATGFDDVRVETADGQQLLVIRPTTIGSLNITGAKMLQNDATKKNLESFGLAQ 120
DB 61 ITKSLYATGFDDVRVETADGQQLLVIRPTTIGSLNITGAKMLQNDATKKNLESFGLAQ 120
OY 121 SQYFNQATLNQAVAGKEEYLGKGLNIQITPKVTKLARNVDITIDTIDEGSAKITDIE 180
DB 121 SQYFNQATLNQAVAGKEEYLGKGLNIQITPKVTKLARNVDITIDTIDEGSAKITDIE 180
OY 181 FEGNQVYSRDKLMRQMSLTGGGIWTLTNSQNEQFAQDMKVTDFYQNNCYFFPRIL 240
DB 181 FEGNQVYSRDKLMRQMSLTGGGIWTLTNSQNEQFAQDMKVTDFYQNNCYFFPRIL 240
OY 241 DTDIQTNEDKTKQITIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKGYERQQ 300
DB 241 DTDIQTNEDKTKQITIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKGYERQQ 300
OY 301 MTAVLGEIQNRMGSAIYSEISVQPLPNAETKTVDFVLHIEPGRKIYNEIHITGNKT 360

Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPRKLIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQMESAPYDTSKLRQSKERVVELLGYFDNVQDPAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQMESAPYDTSKLRQSKERVVELLGYFDNVQDPAVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLSAGWQDVTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSTPDPYFTA 480
Db 421 RSTGSLDLSAGWQDVTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSTPDPYFTA 480
Qy 481 DGVSGLGYDVYKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPQSKLOYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVR 660
Db 601 LPQSKLOYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGNKKNVSAEILLFPMPCAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKNVSAEILLFPMPCAKDARTVRLSLFADAGSVWDG 720
Qy 721 KYDDNSSSATSATGRVQNIYAGNTHKSTFTNELRYSGAGVAVTWLSPGLPMKFRYAYPLKK 780
Db 721 KYDDNSSSATSATGRVQNIYAGNTHKSTFTNELRYSGAGVAVTWLSPGLPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFQFOLGTTTF 797
Db 781 KPEDEIQRFQFOLGTTTF 797

RESULT 2

Q9K1H0 ID Q9K1H0 PRELIMINARY; PRT; 797 AA.
AC Q9K1H0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN OrderedLocusNames=NM00182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_Taxid=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Citterone H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Fizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58";
RL Science 287:1809-1815(2000).
DR EMBL; AE002375; AA040639.1; -.
DR PIR; G81228; G81228.
DR TIGR; NM00182; -.
DR InterPro; IPR000184; Bac surfAg D15.
DR InexPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac surface_Ag_1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.

SQ SEQUENCE 797 AA; 88436 MW; B68BFC5A43D22EE8 CRC64;
Query Match 99.7%; Score 4140; DB 2; Length 797;
Best Local Similarity 99.7%; Pred. No. 2.7e-233;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MKLKQIASLMMLGISPLAPADFTIQDIRVEGLQRTPESTVFYVLPVKVGDYVNDTHGSA 60
Db 1 MKLKQIASLMMLGISPLADFTIQDIRVEGLQRTPESTVFYVLPVKVGDYVNDTHGSA 60
Qy 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITDIE 180
Db 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITDIE 180
Qy 181 FEGNQVYSRKLQMRQMSLTGEGGIWTLTRSNQFNEQKFAQDMKQVDFYQNNGYDFRIL 240
Db 181 FEGNQVYSRKLQMRQMSLTGEGGIWTLTRSNQFNEQKFAQDMKQVDFYQNNGYDFRIL 240
Qy 241 DTDIOTNEDKTKOTIKITVHEGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
Db 241 DTDIOTNEDKTKOTIKITVHEGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPRKLIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPRKLIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQMESAPYDTSKLRQSKERVVELLGYFDNVQDPAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQMESAPYDTSKLRQSKERVVELLGYFDNVQDPAVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLSAGWQDVTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSTPDPYFTA 480
Db 421 RSTGSLDLSAGWQDVTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSTPDPYFTA 480
Qy 481 DGVSGLGYDVYKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPQSKLOYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVR 660
Db 601 LPQSKLOYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGNKKNVSAEILLFPMPCAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKNVSAEILLFPMPCAKDARTVRLSLFADAGSVWDG 720
Qy 721 KYDDNSSSATSATGRVQNIYAGNTHKSTFTNELRYSGAGVAVTWLSPGLPMKFRYAYPLKK 780
Db 721 KYDDNSSSATSATGRVQNIYAGNTHKSTFTNELRYSGAGVAVTWLSPGLPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFQFOLGTTTF 797
Db 781 KPEDEIQRFQFOLGTTTF 797

RESULT 3

Q9JX31 ID Q9JX31 PRELIMINARY; PRT; 797 AA.
AC Q9JX31;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein OMP85.
DE Name=omp85; OrderedLocusNames=NWA0085;
OS Neisseria meningitidis (serogroup A).

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 Klee S.R., Morelli G., Bauman D., Brown D., Chillingworth T.,
 Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis 22491";
 RL Nature 404:502-506(2000).
 DR EMBL; AL162752; CAB83401.1; -.
 DR PIR; D82000; D82000.
 DR InterPro; IPR001084; Bac surfAg D15.
 DR InterPro; IPR010827; Surf Ag VNR.
 DR Pfam; PF01103; Bac surface_Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 KW Complete proteome.
 SQ SEQUENCE 797 AA; 88404 MW; 65DE47E00C9E1D1F CRC64;

Query Match 99.68; Score 4136; DB 2; Length 797;
 Best Local Similarity 99.68; Pred. No. 4.5e-233;
 Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFDDVRVETADQGLLLTVIERPTGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFDDVRVETADQGLLLTVIERPTGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNDVIDITIDEGSKAKITDIE 180
 DB 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNDVIDITIDEGSKAKITDIE 180
 QY 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL 240
 DB 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL 240
 QY 241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKGKWERQQ 300
 DB 241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKGKWERQQ 300
 QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYNEIHTGNKKT 360
 DB 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYNEIHTGNKKT 360
 QY 361 RDEVVRRELQWESAPYDTSKLQSKRERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420
 DB 361 RDEVVRRELQWESAPYDTSKLQSKRERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420
 QY 421 RSTGSLDLSAGVQDQTLGVMSAGVSDNLFQTKGSAALRASRKTTLNGSLSTFDYFFTA 480
 DB 421 RSTGSLDLSAGVQDQTLGVMSAGVSDNLFQTKGSAALRASRKTTLNGSLSTFDYFFTA 480
 QY 481 DGVSGLVDYVKGAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 DB 481 DGVSGLVDYVKGAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPHYADP IKKYGKTGDCGSKGLYKGTGWRGNKTDTSALMPTRCGLYGVNAEIA 600
 DB 541 YNKAPHYADP IKKYGKTGDCGSKGLYKGTGWRGNKTDTSALMPTRCGLYGVNAEIA 600
 QY 601 LPSGKLOYSAETHNQWFFPLSKTFTLMLGGEVGIAGGYRTKEIIPFFENFYGGGLGSVR 660
 DB 601 LPSGKLOYSAETHNQWFFPLSKTFTLMLGGEVGIAGGYRTKEIIPFFENFYGGGLGSVR 660

QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABELLFPMGAKADARTVRLSLFADAGSVWDG 720
 DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABELLFPMGAKADARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGAVTWLSPLGPMKFRYAYPLKK 780
 DB 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGAVTWLSPLGPMKFRYAYPLKK 780
 QY 781 KPEDEIQRTQFQGLGTTTF 797
 DB 781 KPEDEIQRTQFQGLGTTTF 797
 RESULT 4
 P95359 PRELIMINARY; PRT; 792 AA.
 ID P95359
 AC P95359;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Outer membrane protein.
 GN Name=omp85;
 OS Neisseria gonorrhoeae.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=485;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FA19;
 RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
 RA Manning D.S., Reschke D.K., Judd R.C.;
 RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
 are similar to Haemophilus influenzae D-15-Ag and Pasteurella
 multocida Oma87";
 RL Microb. Pathog. 25:11-21(1998).
 DR EMBL; U81959; AAC17600.1; -.
 DR InterPro; IPR000184; Bac surfAg D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac surface_Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 SQ SEQUENCE 792 AA; 87868 MW; 90E32D24AA0513D8 CRC64;
 Query Match 94.8%; Score 3937.5; DB 2; Length 792;
 Best Local Similarity 95.1%; Pred. No. 1.8e-221;
 Matches 758; Conservative 16; Mismatches 18; Indels 5; Gaps 2;
 QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFDDVRVETADQGLLLTVIERPTGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFDDVRVETADQGLLLTVIERPTGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNDVIDITIDEGSKAKITDIE 180
 DB 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNDVIDITIDEGSKAKITDIE 180
 QY 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL 240
 DB 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL 240
 QY 241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKGKWERQQ 300
 DB 241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKGKWERQQ 300
 QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYNEIHTGNKKT 360
 DB 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYNEIHTGNKKT 360
 QY 361 RDEVVRRELQWESAPYDTSKLQSKRERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420
 DB 361 RDEVVRRELQWESAPYDTSKLQSKRERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420

QY 421 RSTGSLDLSAGWVODTGLVMSAGVSDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
 DB 421 RSTGSLDLSAGWVODTGLVMSAGVSDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
 QY 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPTVYDRVNFGLVAEHLTVNT 540
 DB 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPTVYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPHYADFIKKYKTDGDSFGKWLKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
 DB 541 YNKAPHYADFIKKYKTDGDSFGKWLKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
 QY 601 LPGSKLOYYSATHNQWTFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
 DB 601 LPGSKLOYYSATHNQWTFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
 QY 661 GYSGTGLPKVYDEYGEKISYGGNKKANVSAEALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 DB 661 GYSGTGLPKVYDEYGEKISYGGNKKANVSAEALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSATGGRVONIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
 DB 721 RTY-----TAAGNKKSVY-SENAHKSFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 775
 QY 781 KPEDEIQRFOQLGTTTF 797
 DB 776 KPEDEIQRFOQLGTTTF 792

RESULT 5
 Q7NVY6
 ID Q7NVY6 PRELIMINARY; PRT; 771 AA.
 AC Q7NVY6
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Probable outer membrane protein.
 GN OrderedLocusNames=CV2204;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Antonio R.V., Almeida F.C., Andrade E.M., Araripe J., de Araujo M.F.F.,
 RA Alves-Gomes J.A., Baptista A.J., Bataus L.A.M.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrati L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas M.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grisar E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira R.M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.B., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
 RA Silva A.M.R., da Silva A.I.C., Silva D.W., Souza E.M., Souza K.R.L.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Urmenyi T.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals

RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
 DR EMBL; A5016917; AAQ59877.1; -;
 DR InterPro; IPR000184; Bac_surfAg D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac_surface_Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 KW Complete proteome.
 SQ SEQUENCE 771 AA; 85250 MW; 272FA6D8B5F03BE8 CRC64;
 Query Match 49.4%; Score 2052; DB 2; Length 771;
 Best Local Similarity 50.5%; Pred. No. 2.3e-111;
 Matches 404; Conservative 140; Mismatches 224; Indels 32; Gaps 9;
 QY 1 MKLKQIASALMMLGISPLAFA--DFTIQDIRVEGLQRTPEPSTVFNYLPVKVGYNDTHG 58
 DB 1 MKLKRLAVALAMGLTMAVAAADPFVVKDIRVEGLQRTPEPSTVFNYLPVKVGYDTTDAKA 60
 QY 59 SAIIKSLYATGFPDDVRVETADGQLLTIVIERPTIGSLNITGAKMLONDAIKQNLSEFGL 118
 DB 61 KEAIKALFGTGFENDVRVESRGDTLIVTVAERPVIQTQNINGAKESKDQKKALKDNGF 120
 QY 119 AQOYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIITIDEKSKAKITD 178
 DB 121 AESLIFDQALLDGAQVQLKQYYSRGKYSVEITPTVTKLERNRVAVTLDINEGVTAIRE 180
 QY 179 IEPFEGNOVYSDRKLMRQMSLTTEGGIWTWLTNRNQFNEQKFAODMEKVTDFYQNGYDFPR 238
 DB 181 IRIVGANAFQSKLLDDEFLTTGGWLSWITKDDQYSKQKLTGDLKAKAFYQNGYMEFG 240
 QY 239 ILDTDIQTNEDKTKQITIKITVHEGGRFRWGKYSIEGDTNEVPKAELEKLLTWKPGKWER 298
 DB 241 IDSSQVSIQADKKDMYLVINVEGKKTYSVDVRLAGDL-KVPEAEMLKMLQVKRGDTFNN 299
 QY 299 QQMTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGN 358
 DB 300 EKVTESVKALSRLNGEYAFANVNLDPIDREKQTAFTFFVDPGRKTYVRVRVAGNS 359
 QY 359 KTRDEVVRRELQMESAPYDTSKLQSRKERVLLGYDFNVQDPAVPLAGTPDKVDLNMSL 418
 DB 360 KTRDEVIRRELQLEGAPYNAANVKESKERLELLGYFEDVNVETPAVADAPQVDNIGL 419
 QY 419 TERSTGSLDLSAGWVODTGLVMSAGVSDNLFCTGKSAALRASRSKTTTLNGSLSFDPYF 478
 DB 420 KERSTGSLGSLGYVQGEGLVLANISQSNIFGSGKYMSLGMSGTGVKNKYSLSFTDPYF 479
 QY 479 TADGSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPTVYDRVNFGLVAEHLTV 538
 DB 480 TPDGSLGYDLNRYNYP--DATSISAYKTSITGADMRFVGPITEYDRINFTIGAERTDI 537
 QY 539 NTYNKAPHYADFIKKYKTDGDSFGKWLKGTGVMGRNKTDSALWPTRGYLTGVNAE 598
 DB 538 TTYNSNPQYIDFVKQYGNSTY-----VLGTVGWGRDTEDSALWTRGASIRVNAD 589
 QY 599 IALPGSKLOYYSATHNQWTFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGS 658
 DB 590 FGLPGGLQYSLYTHQQTWFFPLSKDFTLMLNGELGYADGYGKTKQLPFFKQFYMGGGLS 649
 QY 659 VRGYESGTLGPKVYDEYGEKISY-CGNKKANVSAEALLFPMPGAKDARTVRLSLFADAGSV 717
 DB 650 VRGYDSSSTGP--YDSVAN--SYLGGNRKAVANVELTFFPFGKONKNSLRTSLFFDAGLT 705
 QY 718 WDCKTYDDNSSATGGRVONIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYP 777
 DB 706 W-----NTNLTAEKAQGI-----TSSPDGFRYSAGLALTWLSPMPGPKFSIANP 751
 QY 778 LKKKPEDEIQRFOQLGTTTF 797
 DB 752 LKKEQGDKIQRFOQLGTAF 771

RESULT 6
 Q82U03

ID Q82U03 PRELIMINARY; PRT; 758 AA.
AC Q82U03;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bacterial surface antigen (D15).
GN OrderedLocusNames=NE1710;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IF0 14298;
RX MEDLINE=22586410; PubMed=12700255;
DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
HAUSER L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea";
RL J. Bacteriol. 185:2759-2773 (2003).
DR EMBL; BX321862; CAD85621.1; -;
DR InterPro; IPR000184; Bac surfAg D15.
DR InterPro; IPR010827; Surf Ag VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; Surf Ag VNR; 5.
KW Complete proteome.
SQ SEQUENCE 758 AA; 85016 MW; 6B9630B7124B06C9 CRC64;

Query Match 37.5%; Score 1555.5; DB 2; Length 758;
Best Local Similarity 38.4%; Pred. No. 2.3e-82;
Matches 306; Conservative 167; Mismatches 285; Indels 39; Gaps 7;

QY 1 MKLQIASALMMLG18PLAFADTIQDIRVEGLQRTPESTVFYLPVKVGDYNDTHGSA 60
DB 1 MKLRFILFSLVSLGCMANDSLVWRDIRVEGIQRTPEAGTVFSLPVKVGDVLDKSKASA 60
QY 61 IIKSLVATGFFDVRVETADQGLLTIVERTPTGSLNITGAKMLQNDKAKNLESFGLAQ 120
DB 61 AIKALYATGFFSDVGLKSEGLLIVQVQERPAIAQISNGAKEFDKDKLKEGLKQAGLE 120
QY 121 SQVFNQATLNOAVAGLKEEYGLRGKLNIOITPKVTKLARNRVIDITIDGKSAKITDIE 180
DB 121 SRIFSRLLEKAEQELKQVIRSKGKAVKITTPTPLERNRIGINDIPEGKTAIRIKQIN 180
QY 181 FEGNQVYSDKLRQMSLREGGWTWLTNRNQNEQKFAQDMKVTDYFQNNGYDFDFRIL 240
DB 181 IVGNHVFPEDDLVDLSLTKPGFWFTKDDQYSKQKLSADLETLSYVLDRCYLEFNIE 240
QY 241 DTDIQNEDKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAEKLLTWKPKVYERQ 300
DB 241 STQVSTIPDMKDIYITVNVTEGPQYTVSDIKLAGEL-LVPEELRLKLIKLEPGGIFVREK 299
QY 301 MTAVLGEIQNEMSGAVYSEISVQPLPNAETKTVDVLHIEPRKIYNEIHTGNKKT 360
DB 300 LTSIKLISDLRGNDGYAFANVASPELDKETRTAFTFFIDPGRVYVRINISGNERT 359
QY 361 RDEVRRELQMESAPYDTSKLOKSERVELLGVFQNVQPDVAPLACTPKVDLNNLSLTE 420
DB 360 RDEVIRREFQMEGGWHSTEQINRSQRVDRLOFFFTGVNIETFPVADVPQVDINNVVE 419
QY 421 RSTGSLDLSAGVQDTGLNMGVAGVSDNLFGTKSAALRASRKTTLNGSLSTFDYFFTA 480
DB 420 KPTGAIMFGAGYSDREGIILNGSLTAQNNILGTGNFLSLQVNTGSKVNVKVSASFNPNYTI 479
QY 481 DGVSLGVDYVKGAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHTVNT 540
DB 480 NGVSLGLEAFKRDINTSLSL-SVGMFNTDTGANIRFGIPVAENDIVSLGLGYEHTKIDL 538
QY 541 YNKAHPHYADFIKYGKTKDGTGDSFGKWLKGTGWRGNKNTDSDLPTTRGKYLGVNAEIA 600
DB 539 RDSQPQRKFVDVQFGKTSNN-----LPITLSWARDRRNSAIWTTSGMTQRLFGFEG 590

QY 601 LPSGKLOYYSATHNOTWTFPLSKTFTMLGGEVGIAGGYGRKTEIPFFENFYGGGLGSVR 660
DB 591 LPEGLDLYYKVSVEQRWFVFTKMTFLMLNGEVGVDGYS-DKPLFFKXNFFAGGNSVR 649
QY 661 GYESGTLPKPYDVEYGEKISYGCNKKANYSAELLFPMPGAKAARTVRLSLFADAGSVWDG 720
DB 650 GYNINTLGPDRSDDR---VLGSKRIVGNIEVLFPVPFWMKEDKSVRLSAFADGGTI--- 702
QY 721 KYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPKPKFYAYPLKK 780
DB 703 -----VNSFSLG-----FDDFRYSAGLAATWISPMGLPKFSVAQPLNN 741
QY 781 KPDEIQRFQFQLGTTTF 797
DB 742 QSGDKLQRFQFQGGTF 758

RESULT 7
Q8XZ13 PRELIMINARY; PRT; 765 AA.
ID Q8XZ13;
AC Q8XZ13;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.
GN Name=RS05280; OrderedLocusNames=RScl412;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunnac S., Denange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502 (2002).
DR EMBL; AL646064; CAD15114.1; -;
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; Surf Ag VNR; 5.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 36.1%; Score 1497.5; DB 2; Length 765;
Best Local Similarity 37.5%; Pred. No. 5.7e-79;
Matches 301; Conservative 161; Mismatches 294; Indels 47; Gaps 9;

QY 3 LKQIASALMMLG18PL-----AFADTIQDIRVEGLQRTPESTVFYLPVKVGDYND 54
DB 2 IQRHFPPLSMLAASVLTVCAGAHAVEPVIKDIRVEGVRVPEPVGTVFGLPVKVGTF 61
QY 55 DTHGSAIKSLVATGFFDVRVETADQGLLTIVERTPTGSLNITGAKMLQNDKAKNLE 114
DB 62 DDKGAESIRALYNTGFFKDVQIRAEGLVVRVEERPAISQLEFIGKEFDKDLRLSLR 121
QY 115 SFGLAQSVFNQATLNOAVAGLKEEYGLRGKLNIOITPKVTKLARNRVIDITIDGKSA 174
DB 122 GGVAEARYYDKSLIDRAEQELKQYVSRGYAAADVQTTVPVDANRVSFTFVDEGPA 181
QY 175 KITDIEFEGNQVYSDKLRQMSLREGGWTWLTNRNQNEQKFAQDMKVTDYFQNNGY 234
DB 182 KIRQINIVGNKAFSEGLDRDEMQLSTPNWLSWYTKNDLYSKQKLTADLRLSRYLDGRY 241
QY 235 FDFRILDTDIQNEDKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAEKLLTWKPKG 294
DB 242 LSFATESTQVSTPDKDIYILNINHEGQYKVSIDIKLTGELLS-KQAEWEKLIKLGQD 300


```

SEQUENCE FROM N.A.
RC STRAIN=ATCC 23344;
RA Niezman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA Davidson T.D., Debroy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RR Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
RL EMBL: CP000010; AAU47747.1;
SQ SEQUENCE 769 AA; 84848 MW; AADDJDEI446B20E0 CRC64;

Query Match          35.5%; Score 1476; DB 2; Length 769;
Best Local Similarity 37.7%; Pred. No.1e-77;
Matches 298; Conservative 163; Mismatches 294; Indels 36; Gaps 7;

QY      7 ASALMLGIGSLPAPADTTIQDIRVEGLQRTEPSVFNVLPVKVGDTYNDTHGSAAIKLSLY 66
DB      15 AALAAGHLAHAHATAFPFVVDQIEKGQLGRVEAGSVFAYLPFKQGDFTFDGKASEAIRALY 74
QY      67 ATGFDDVRVETADQQLLTIVIERPTTGLSNIITGAKMLQNDAIKKNLSEGLASQVFNQ 126
DB      75 ATGFENDVRLATQGQGVVIQVOERPAIASIDFTGIKEFDKNLNKALKAVGLSGRYDYDK 134
QY      127 ATLNAQVAGLKEEYLGRGLNIIQTTPVKTLARNVDIIDTDGKSAKITDIEFGNOV 186
DB      135 ALVDKAQBELKRQVLITRGFFAAEVSTVTVPDANRVSIILFAVAGPPAKIRINFINCKA 194
QY      187 YSRDKLMRQMSLTEGGIWTWLTNRSNQFNQEKFAQDMKVTFDYQNNGYFYDFRIILDIOIT 246
DB      195 FKTSTLRDEMQLSTPNWFWSWTKDLYSKEKLTGDLNVRSYYLNRGVLEFNIBESTQVISI 254
QY      247 NEPKTKOTIKITWHEGGRFRMGKVSISGDTNEVPKAELEKLLTMKPCKWTERQOMTAVLG 306
DB      255 SPDKNMYLTVALLHGEGRPYTSSVSKLAGNLDD-RQAELKLVTKPGDRFSAEKLQOTTK 313
QY      307 EIQRMGSGAGYAYSEISVQPLPNAETKTVDVFLHI EPGRKIYVNEIHITGNKTRDEVVR 366
DB      314 AIYDKLGOYGAFATVNAQPEIDQATHKVGILTVDPSRRVYVRRINI VGNTRTRDEVVR 373
QY      367 RELRWESAPYDTSKLQRKSERVELLYGYFDNVQFDAPVLAGTPDKVDLNMSLTERSTGSL 426
DB      374 REMRQLESSWFDSSRLALS KDORVNLGYFTDVDTTVFVTEGNDQVDVNKVVAEKPITGAI 433
QY      427 DLGAGWQDGTGLVMSAGVSODNFLGTCGKSAA LRASRKTIINGLSLSTDPDYFTADGVSLG 486
DB      434 TLGAGFSSTDKVWLVSAGISODNFVGSCTSLAVNVNTAKSYRTLTVTQVDYFTVDGIKRI 493
QY      487 YDVYGAFDPRKASTSIKYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPK 546
DB      494 TDVFIPTYQPLYSTN--SSFRITAGNLKFGIPFSETDVIYFAGFEQRNLDOVDSMTQP 552
QY      547 HYADFPIKCYKTDGTGDSFGKWLGYKGTVGWRNKNTDSALMPTFRGYLTGVNAEIALPGSKL 606
DB      553 SYQDYVNEFGRVNT-----VPLTIGSWRDARDSALLIPSRGYFTQANAEGYGPVGKI 604
QY      607 QYYSATHNQTWTFPLPKSKTFTFM LGGEVGIAGGYGRTEKIEIPPFENFYGGGLGSGVRGESGT 666
DB      605 QYTYMDVQQGYYSYSFARGFTGLGNLFQAGYGNIGG--NPYPYIFKNYTAGGICSGVRGEPSS 662
QY      667 LGRPVDYEYCEKISYGNKKKANVASSELLFWPMGAKADARTVRLSIFADAGSVWDGKTYDDN 726
DB      663 LGPR---DVTNTDPIGGRKMVMVNGIELTTFPLPGTGYPDTRLVTFFLDGGNNW----- 711
QY      727 SSSATGCRVQNYCAGNTHKSTFTNELRESAGGAVTWLSPGLPMKFRYAYPLKKKPBDEI 786
DB      712 -GNAPG-----TSTGANGLRYGVGICLAWISPGLPLKSLGFLPQKHGEDQY 758
QY      787 QRFOFOLGTTTF 797
DB      759 QKFQFQIGTAGF 769

```

RESULT 10	
Q7VYC2	
ID Q7VYC2 PRELIMINARY; PRT; 778 AA.	
AC Q7VYC2;	
DT 01-OCT-2003 (TrEMBLrel. 25, Created)	
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)	
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)	
DE Probable surface antigen.	
GN OrderedLocusNames=BPI1427;	
OC Bordetella pertussis.	
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	
OC Alcaligenaceae; Bordetella.	
OX NCBI_TaxID=520;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;	
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngl277;	
RA Parikh J.J., Sebailia M., Preston A., Murphy L.D., Thomson N.R.,	
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,	
RA Cardeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,	
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,	
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,	
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,	
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,	
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,	
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,	
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;	
RT "Comparative analysis of the genome sequences of Bordetella pertussis,	
RT Bordetella parapertussis and Bordetella bronchiseptica.";	
RL Nat. Genet. 35:32-40(2003).	
DR EMBL; BX640415; CAE4171.1; -	
DR InterPro; IPR000184; Bac_surfAg_D15.	
DR InterPro; IPR005479; Cphg_synth_L_D2.	
DR InterPro; IPR010827; Surf_Ag_VNR_	
DR Pfam; PF01103; Bac_surface_Ag; 1.	
DR Pfam; PF07244; Surf Ag VNR; 5.	
DR PROSITE; PS00867; CPASA2_2; UNKNOWN_1.	
KW Complete proteome.	
SQ SEQUENCE 778 AA; 86408 MW; 41E3A869DBF0BACC CRC64;	
Query Match	33.6%; Score 1395.5; DB 2; Length 778;
Best Local Similarity	36.0%; Pred. NO. 5.3e-73;
Matches 287; Conservative	169; Mismatches 239; Indels 43; Gaps 12

Query Match	33.6%	Score 1395.5	DB 2	Length 778
Best Local Similarity	36.0%	Pred. No. 5.3e-73		
Matches	287	Conservative 169	Mismatches 299	Indels 43
Gaps	12			
QY	6	IASALMMIGISPLAFADFTIQDIRVEGLQRTSTVENYLPVKVGDYNDTHGSAIKSL	65	
DB	18	LAALALAPALAH-APEPFVVRDIRVEGIQRTDAGTVFGYLPVKRGKFTDEEATEAVRRL	76	
QY	66	YATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFN	125	
DB	77	YGTGFFSDVQIQTDNNVVVVVQVERPTIASISFNGMRFPDSKAITKSLAQVGFGEGRIFD	136	
QY	126	QATLNQAVAGLKEEYLRGKLNLIQTPVKYLARNRVIDITTDGBKSAKITDIEFGNQ	185	
DB	137	QSMLERAEYELKEOYLAKGKYGEVETATVPLPRNRVGVSFDPFEGEVAKIREIRVVGSK	196	
QY	186	VYSDRKLMRQMSITEGGIWTWLTFRSNQFNQKQPAQDMKEVTFYQNNGYFDFRILDDIQ	245	
DB	197	AFSEGELLOQFDLTTPGWLTYWNTDKYSREKLEGGDIERLSFVLDQGLYEFTVEPQVT	256	
QY	246	TNEDKTKQTIKITIVHGGRRFWGKVISIEGDTNEVPKAELEKLTMTKPKGWYERQOMTAVL	305	
DB	257	ISDPDRDIYITIVHGEPEPYKVRREVLAGNLMGL-DSEINNVLVEIKPGEVPSAAKNNSA	315	
QY	306	GETQNRMGAGYAYSEISVQPLNNAETKTVDVFLVHTEPGRKIYVNEIHTGNKNTREVV	365	
DB	316	KAITNLGLDGLYAFANNPNPQIDRAKHEADVTFFYVDPSSRVVRRIQIGNTKTRDEV	375	
QY	366	RRELQMEAPYDTSKLQRSKERVELLGYPDNYQFQDAVPLAGTDPKVDLNMSLTERSTGS	425	
DB	376	RRBMRQOEAAWYDAGDIPKYSRSDVRLGYENEVNKTDPVPSGPDVDVNDVVKKEPTGI	435	

RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J.E., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cordero-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640427; CAE36837.1; -;
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR005479; Cphp synth_L_D2.
DR InterPro; IPR010827; Surf_Ag_VNR_1.
DR Pfam; PF01103; Bac_surfAg_1.
DR Pfam; PF07244; Surf_Ag_VNR_5.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 778 AA; 86342 MW; 15C8F0F43B865298 CRC64;

Query Match 33.3%; Score 1384.5; DB 2; Length 778;
Best Local Similarity 35.8%; Pred. No. 2.3e-72;
Matches 286; Conservative 169; Mismatches 300; Indels 43; Gaps 12;

QY 6 IASALMMLGSLPLAFADFTTQDIRVEGLQRTPESTVFNPLPVKVGDTYNDTHGSATIKSL 65
DB 18 LAAALLAPALAH-AFPEFVVRDVRVEGIQRTDAGTVFGLPVKVGKFTDEATEAVRRL 76

QY 66 YATGFFDDVRVETADGQLLTIVIERPTIGSLNTGAKMLQNDIAKKNLESFGLAQSYFN 125
DB 77 YGTGFFSDVQIQTDNNVVVVQVQERPTIASISFNGKREPDSKAITKSLAQVGEGRIPD 136

QY 126 QATLQNAVAGLKEEYLGRKLNLTQIPKVTKLARNRVDIDITDEGSAKITDIEFEGNQ 185
DB 137 QSLMRAEYELKEQYLAQKGYGEVATVTPLPNRVGVSGFDVFEGEVAKIREIVVGSK 196

QY 186 VYSDRLKRMQSLTEGGIWTWLTFRSQFNQFNQKFAQMEKVTDFYQNNGYDFDRIIDTDIQ 245
DB 197 AFSEGLLDQFDLTTPGLWTWYNTDKYSREKLEGIERLSYLOQGYLEFTEVPQVT 256

QY 246 TNEDEKTKQTITITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQTAVL 305
DB 257 ISPDKDIYITITVHEGEPYKREVKLAGNLMGL-DSEINNLVEIKSGEVFSAKANSNA 315

QY 306 GEIQNRMGSGYAYSISVQPLNATKTVDFVLHIEPGRKIYVNIHITGNKTRDEVV 365
DB 316 KAITDYLGLDGLYAFANVNPQDRAKHEADVTFFYDPSRRVVRRIQIGGNTRTRDEVV 375

QY 366 RRELQWESAPYDTSKLQSKERVELLYGPDNVQFQDAVPLAGTPDKVDLNMSLTERSTGS 425
DB 376 RREMRQEAANYDAGIKVSRDRVRLGLFNVNVKTDVPVGSQPDQVNVVDVKEKPTGI 435

QY 426 LDLSAGVQDQTLVMSAGVSQDNLFGTGKSAALRASRSKTLTLNGSLSFDPYPTADGVSL 485
DB 436 INLGVGSGSEKAILSGAISDNVFGSGTNLTQLNTSKTNRAVLSDHTDPYTKDGISR 495

QY 486 GYDVYKAFDPRKASTSIQYKTTTAGAGIRMSVPVTEVDNRVNFGLVAEHLTVNTYKAP 545
DB 496 TTSAYRVTEPWNNDG--DYRVKAMGLGMNFGVPISEYDRIFLGGTFFERNQDLYNNSP 553

QY 546 KHVADFTKYGKTDGDSGPKGLYKGTVCWGRNKTDLSALWTPTRGYLTGVNABIALPGSK 605
DB 554 QATRDVQDQG--DSTNALI-----FNTGSKDTRDSALAPTKGAYTRKLGDFST--MD 603

QY 606 LQYISATHNQTFPPLSKFTFLMLGGEVGIAGGYGRTKETLPPFNFGGLGSGVRGYESG 665
DB 604 LKYYLLTAQOQYYLPLGRSYTLALNGMIDYGRSYGGL-DYFVTKVNYAGGIGTVRGYEGA 662

QY 666 TLGP--KVYDEYGEKISYGNKKANVSAELLPMPGKAKDARTVRLSLFADAGSVWDGKTY 723
DB 663 SLGPRDLITGDY-----IGSRRWANAQYILFPFGASKDRTLRWVFTDAGQVAAQ--- 714

QY 724 DNSSSATGGR-----YQNIYAGNTHKSTFTTNELRYSAGGAVTWLSPGLGPMKERYAYPLK 779
DB 715 --SGMCTAGKPGSEVEDPCG-----WRFSAGIGLSMQSPGLGQLSLYARPLN 760

QY 780 KPEDIQRPQOLGTTTP 797
DB 761 SKSGDDTQAFQIGTGF 778

RESULT 13
Q886N5 PRELIMINARY; PRT; 795 AA.
AC Q886N5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN OrderedLocusNames=PSPT01542;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Dougherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000."
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AS016861; AA055062.1; -;
DR TIGR; PSPT01542; -;
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surfAg_1.
DR Pfam; PF07244; Surf_Ag_VNR_5.
KW Complete proteome.
SQ SEQUENCE 795 AA; 87504 MW; 7DCAA623FBA087B1 CRC64;

Query Match 31.8%; Score 1320; DB 2; Length 795;
Best Local Similarity 33.6%; Pred. No. 1.4e-68;
Matches 274; Conservative 167; Mismatches 335; Indels 40; Gaps 8;

QY 1 MKLKQIASALMMLGSLPLAFADFTTQDIRVEGLQRTPESTVFNPLPVKVGDTYNDTHGSA 60
DB 1 MKRLLLTAVLSALMTAEVHAESFTTDIRVNGLQVRVSGSVFGALPLNVGEQADGLVD 60

QY 61 ITKSLVATGFPDDVRVETADGQLLTIVIERPTIGSLNTGAKMLQNDIAKKNLESFGLAQ 120
DB 61 ATRSLFKTGTFFQDIQLGRDGNVLVINVERPSVASIEIEGNAKISTEDLMKLGKQSGLA 120

QY 121 SOYFQATLQNAVAGLKEEYLGRKLNLTQIPKVTKLARNRVDIDITDEGSAKITDIE 180
DB 121 GEIFQRTALEGVNRELQRYVAGRYSAEVADEVVQPPENRVCLKININEGTVASQIHIN 180

QY 181 FEGNQVYSRDKLMRQMSLTFEGGIWTWLTFRSQFNQFNQKFAQMEKVTDFYQNNGYDFRIL 240
DB 181 VVGVNTVFSDEDLTDLFELKTSNWLSPFKNDKDYAREKLSGDLRLRSYYLDRGYINMDIA 240

QY 241 DTDIQTNEKTKQITIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQ 300

Db 241 STQVSTPDKKNVITVNNNEGEKYSVKVSLSGDL-KVPEDQVKSLLLLVQPGQVFSRKV 299
QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHITGNKKT 360
Db 300 MTTTSELITRLNEGVTYFANVGVPTPNNEHTVDITFVVDGKRAYNRYNRGNKTS 359
QY 361 RDEVVRELROMESAPYDTSKLRQSKRVERVELLYGFONVQPDVPLAGTPDKVLDLNSLSTE 420
Db 360 EDEVLRREMRQMEGMASTYLDQSKTRLDRLGFFKEVNVETPPVPGTDQDVNDVAAVEE 419
QY 421 RSTGSLDLSAGVQDGLVMSAGVSQDNLFCTGSAALRASRSKTTLNGSLSTFDYFFTA 480
Db 420 QASGSITASVGFQASAGLILGGSISQNNFLGTGNKVSIGUTRSEYQSRYNFSYVDPYTP 479
QY 481 DGVSLGVDYVKGAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 480 DGVSLGVSAYRRTNYDDLDVDVASYAVDSLGAAGINLGYPISETSRLYTGLTQQDEIKT 539
QY 541 YNKAPHYADFIKKYKGTGDTGDSFGKWLKYGTVGWRNKTKDSALMPTRGYLTVGVNAEIA 600
Db 540 GRVTVDEIFDVQKEG-----KYLNFKSGISGSESTLNKGVLATRGHSQSLVFEST 591
QY 601 LPQSKLOYYSATHNQTFWFFPLSKFTFLMLGGEVGIAGGYCRTKEIPFFENFYGGGLGSVR 660
Db 592 LPQSDLSFFKLDYRAQYFHPITDNYTLRLHTELGYGDYGSTGLPFFENYAGGFNSVR 651
QY 661 GYBSGTLGPKVYDEYG-----EKISYGGNKKANVSAAELLPMPGAKDART 705
Db 652 GPKDSTLGPSTPSRGVAVTGNQGTDPDQDPLPFGGNALVOGGEVMEPLFIKDQRS 711
QY 706 VRLSLFADAGSVMDGKTYDDNSSATGGRVQ--NIYGAGNTHKSTFTNELRYSAGGAVTW 763
Db 712 LRTSVFVDVGNVFD-TNCDSTRTASGKVCENIDLSG-----MASSVGIGVTW 760
QY 764 LSLPGMPKRYAYELKKPED--EIQRFQFQLGTF 797
Db 761 ITALGPLSFALAMPI-KKPDDEAETQVFQSLGQTF 795

RESULT 14
Q88MH2 PRELIMINARY; PRT; 786 AA.
AC Q88MH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein, bacterial surface antigen family.
GN OrderedLocusNames=PP1599;
OC Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA NELSON K.E., Weinel C., Paulsen C., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzaz A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808 (2002).
RL ENBL; AE016779; AAN67220.1; -.
DR TIGR; PP1599; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.

KW Complete proteome. 86513 MW; D88E288A938D9E98 CRC64;
SQ SEQUENCE 786 AA; 31.2%; Score 1295; DB 2; Length 786;
Query Match 33.2%; Pred. No. 4e-67;
Best Local Similarity 163; Mismatches 334; Indels 44; Gaps 7;
Matches 269; Conservative 163;
QY 3 LKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTFVNVLPVKVGTDYNTHGSAII 62
Db 6 LTAVMSALM--IAEVHAESFTISDIRVNGLQVRSAGSVFGALPLNVGDAQDRLRLVDST 62
QY 63 KSIYATGFPDDVRVETADGOLLTVIERFTIGSLNITGAKMLQNDAIKNLESFGLAQSQ 122
Db 63 RSLFKTGFPFDIQLSRDGNVLIINVVERPSVSSIEIEGNKAISTEDLMKGLQSGLAEGE 122
QY 123 YFNOATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNVDIDITIDEGSKAKITDIEPE 182
Db 123 IFORATLEGVRNELQYVQAQGRYSAEDVAEVVPPQPNRNVALKIKINEGTVAIAQHINIV 182
QY 183 GNQVYSDRKLMRQMSLTEGGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYPDFRILD 242
Db 183 GNNVPDETLGOLFELKTTNWLSPFKNDKDYAREKLSGDLRLRSYYLDRGVYINMDIAT 242
QY 243 DIQTNEDETKQTIKITVHEGGRFKWGKVISIEGDTNEVPKAELEKLLTMKPGKWKYERQOMT 302
Db 243 QVSITPDKKHVYITVINEGEKYTVRDVKSGLD-KVPEDQVKSLLLLVQPGQVFSRKVMT 301
QY 303 AVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHITGNKTRD 362
Db 302 TTSSELITRLNEGVTYFANVGVPTPNNEHTVDITFVVDGKRAYNRYNRGNKTKED 361
QY 363 EYVRELROMESAPYDTSKLRQSKRVERVELLYGFQNDVQFADVPLAGTPDKVLDLNSLSTE 422
Db 362 EVLRREMRQMEGMASTYLDQSKTRLERLGFKEVNVETPPVPGTDQDVNDVYVEEQ 421
QY 423 TGSLLDSAGVQDGLVMSAGVSQDNLFCTGSAALRASRSKTTLNGSLSTFDYFFTA 482
Db 422 SGSITASVGFQASAGLILGGSISQSNFLGTGNKVSIGLTRSEYQTRYNFGVDPYFTADG 481
QY 483 VSLGVDYVKGAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542
Db 482 VSLGYNVAFRSTPDYDDLDVDVASYAVDSYAGVSLGYPISETSRLYTGLSVQDQKIKTGK 541
QY 543 KAPKHYADFIKKYKGTGDTGDSFGKWLKYGTVGWRNKTKDSALMPTRGYLTVGVNAEIALP 602
Db 542 YTVDEIFDFLEEG-----DNFLN--FKASIGWSESTLNKGVLATRGHSQSLSTE 593
QY 603 GSKLQYYSATHNQTFWFFPLSKFTFLMLGGEVGIAGGYCRTKEIPFFENFYGGGLGSVRGY 662
Db 594 GSDLSFPKLDYRGQLFKPITSYTLRLHTELGYGDYGSTGLPFFENFYAGGFNSVRGF 653
QY 663 ESGTLGPKVYDEYGE-----KISYGGNKKANVSAAELLPMPGAKDARTV 707
Db 654 KQSLGPRSTPSIGEAAAGKPGTIADPDQDPLPFGGNVIVQGAELLLFLPFPVKDQRSUR 713
QY 708 LSLFADAGSVMDGKTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSP 767
Db 714 TSFVMDVGNVFD-----TNCNKPDCXKVGFSG-MASSVGLGVTWTAL 756
QY 768 GPMKRYAYPLKKPDEIDQRFQFQLGTF 797
Db 757 GPLSFLAMPVKPKPDADTQVFQSLGQTF 786

RESULT 15
Q9HXY4 PRELIMINARY; PRT; 797 AA.
AC Q9HXY4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable outer membrane protein.
GN OrderedLocusNames=PA3648;

OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.H., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Loty S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004784; AAG07036.1; -.
DR PIR; H83190; H83190.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surfAg_1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88286 MW; 71799EF15BC89476 CRC64;

Query Match 30.8%; Score 1279.5; DB 2; Length 797;
Best Local Similarity 33.3%; Pred. No. 3.3e-66;
Matches 273; Conservative 157; Mismatches 338; Indels 51; Gaps 7;

QY 3 LKQIASALMMLGISPLAFADPTTQDIRVEGLQRTPEPSTVFNYLPVKVGYDYNTHGSAII 62.
DB 6 LPALLSALM--TAEVHAESFTVSDIRNGLQVRVAGSVFAALPLNVGETIDQALVOAT 62

QY 63 KSLYATGFFDDVRVETADGOLLTVIERPTIGSLNITGAKMLQNDALKNLESFGLAQSQ 122
DB 63 RSLFKTGFFQDIQLGRDGNLVTVVERPSISIEIEGNKAISKEDLLKGLKQSLAEGE 122

QY 123 YFQATLNQAVAGLKEYLGRGKLNIOITPKVTKLARNVDIIDITIDEGSAKITDIEFE 182
DB 123 IFQRATLEGVRNELQRYVAQGRYSABEAEVTPQPRNVALKININEGTVAISHINVV 182

QY 183 GNOVYSDRKLWQMSLTGEGGIWTLTSNQFNQKFAQDMKVTDFYQNNGYDFDRLDIT 242
DB 183 GNTVFESEDTIDFELKTTNWLSPFKNDDKYAREKJSGDLRLRSYYLDGRYINMDIAT 242

QY 243 DIQTNEDEKTKQTITKITVHEGGRFRWGVSTEGDTNEVPKAELEKLLTMKPKWYEQOMT 302
DB 243 QVSTTPDKKHVYITVNIENGEKTIIRDVKLTGDL-KVPEEEVKRLLLVQKGQVFSRKVMT 301

QY 303 AVLGEIQNRMSAGAYSEISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNKTRD 362
DB 302 TTSDLTIRRLNGEYTFANVNGVPEAHDDKTVSVTFVDPGKRAYVNRINFRGNTKTD 361

QY 363 EVVRRELROMESAPYDTSKLORSKERVLLGYFDNVQFADVLACIAPDKVDLWMSLTERS 422
DB 362 EVLRERKQMEGWASLYLIDQSKARLERLGYPKEVNVETPAVPGTDDQVDVNVSVEEQP 421

QY 423 TGSLLDSAGWVQDTGLVMSAGVQDNLFPGTGSAAALRASRKTTLNGSLSFDPYFTADG 482
DB 422 SGSITASVGAQAGNLLGSLISQNNFLGHNKVSIGLTRSEYQTRYNFGVDVYFVVDG 481

QY 483 VSLGYDVGKAFDPKRAKSTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542
DB 482 VSLGYNAPYRKTVDYDELDVDVASYSVNSLGAAGMSIGYPISETSLTYGLSVQRDQIDTGR 541

QY 543 KAPKHYADFIKKYKTKDGTGSGFKGWLKGTGVGRNKTDSALWPTRGYLTGVNAEIALP 602
DB 542 YTVDEIYDFLDKEG-----DNFTN--FKASIGWSESTLNKGLVATRGHSQSILTLETL 593

QY 603 GSKLQYYSATHNQTFPPLSKTFTLMLGGVGIAGGYGRKTEIPFEENFYGGGLGSRGY 662
DB 594 GSDLSFYKIDYRGQVAFPLTDNVTMRPHTELGYGDGYGSTGERLPFFYENYAGGFNSVRGF 653

QY 663 ESCTLGP-----KVVDEYGEKISYGNKKANVSALLPMP 698
DB 654 KDTLGRSTPSPVARNPDTGTPMKNQGPDSKGRYTDPDQDPEAFGGNILLITGGAEILLPLP 713
QY 699 GAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYGAGNTHKSTFTTNELYSAG 758
DB 714 FVKDQQLRTVLFWDVGS-----TFDTDCPTKTTTNCDDGIK-----TDNLASSVG 758
QY 759 GAVTWLSPLGPMKFRVAYPLKKPKPEDEIQRPQFOLGTTF 797
DB 759 VGLTWITALGPLSFSLATPIKKPDNAETQVFQPSLGQTF 797

Search completed: July 6, 2005, 15:18:02
Job time : 228.937 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:05:39 ; Search time 61.3077 Seconds
(without alignments)
970.438 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 4152

Sequence: 1 MKLKQIASALMMLGISPLAF.....LKKKPEDEIQRFQGLGTTF 797

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4152	100.0	797	4	US-09-594-192-4
2	3937.5	94.8	792	4	US-09-594-192-2
3	1286	31.0	821	4	US-09-252-991A-21013
4	1266.5	30.5	865	4	US-09-328-352-7498
5	1259	30.3	827	4	US-09-543-681A-6425
6	1213.5	29.2	815	4	US-09-489-039A-12469
7	1187.5	28.6	825	4	US-09-489-039A-8469
8	1136	27.4	797	3	US-08-433-522A-2
9	1136	27.4	797	3	US-08-433-522A-4
10	1136	27.4	797	3	US-08-433-522A-6
11	1136	27.4	797	3	US-09-135-166-2
12	1136	27.4	797	3	US-09-135-166-4
13	1136	27.4	797	3	US-09-135-166-6
14	1136	27.4	797	3	US-08-942-046-2
15	1136	27.4	797	3	US-08-942-046-4
16	1136	27.4	797	3	US-08-942-046-6
17	1114	26.8	793	3	US-08-433-522A-10
18	1114	26.8	793	3	US-09-135-166-10
19	1114	26.8	793	3	US-08-942-046-10
20	1112	26.8	813	4	US-09-540-236-3472
21	1109.5	26.7	792	3	US-08-433-522A-8
22	1109.5	26.7	792	3	US-09-135-166-8
23	1109.5	26.7	792	3	US-08-942-046-8
24	1109	26.7	813	4	US-09-701-711-2
25	1109	26.7	813	4	US-09-701-711-4
26	703	16.9	896	4	US-09-689-065B-5
27	454.5	10.9	795	4	US-09-198-452A-314

28	454.5	10.9	795	4	US-09-438-185A-302	Sequence 302, Appl
29	304.5	7.3	605	4	US-09-252-991A-31355	Sequence 31355, A
30	233	6.1	889	4	US-09-914-168-4	Sequence 4, Appli
31	253	6.1	919	4	US-09-914-168-2	Sequence 2, Appli
32	251	6.0	609	4	US-09-857-669-2	Sequence 2, Appli
33	251	6.0	609	4	US-09-857-669-4	Sequence 4, Appli
34	250	6.0	947	4	US-09-540-236-1991	Sequence 1991, Ap
35	237	5.7	587	4	US-09-857-669-6	Sequence 6, Appli
36	232.5	5.6	913	4	US-09-328-352-7024	Sequence 7024, Ap
37	221	5.3	586	4	US-09-489-039A-8950	Sequence 8950, Ap
38	194.5	4.7	583	4	US-09-543-681A-5823	Sequence 5823, Ap
39	184.5	4.4	759	4	US-09-252-991A-17841	Sequence 17841, A
40	161.5	3.9	447	4	US-09-902-540-9863	Sequence 9863, Ap
41	160.5	3.9	1220	4	US-09-206-942-28	Sequence 28, Appl
42	160.5	3.9	1226	4	US-09-206-942-26	Sequence 26, Appl
43	156	3.8	915	4	US-09-206-942-35	Sequence 35, Appl
44	156	3.8	1222	4	US-09-206-942-37	Sequence 37, Appl
45	156	3.8	1228	4	US-09-206-942-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1

US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UMS9C147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match	100.0%	Score 4152	DB 4	Length 797
Best Local Similarity	100.0%	Pred. No. 0		
Matches 797	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	MKLKQIASALMMLGISPLAFADFTTQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60	
DB	1	MKLKQIASALMMLGISPLAFADFTTQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60	
QY	61	ITKSIYATGFFDDVAVETADGQLLTIVTERTPGISNITGAKMLQNDATKKNLESFGLAQ	120	
DB	61	ITKSIYATGFFDDVAVETADGQLLTIVTERTPGISNITGAKMLQNDATKKNLESFGLAQ	120	
QY	121	SOYFNOATLNQAVAGLKEEYLGRGKLNQITPKVTKLARNRVDDITIDEGKSAKITDIE	180	
DB	121	SOYFNOATLNQAVAGLKEEYLGRGKLNQITPKVTKLARNRVDDITIDEGKSAKITDIE	180	
QY	181	PEGNOVYSRDKLMRQMSLTGGIWTLTRSNQFNQKFAQDMKEKVTDFYQNNGYDFRLL	240	
DB	181	PEGNOVYSRDKLMRQMSLTGGIWTLTRSNQFNQKFAQDMKEKVTDFYQNNGYDFRLL	240	
QY	241	DTDIOTNEDKTKQTKITITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPKGKMYEROQ	300	
DB	241	DTDIOTNEDKTKQTKITITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPKGKMYEROQ	300	
QY	301	MTAVLGEIQNRMGSAAGYAYSETSVOPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT	360	
DB	301	MTAVLGEIQNRMGSAAGYAYSETSVOPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT	360	

```
QY 361 RDEVVRRELQMESAPYDTSKLORSKERVVELLGYFDNVQFDVPLAGTDPKVDLNNLSL 420
Db 361 RDEVVRRELQMESAPYDTSKLORSKERVVELLGYFDNVQFDVPLAGTDPKVDLNNLSL 420
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480
Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480
QY 481 DGVSGLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPHYADFIKKYKGTGDTGDSFGKWLKGTGKSAALRASRSKTTLLNGSLSFDPYFTA 600
Db 541 YNKAPHYADFIKKYKGTGDTGDSFGKWLKGTGKSAALRASRSKTTLLNGSLSFDPYFTA 600
QY 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSR 660
Db 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABELLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABELLFPMGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFOQLGTTTF 797
Db 781 KPEDEIQRFOQLGTTTF 797

RESULT 2
US-09-994-192-2
; Sequence 2, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Manning, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2

Query Match 94.8%; Score 3937.5; DB 4; Length 792;
Best Local Similarity 95.1%; Pred. No. 0;
Matches 758; Conservative 16; Mismatches 18; Indels 5; Gaps 2;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFDVVRVETAGQILLTVIERPTTGLSNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDVVRVETAGQILLTVIERPTTGLSNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDIDEGKSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDIDEGKSAKITDIE 180
QY 181 PEGNQVTSRKLMRQMSLTGEGGIWTLTRSNQFNQEQFAQDMEKVTDFYQNGYFDFRIL 240
Db 181 PEGNQVTSRKLMRQMSLTGEGGIWTLTRSNQFNQEQFAQDMEKVTDFYQNGYFDFRIL 240
```

```
Db 181 PEGNQVTSRKLMRQMSLTGEGGIWTLTRSDRDPDROKFAQDMEKVTDFYQNGYFDFRIL 240
QY 241 DTDIQTNEDEKTKQTIKITVHEGGRFRWGVKSIEGDTNEVPKAELEKLLTMKPGKWYERQQ 300
Db 241 DTDIQTNEDEKTKQTIKITVHEGGRFRWGVKSIEGDTNEVPKAELEKLLTMKPGKWYERQQ 300
QY 301 MTAVLGEIQRNMGSAAGYAYSEISVQPLPNAETKTVDVFLHIHPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQRNMGSAAGYAYSEISVQPLPNAETKTVDVFLHIHPGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELQMESAPYDTSKLORSKERVVELLGYFDNVQFDVPLAGTDPKVDLNNLSL 420
Db 361 RDEVVRRELQMESAPYDTSKLORSKERVVELLGYFDNVQFDVPLAGTDPKVDLNNLSL 420
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480
Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480
QY 481 DGVSGLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPHYADFIKKYKGTGDTGDSFGKWLKGTGKSAALRASRSKTTLLNGSLSFDPYFTA 600
Db 541 YNKAPHYADFIKKYKGTGDTGDSFGKWLKGTGKSAALRASRSKTTLLNGSLSFDPYFTA 600
QY 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSR 660
Db 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABELLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABELLFPMGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGPMKFRYAYPLKK 780
Db 721 RTY----TAAENGNNKSVY-SENAHKSTFTNELRYSAGGAVTWLSPGPMKFRYAYPLKK 775
QY 781 KPEDEIQRFOQLGTTTF 797
Db 776 KPEDEIQRFOQLGTTTF 792

RESULT 3
US-09-252-991A-21013
; Sequence 21013, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21013
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21013

Query Match 31.0%; Score 1286; DB 4; Length 821;
Best Local Similarity 33.8%; Pred. No. 5.8e-100;
Matches 276; Conservative 157; Mismatches 335; Indels 48; Gaps 9;

QY 3 LKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAII 62
Db 33 LPALLSALM---IAEVHRESFTVSDIRVNGLQVRVSAGSVFAALPLNVGETIDDOALVQAT 89
```

63 KSLYATGFFDDVRVETADGOLLITVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQ 122
 90 RSLFKTGFFDQIOLGRDGNVLVTVVERPSISIEIGNKAIKSKEDLLKGLKQSLAGE 149
 123 YFNOATLNQAVAGKEBYLGRGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITDIEFE 182
 150 IFORATLEGRVNELOQYVAQGRYSABINAEVIPPQPNRVALKININEGTVAASHINVV 209
 183 GNOVYSRDKLMRQMSLTGEGITWLTSTNQNPFQAKMEKVTDFYQNNGYDFPRLIDT 242
 210 GNTVFSSEEDTJDFELTKTNWLSFFKNDNDKYAREKUGSGLRLRSYDLDGYINMDIAT 269
 243 DIOTNEDTKQTITITVHEGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPKWYERQOMT 302
 270 QVSTTPDKHVIYTVNINEGKTYIRDVKLTGDL-KYPEEVEVKRLILVQGVFSRKVMT 328
 303 AVIGEONRMSAGAYSEISVOPLPNAETKTVDVFLHIEPGRIKYVNEIHTGNKTRD 362
 329 TTSDLITRRLGNEGYPANVGVPEAHDDDKTYSVTFTVDPGKRAYVNRINFRGNTKTD 388
 363 EVVRRELROMESAPYDTSKLQSKERVELLGYPDNQDFDAPVPLAGTDPKVDLNMSLTERS 422
 389 EVLREROMEGGWASTYLLIDQSKARLERLGYFKEVNVETPAVPGTDDQVDVNVSVBEP 448
 423 TGSILDSAGWQDTGLVMSAGVSDNLFGRGKSAALRASRSKTTLNGSLSFDTDPYFTADG 482
 449 SCSITASVGAQAGNLLIGSISONNPLGTGNKVSIGLTRSEYQTRNFYFVDPYWTVDG 508
 483 VSLGVDYVYKAPPRKASTSIKQYTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542
 509 VSLGYNAPYKTDYDELDDVDVASVSNLSGAGMSIGYPISETSRLTYGLSVQRDDIDTGR 568
 543 KAPKHADFTKTKYKTDGTSFGKMYLKTGVWGRNKTDSALWPRGYLTGVNAELALP 602
 569 YTVDEIYDFLDKEG-----DNFTN--FRASIGWSESTLNGVLAIRGHSQSLETLTP 620
 603 GSKLOYVSAHNTQWFRPLSKTFTMLGGBVAGGYGRKTEIPFPENFYGGGLGSRGY 662
 621 GSDLSPKIDYRGQVAPLNDYNTMRHTELGYDGDGYSGERLFPFENYAGGFNSVRGF 680
 663 ESGTLGP-----KVY-----DEYG-----EKISYCGNKKANVSARELLFPMPGAK 701
 681 KDSITLGRSPSRAYKDGKIIIPGDERGRVTDPPDQDPEAFGGNILLITGGAEILLFPLFPVK 740
 702 DARTVRLSLFADAGSVWDGTYDDNSSATGGRVQNIYAGNTHKSTFTTNELRYSGAGV 761
 741 DQRLRLVLPWDVGS-----TFDTCPTKTTNCDGK-----TDNLASSVGVGL 785
 762 TWLSPLGPMKFRYAYPLKKPEDEIQRFQGLGTF 797
 786 TWITALGPLSFLATPIKPPDNPAETQVQFSLGQTF 821

RESULT 4
 US-09-328-352-7498
 ; Sequence 7498, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GFC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 7498
 ; LENGTH: 865
 ; TYPE: PRT
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-7498

Query Match 30.58; Score 1266.5; DB 4; Length 865;
 Best Local Similarity 33.74; Pred. No. 2.8e-98;

Matches 280; Conservative 153; Mismatches 329; Indels 69; Gaps 13;
 QY 22 DFTIQDIRVEGLQRTSPSTVFVNVLPVKVGDYNDTHGSAIKLSYATGFPDDVRVETADG 81
 Db 49 DFVVRDIHVNGVLRLTPANVYTWLPINSGDRVNEPMIAEIRTYLATGLFDDDLKASKEND 108
 QY 82 QALLTVIERPTTGLSLNITGAKMLQNDIAIKKNLESFGLAQSYQFNQATLNQAVAGLKEEYL 141
 Db 109 TLVFNVIERPIISLKEFPKGNKLLIPKEALSQGLKMGIAEVEFKKSALQTIETIEEQYT 168
 QY 142 GRGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITDIEFEGNQVYSDRKLMEQMSLTEG 201
 Db 169 QQGRYDADVTVDTPARPNRVELKINFNEGTAKVFDINVIGNTVFKDSIKQAFVAKES 228
 QY 202 GIWTLTRSNQFNEQFAQDMKVTDFYQNNGYDFRILDDTIDQTNEDTKQITIKITVHE 261
 Db 229 GWASVVRTRNDYAREKWAASLEALRAMYLKNGYINFNINNSQLNISEDKKHIEFVADVE 288
 QY 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKWYERQOMTAVLGEITQNRMGAGAYSE 321
 Db 289 GSQFKEGQTKFLGDALYKPE-ELQALKIYKDGDTYSQEKVNAVQKLLRLKYGNAGYFAD 347
 QY 322 ISVQPLPNAETKTVDVFLHIEPGRIKYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 381
 Db 348 VNIVPOINNETGVVDLNVYVNPQGVTVRRINFTGNSKTSDEVLRREMRQMEGALASNEK 407
 QY 382 LQBSKERVLLGYPDNQDFDAPVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 441
 Db 408 IDLSKVRLEBRTGFFKTVDIKPARIPNSPDQVDLNVNEEQHSGSTTLTLAGYSQSGITFQ 467
 QY 442 AGVSQDNLFCTGSAALRASRSKTTLNGSLSFDTDPYFTADGVSGLGDYDVYKAFDPRKAST 501
 Db 468 AGLSQNFMTGTRVVAIDLSRSETQDYNLVSVTDPTFTIDGVSRGVNY-----YRKTCL 522
 QY 502 ----SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADFI----- 552
 Db 523 NDDYNVNVVTSFSGSLSGFVPIDENQSLASVGVNDTKVTGTPVYSTVRYVLLANGG 582
 QY 553 KKYGKT-----DGTGSGFKW-----LYKGTVCGRNKTDSA 584
 Db 583 KATGKSWCPGSKNKTDPNTQOPIDPTCEGGEFDYNSAFEGEFTYNLNLGWSYNTLNR 642
 QY 585 LMPTRGYLGVNAEIALPGSKLOYYSATNQWFFPLSKT-FTMLMGEGVGIAGGYGRTK 643
 Db 643 IPTGSMHRVGLGLEIGLPGSDVDYQKTYDQTAFFPIGTGFLRGVGLK-----GYG--N 696
 QY 644 EIPFPENFYGGGLGSRVYESGTLGPK-----VYDEYGEKISYCGNKKANVSARELLF 695
 Db 697 DLFPYKFNFYAGGYGSRGYDNLGPKYASVNLQETKQNDGSPPEEVGNALVQFGLVL 756
 QY 696 PMPGAKD-ARTVRLSLFADAGSVWDGTYDDNSSATGGRVQNIYAGNTHKSTFTTNE-- 752
 Db 757 PMPFKGDWTRQVRPVLFAEGGQVDFTKCNIDN--SVYGNKGMKINGQITIDVRKYCEDNY 814
 QY 753 -----LRYSGAGVMTLSPGLGPMKFRYAYPLKKPEDEIQRFQGLGTF 797
 Db 815 GFDLGNLRYSVGVGTWITMIGLPLSYAPPLNDKPGDETKETQFIEGRTF 865

RESULT 5
 US-09-543-681A-6425
 ; Sequence 6425, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344

[illegible]

RESULT 6
US-09-489-039A-12469
; Sequence 12469, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al

RESULT 7
US-09-489-039A-8469
; Sequence 8469, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8469
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8469

Query Match 28.6%; Score 1187.5; DB 4; Length 825;
Best Local Similarity 33.3%; Pred. No. 1.3e-91;
Matches 276; Conservative 156; Mismatches 343; Indels 53; Gaps 15;

Qy 1 MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Db 20 LKTHIISGLLIAPLTLYAATSQVDDIRPEGLQRVTIGAILLSMPLHAGDVA TPEDVSE 79

Qy 61 IISLYATGFEVDVVRVETADQGLLTIVERTIGSLNITGAKMLQNDAILKNLESFGLAQ 120
Db 80 AVRALYASGNFENVQILRDGKTLVVQKERTIASVSFGNKAVKDALXENITASGISA 139

Qy 121 SQYFNQATLQAVAGLKEEYVGRKLNQITPKVTKLARNVDITIDEGSKAKITDIE 180
Db 140 GSALDRNLSIEIEKGLQDFYSACKYSAQVAVVTPIPRNRVDLTVPFQEGISAKIAQIN 199

Qy 181 FEGNQVYSDRKLMPQMSLTEGGITWITLRSNQFNEQKPAQMEKVDYFQNNGYFDFRIL 240
Db 200 IIGNQAFREETLLDQLRLDNVPMWNVVADKKYQKLEADLETLSFYLDRGVAREFAIE 259

Qy 241 DTDIQTNEKTKQIKITVHEGGRFRGKYSIEGDTNEVPKAELEKLTWKPKGWYERQ 300
Db 260 STQVSMTPDKSLYITLALNEGERYRVDRTQVTGDLAQ-HGPEIEALAQPLAGAWYSGAQ 318

Qy 301 MTAVLGIGNRMSGAGYAYSEISVOP-LPNAETKTVDFVLHIE--PGRKIYVNEIHITGN 357
Db 319 VTTVNEIKKHFGKYGAWPQVSTPEIDDAHRV---VLHIQVNGRRYSVRQIRFSGN 375

Qy 358 NKTRDEVVRRELQMSAPYDTSKLQSRKERVLLGYFDNVQFQDAVPLAGTPDKVDLNM 417
Db 376 DTSRDAVLRREMRQMEGAWLNNEKVDQKVLDRDTGFFENVEQQIVPVSGTADQVDVYVK 435

Qy 418 LTERSTGSLDSAGWODTGLMSAGVSDNLFTGKSAALRABRSKTTLNGSLSFDPDY 477
Db 436 VKERNTGSFNVGLGFGTDSGYSYQLGVTQDNWLGTGNSVSPNGTRNSYQSYLEIGATNP 495

Qy 478 FTADGVSIGVDVYKADPRKASTSIQYKTTTAGAGIRMSVPVTEYDRNFGVLAH-- 535
Db 496 FTVDGISLGGKIFNYSYDADADAG--SYNQSYGLGSTTGFPISENNSLNLDYVYHNR 553

Qy 536 -----LTNVTYNKAPKHYADFKIKYKTKGTGTDGS-FKGWLYKGTVGWGRNKDTSALWP 587
Db 554 LTNMDPELTWRYLSSRGIEPSVTK-----DGDGSAKYSANDYFASLGWNGVNDLDRGFFP 609

Qy 588 TRGYLTGVNABIALPGSKLOYSAATHNQTFWPLS--KTFTLMJGGVGIAGGYGRKTEI 645
Db 610 RAGNKSLSGKVTLPQSDNSYYKLSFDTAQYLPLSNKRNMWRERLRAVAGGLD-GKSV 668

Qy 646 PPFENFYGGGLGSRVGYESGTLPKV--YDEYGEKISY-----GKNKANVSA 691
Db 669 PFYDNFYAGGSSSVRGFSSNTIGPKAAYYRCNGSESSYACPLDASSDAVGGNAMAVALNS 728

Qy 692 ELLFPMPGAKD--ARTVRLSLFADAGSVMDKTYDDNSSSATGRRVQNIYAGNTHKSTF 749
Db 729 EFIIPTFPVNDKYADSLRSLTSLFVDAGTVMSTWHNTAQTLAAG-----IPDYGD----- 777

Qy 750 TNELRYSAGGAVTWLSPGLPMKFRYAYPLKKKPEDEIQRFQFQLGTTFF 797
Db 778 PSIRLSAGIAGVQWMSPLGLPLVFSWAEPPFKYDGDKAEOQFQFNIGKTW 825

RESULT 8
US-08-433-522A-2
; Sequence 2, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,522A
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-522A-2

Query Match 27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

Qy 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTVAAPFVAKDIRVDVGQDLEQQIRASLPVRAGORVTDNDVANI 60

Qy 62 IKSLYATGFPDDVVRVETADQGLLTIVERTIGSLNITGAKMLQNDAILKNLESFGLAQ 121
Db 61 VRSLSVSGRFDVKAHQEGDVLVSVVAKSIIISDVKIKGNSVITPEALKQNDLNGFKVG 120

Qy 122 QYFNQATLQAVAGLKEEYVGRKLNQITPKVTKLARNVDITIDEGSKAKITDIEF 181
Db 121 DVLIREKLNFAKSVKHEVASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF 180

Qy 182 EGNQVYSDRKLMPQMSLTEGGIW-TWLTNRNQFNEQKFAQMEKVDYFQNNGYFDFRIL 240
Db 181 KGNESVSSSTLQSQMELQPDSSWWKLM---GNKPEGAQFEKQDSIRDYILNNGYAKAQIT 237

RESULT 10
US-08-433-522A-6
; Sequence 6, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,522A
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-522A-6

Query Match 27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;
QY 3 LKQIAGALMLGISPLAF-ADFTIQRVEGLQRTPESTVFNPLPVKVGDTYNDTHGSAI 61
DB 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVGVQDLEQQIRASLPVRAGQRTDNDVANI 60
QY 62 IKSIXATGFDDVRVETADQQLLTWERTIGSLNITGAKMLQNDAIKNLESFGLAQS 121
DB 61 VRSLLFSGRFDVKAHQEGDVLVSVVAKSIIISDVKIKGNSVIPTKALQNDKANGFKVG 120
QY 122 QYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIITIDEKSKAKITDIEF 181
DB 121 DVLIRKLENEFAKSVKHYASVGRYATVPIVNTLPNNRAELIQINEDDKAKLASLTF 180
QY 182 EGNQVSDRKLMEQMSITGGI-WLTRSNQFNEQKFAQDMKVTDFYQNNQYDFRIL 240
DB 181 KGNESVSSSTLQEQMELQDSSWKLW---GNKFEQAQFEKDLQSIKDYLLNNGYAKAQIT 237
QY 241 DTDIOTNEDTKTQIKITVHEGGRFNGKYSISGDTNEVPKAELEKLT-MKECKWYERQ 299
DB 238 KTDVQLNDEKTKNVNITDVNNEGLQDLRSARIITGLGM-SAELEPLLSALHLNDFRS 296
QY 300 QMTAVLGEIQNRMSAGYAVSEISVQPLPNAETKTVDVLHIEPGRKIYNEITHGNK 359
DB 297 DIADVENAIKALGERGYGATVNSVPDFDDANKTLAITLVDAGRRLTVRQURFEGNTV 356

QY 360 TRDEVVRRELROMESAPYDTSKLQRKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLT 419
DB 357 SADTLRQEMRQOEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDEVDVYTKVK 416
QY 420 ERSTGSLDLSAGWVQDTGLVMSAGVQDNLFGTGKSAALRASRSKTTTLNGSLSTFDTPYFT 479
DB 417 ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAASVSTAGTKNDYGTSVNLGYTEPYFT 476
QY 480 ADGVSLGYDYGKAFDPRKASTSIKOKYKTTTAGAGIRMSVPTVEYDRVNFGLVAEHLTVN 539
DB 477 KDCVSLGNGVFFENYDNSKSDTS-SNYKRTTYGNSVTLGPPVNNENNSYYVGL-----GH 529
QY 540 TYNKAPKH-----YADFIKKYG--KTDGCTGSGFKGWLKGTVMGRNKTDSALMPT 588
DB 530 TYNKISNFALEYNRNLIQSMKFKNGIKTNDPFSF-----GWNYSNLRGYFT 580
QY 589 RGYLTGVNAEIALPGSKLOVYSATHNOTFFPLSKTFTLMLGGE--VGIAGGYGRTEIP 646
DB 581 KGVKASLGGRTVTPGSDNKYKLSADVQGFYPLDRDHLWVWSAKASAGYANGFG-NKRLP 639
QY 647 FFENFYGGGLSGVRGYESGTLGPK-VYDEYG-----EKIS---YGNKKANVSAELL 694
DB 640 FYOTYTAGGIGSLRGFAYGSGIPNAYIAYBYGNGSGGTGTFKIKISSDVIGGNAIATASAEI 699
QY 695 FPMF--GAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNI-----YGAGNTHK 746
DB 700 VPTFPVSDKSQNTVRTSLFVDAASVWNTKWSKDN-----GLESDDLKRLPDYK----- 749
QY 747 STFTNELRYSAGGAVTWLSPGLGPKRYAYPLKPKPEDEIQRFOFOLGTTFF 797
DB 750 ---SSRIRASTGVGFQWQSPFGLVPSYAKPIKKYENDVDEQFOFSIGSGF 797
RESULT 11
US-09-135-166-2
; Sequence 2, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-135-166-2

Query Match          27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

QY  3 LKQIASALMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAI 61
DB  1 MKKLLIASLLFGITTTVFAAPFVAKDIRVDVGQDLEQQIRASLPVRAGQRTDNDVANI 60

QY  62 IKSLEYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQS 121
DB  61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVIPTALKQNDANGFKVG 120

QY  122 QYFNQATLNOQAVAGLKEEYLGKGLNIQITPKVTKLARNVDIDITIDEGSKAKITDIEF 181
DB  121 DVLIREKLNFEAKSVKHYASVGRYNATVEPIVNTLPNNRAELIQINEDDKAKLASLTF 180

QY  182 EGNQVYSDRKLMRQMSLTGEGIW-TWLTRSNQFNEQKFAQDMKVTDFYQNNGYDFRIL 240
DB  181 KGNESVSSSTLQEQMELQPDSSWKLM--GNKPEGAQFEKDLQSIDRYLNNGYAKAQIT 237

QY  241 DTDIQTNEDKTKQTIKITVHEGGRFWKGVSIIGDNTNEVPKAELEKLLT-MKPGKMYERQ 299
DB  238 KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGGM-SAELEPLLSALHLNDTFRS 296

QY  300 QMTAVLGEIQNRMGSGAGYASEISVQPLPNAETKTVDVLHIEPGRKIYVNEIHTGNKK 359
DB  297 DIADVENAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQLRFEGNTV 356

QY  360 TRDEVVRRELQMESAPYDTSKLQRSKVERVELLGYFDNVQFADVPLAGTDPKVDLNNSLT 419
```

RESULT 12

US-09-135-166-4

; Sequence 4, Application US/09135166

; Patent No. 6083743

```
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS.jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-135-166-4

Query Match          27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

QY  3 LKQIASALMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAI 61
DB  1 MKKLLIASLLFGITTTVFAAPFVAKDIRVDVGQDLEQQIRASLPVRAGQRTDNDVANI 60

QY  62 IKSLEYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQS 121
DB  61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVIPTALKQNDANGFKVG 120

QY  122 QYFNQATLNOQAVAGLKEEYLGKGLNIQITPKVTKLARNVDIDITIDEGSKAKITDIEF 181
DB  121 DVLIREKLNFEAKSVKHYASVGRYNATVEPIVNTLPNNRAELIQINEDDKAKLASLTF 180

QY  182 EGNQVYSDRKLMRQMSLTGEGIW-TWLTRSNQFNEQKFAQDMKVTDFYQNNGYDFRIL 240
DB  181 KGNESVSSSTLQEQMELQPDSSWKLM--GNKPEGAQFEKDLQSIDRYLNNGYAKAQIT 237

QY  241 DTDIQTNEDKTKQTIKITVHEGGRFWKGVSIIGDNTNEVPKAELEKLLT-MKPGKMYERQ 299
DB  238 KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGGM-SAELEPLLSALHLNDTFRS 296

QY  300 QMTAVLGEIQNRMGSGAGYASEISVQPLPNAETKTVDVLHIEPGRKIYVNEIHTGNKK 359
DB  297 DIADVENAIKAKLGERGYGSATVNSVPDFDDANKTLAITLVVDAGRRLTVRQLRFEGNTV 356

QY  360 TRDEVVRRELQMESAPYDTSKLQRSKVERVELLGYFDNVQFADVPLAGTDPKVDLNNSLT 419
```

Db 357 SADSTLRQEMRQBGWYNSOLVELKIRLDRDGTGFETVENRDPINGSNDEVDVYKVK 416
Qy 420 ERSTGSLDLGAGWQDTGLVMSAGVSDNLFPGTKSAALRASRKTTLNGLSFTDPYFT 479
Db 417 ERNTGSIINFGIGYGTESGISYQASVKQDNFLGTGAASVIAAGTKNDYGTSLNGLVTEPYFT 476
Qy 480 ADGVSILGVDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVN 539
Db 477 KDGVSILGCVFFENYDMSKSDTS-SNYKRTYGSNVTGLGPPVNNNSYYVGL-----GH 529
Qy 540 TYNKAPKH-----YADFIKKYG---KTDGTDGSPKGLWLYKGTGWSGNKTKDSALWPT 588
Db 530 TYNKISNFALEYNRLYIOSMKPKNGIKTNDPFSF-----GWNYSNLNRGYFPT 580
Qy 589 RGYLTGVNAEIALPGSKLOYSATHNOTWFFPLSKTFTLMLGGE--VGIAGGYGRTKETIP 646
Db 581 KGVKASLGRVTPFGSDNKYKLSADVQGFYPLDRDLHWVSASAKAGYANGFG-NKRLP 639
Qy 647 PFENFYGGGLSGVRGYESGTLGPK-VYDEYG-----EKIS---YGGNKKANVSAELL 694
Db 640 FYQTYTAGGIGSLRGFAYSIGNNAIYAEYGNNGSGTGTFTPKISSDVIGGNAIATASAEI 699
Qy 695 FPMF--GAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVONI-----YGAGNTHK 746
Db 700 VPTPFVSDKSQNTVRTSLFVDAASVWNTKWSKDN-----GLESVULKRLPDYK 749
Qy 747 STFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKKKPEDEIQRFOFOLGTTFF 797
Db 750 ---SSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYENDDDVEQFQSIGGSF 797

RESULT 13

US-09-135-166-6
; Sequence 6, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-135-166-6

Query Match 27.4%; Score 1136; DB 3; Length 797;

Best Local Similarity 31.8%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

Qy 3 LKQIASALMMLGISPLAF-ADFTIQIRVEGLQRTPEPSTVFNYLPVKVGDTYNDTHGSAI 61
Db 1 MKKLLTASLLFGTTTVPAPFVAKDIRVDGVQGDLEQQIRASLPVRAGORVTDNVANI 60
Qy 62 IKSLYATGTFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLSFGLAQS 121
Db 61 VRSLPVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVIPTKALQNLDANGFKVG 120
Qy 122 QYFNQATINQAVAGLKEEYVLRGKLNIOITPKYTKLARNRVIDIITIDEGSKAKITDIEF 181
Db 121 DVLIRREKLNPEAKSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKASLT 180
Qy 182 EGNQVYSDRKLKRMQSLTEGGIW-TWLTRSNQFNEQKFAQDMKVKTDYFONNGYFDFRIL 240
Db 181 KGNESVSSSTLQEQMELQPDSSWKLW---GNKPEGAQFQKQSDIRDYILNNYAKAQIT 237
Qy 241 DTDIQTNEDKTKQTIKITVHEGGRFRWGVKVSIEGDTNEVPKAELEKLT-MKPGKWYERQ 299
Db 238 KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGM-SAELEPLLSALHLNDFRRS 296
Qy 300 QMTAVLGEITONRMSAGYAYSEISVQPLNPAETKTVDFVHLIEHPGRKIYNEIHIITGNK 359
Db 297 DIADVENAIAKALGERGYGSATVNSVPDFDDANKTLAITLVWDAGRRLTVROLRFEGTV 356
Qy 360 TRDEVVRRELROMESAPYDTSKLQSKERVELLGYEDNVQDFDAVPLAGTPDKVDLMSLT 419
Db 357 SADSTLRQEMRQBGWYNSOLVELKIRLDRDGTGFETVENRDPINGSNDEVDVYKVK 416
Qy 420 ERSTGSLDLGAGWQDTGLVMSAGVSDNLFPGTKSAALRASRKTTLNGLSFTDPYFT 479
Db 417 ERNTGSIINFGIGYGTESGISYQASVKQDNFLGTGAASVIAAGTKNDYGTSLNGLVTEPYFT 476
Qy 480 ADGVSILGVDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVN 539
Db 477 KDGVSILGCVFFENYDMSKSDTS-SNYKRTYGSNVTGLGPPVNNNSYYVGL-----GH 529
Qy 540 TYNKAPKH-----YADFIKKYG---KTDGTDGSPKGLWLYKGTGWSGNKTKDSALWPT 588
Db 530 TYNKISNFALEYNRLYIOSMKPKNGIKTNDPFSF-----GWNYSNLNRGYFPT 580
Qy 589 RGYLTGVNAEIALPGSKLOYSATHNOTWFFPLSKTFTLMLGGE--VGIAGGYGRTKETIP 646
Db 581 KGVKASLGRVTPFGSDNKYKLSADVQGFYPLDRDLHWVSASAKAGYANGFG-NKRLP 639
Qy 647 PFENFYGGGLSGVRGYESGTLGPK-VYDEYG-----EKIS---YGGNKKANVSAELL 694
Db 640 FYQTYTAGGIGSLRGFAYSIGNNAIYAEYGNNGSGTGTFTPKISSDVIGGNAIATASAEI 699
Qy 695 FPMF--GAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVONI-----YGAGNTHK 746
Db 700 VPTPFVSDKSQNTVRTSLFVDAASVWNTKWSKDN-----GLESVULKRLPDYK 749
Qy 747 STFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKKKPEDEIQRFOFOLGTTFF 797
Db 750 ---SSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYENDDDVEQFQSIGGSF 797

RESULT 14

US-08-942-046-2
; Sequence 2, Application US/08942046
; Patent No. 6284954
; GENERAL INFORMATION:

APPLICANT: CHONG, Pele
 APPLICANT: THOMAS, Wayne
 APPLICANT: YANG, Yan Ping
 APPLICANT: LOOSMORE, Sheena
 APPLICANT: SIA, Dwo Yuan Charles
 APPLICANT: KLEIN, Michel
 TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
 NUMBER OF SEQUENCES: 55
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sim & McBurney
 STREET: 6TH Floor, 330 University Avenue
 CITY: Toronto
 STATE: Ontario
 COUNTRY: Canada
 ZIP: M5G 1R7
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/942,046
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/433,522
 FILING DATE: 12-SEP-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: STEWART, Michael I
 REGISTRATION NUMBER: 24,973
 REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (416) 595-1155
 TELEFAX: (416) 595-1163
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 797 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-942-046-2

Query Match 27.4%; Score 1136; DB 3; Length 797;
 Best Local Similarity 31.6%; Pred. No. 2.9e-87;
 Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

QY	3	LKQIASALMMLGISPLAF-ADTIQDIRVEGLQRTSTPVNLYPVKVGDTYNDTHGSAI	61
DB	1	MKKLLIASLFLGTTTTFVFAAPFAVKDIRVDGVQGDLEQIRASLPVAGQRTVDNVANI	60
QY	62	IKSLVATGFDDVRVETADGQLLTIVERTPTIGSLNITGAKMLQNDALIKNLESFGLAQS	121
DB	61	VRSFLVSGRFDFFDKAHQEGDVLVSVVAKSIISDVKIKGNSVITPEALUKQNDANGFKVG	120
QY	122	QYFNQATLNQAVAGLKEEYLGKGLNIQITTPKVTKLARNRVDIDITIDEGKSAKITDIEF	181
DB	121	DVLIREKLNFEAKSVKEHVASVGRYNATVEPIVNTLPNNRAEILQINEDDKAKLASITF	180
QY	182	EGNQVYSDBKLWRMSLTGEGTW-TWLTFSQNFQKFAQMEKVTDFYQNNQYDFDFRIL	240
DB	181	KGNESVSSSTLQEQBELQDPSWKLW--GNKFEQAQPEKQLQSDIRDYLLNNGYAKAQIT	237
QY	241	DTDIDQNEKTKOTIKITVHEGGRFRWGKVSLEGDTNEVPKAELEKILT-MKPGKWYERQ	299
DB	238	KTDVQNDSEKTKVNTVDVNEGQVLDLSARIIGNLGM-SAELEPLLSALHNDTPFRS	296
QY	300	QMTAVLGETQNRMGSGAYSEISVQPLPNAETKTVDVFLHTEPGRKTYVNEIHTGNKK	359
DB	297	DIADVENAIKALGERGYGSATVNSVPDPPDDANKLTAITLVVDAGRLTVQLRFEQNTV	356
QY	360	TRDEVVRELQWESAPYDTSKLRQSKRVELLGVFDNVQFDPVPLAGTPDKVDLNMSLT	419

357 SADSTLRQEMRQOEGTWYNSQLVELGKIRLDRTGTFETVENRIDPINGSNDEVDVVYKVK 411
 420 ERSTGSLDLSAGWVQDTGLVMSAGVQDNLFCTGKSAALRASRSKTTLLNGSLSTDPYFT 479
 417 ERNTGSIINFIGVGTESGISYQASVKQDNFLGTGAASVLAGTKNDYGTGVNLTGYTEPYFT 476
 480 ADGVSIGVDYVKAFDPKRASTSIKQYKTTTATAGIRMSVPVTEYDRVNFVGLVAHSLTW 539
 477 KCGVSLGNGVFPFENYDNSKSDTS-SNYKRTTYGSSNVTLGFPVNENNSYYVGL-----GH 529
 540 TYNKAPEK-----YADFIKKYG---KTGCTGDSFGKWLKYGTVGGRNKTDSALWPT 588
 530 TYNKISNFALEYNRNLYIOSMKPKNGIKINDPDSF-----GWNYSNLNRGYEPT 580
 589 RGYLTGVNAEIALPGSKLOYYSATHNQTFWFFPLSKTFTIMLGE--VGIAGGYGRTKEIP 646
 581 KGVKASLGGRTVTPGSDNKYKLSADVQGVFELDRDLWVWSAKASAGVANGFG-NKRLP 639
 647 FFENFYGGGLGSGVRGYESGTLPK-VYDEYG-----EKIS-----YGNKKANVSARELL 694
 640 FYQTYTAGGIGSLRGFPAYGSGIGNAIYAEYGNCGSGTGTGPKIISDVIGGNATATASAEII 699
 695 FPMF--GAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNI-----YGAGNTHK 746
 700 VPTPFVSDKSQNTVTSLEFVDAASVNTKWKSDKN-----GLESVLRKLDPYK----- 749
 747 STFTNELRYSAGGAVTWLSPGLGPMKFRYAYPLKPKPEDEIQRFQFQLGTTF 797
 750 ---SSIRASTGVGFQWQSPIGPLVFSYAKPIKKYENDDDVEQFQSIGGSF 797

RESULT 15
 US-08-942-046-4
 ; Sequence 4, Application US/08942046
 ; Patent No. 6264954
 ; GENERAL INFORMATION:
 ; APPLICANT: CHONG, Pele
 ; APPLICANT: THOMAS, Wayne
 ; APPLICANT: YANG, Yan Ping
 ; APPLICANT: LOOSMORE, Sheena
 ; APPLICANT: SIA, Dwo Yuan Charles
 ; APPLICANT: KLEIN, Michel
 ; APPLICANT: STEWART, Michael I
 ; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
 ; NUMBER OF SEQUENCES: 55
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sim & McBurney
 ; STREET: 6TH Floor, 330 University Avenue
 ; CITY: Toronto
 ; STATE: Ontario
 ; COUNTRY: Canada
 ; ZIP: M5G 1R7
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/942,046
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/433,522
 ; FILING DATE: 12-SEP-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: STEWART, Michael I
 ; REGISTRATION NUMBER: 24,973
 ; REFERENCE/DOCKET NUMBER: 1038-732 MIS:jb
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (416) 595-1155
 ; TELEFAX: (416) 595-1163
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 797 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-942-046-2

```
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-942-046-4

Query Match      27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

Qy 3 LKQIASALMMIGISPLAF-ADFTIQDIRVEGLQRTPESTVENYLPVKVGDYTNTHGSAI 61
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MKLLIASLLFGTTTTFVFAAPFAVDKIRVQGVQGDLEQOIRASLPVRAGQRTDNDVANI 60
Qy 62 IKSIIYATGFFDDVRVETADGQGLLLTVTERPTIGSINITGAKMLQNDAIKNLESFGLAQ 121
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 VRSLSVSGRFDVQAHQEGDVLVSVVAKSIIISDKIKGNSVIPTKALKQNLDFANGFKVG 120
Qy 122 QYFNOATLNOAVAGLKEEYLRGKLNQITPKVTKLARNRVDIDITIDEGSKAKITDIEF 181
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 DVLIREKLNPAKSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF 180
Qy 182 EGNQVYSRDKLMRQMSLTEGGIM-TWLTNRNQFNEQKFAQDMKVTDFYQNNGYDFEPRIL 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 KGNESVSSSTIQEQMELQPDSSWKLW---GNKFEQAQPEKDLQSIQIRDYLLNNGYAKAQIT 237
Qy 241 DTDIQTNEDKTKQIKITVHEGGRFRGKVSIEGDTNEVPKAELEKULT-MKPGKWYERQ 299
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
238 KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGM-SAELEPLLSALHLNDTPRRS 296
Qy 300 QMTAVLGEIQNRMSAGVAYSEISVQPLPNAETKTVDVLHIEPRKIYVNEIHTGNK 359
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
297 DIADVENAIKAKLGERGYGSATVNSVDFDANKTLAITLVVDAGRRLTVRQLRFEQNTV 356
Qy 360 TRDEVWRRELKQMSAPDYTSKQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNMSLT 419
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
357 SADSTLREQEWRQEGTWNSQVLSQVGLKIRLDRTOFFETVENRIDPINGSNDEVVVYKVK 416
Qy 420 ERSTGSLDLGAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLNGSLSTDPYFT 479
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
417 ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAASVSIAGTKNDYGTSVNLGYTEPYFT 476
Qy 480 ADGVSIGYDVYKGFDPKASTSIKQYKTTAGAGIRMSVPVTEYDRNFGLVAEHLTVN 539
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
477 KDGVSIGGNVFFENYDMSKSDTS-SNYKRTTYGSNVTLGFPVNNNSYYVGL-----GH 529
Qy 540 TYNKAPKH-----YADFIKKYG---KTDGTDGSPFGKMLYKGTGVMGRNKTDSALWPT 588
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
530 TYNKISNFALEYNRNLVIQSMKFGKNGIKINDPFSF-----GWNYSNLNRGYFPT 580
Qy 589 RGYLTGVNABIALPGSKLOYSATHNQTFWFPPLSKTFTLMIGGE--VGIAGGYGRTKEIP 646
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
581 KGVKASLGGRTVTFGSDNKYKLSADYQGFYPLDRDLWVVSASAKASAGYANGFG-NKRLP 639
Qy 647 PFENFYGGGLGSRVGYESGTLGPK-VYDEYG-----EKIS---YGGNKKANVSALL 694
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
640 FYQTYTAGGIGSLRGFAFGYGNPAIYAEYGNSGSGTGTFFKKISSDVIQGNALATASAEI 699
Qy 695 FPMF--GAKDARTVRLSIFADAGSVWDGKTYDDNSSSATGGRVQNI-----YGAGNTHK 746
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
700 VPTPFVSDKQNTVRTSLFVDAASVWNKWKSDKN-----GLESDELRLPDYDK----- 749
Qy 747 STFTNELRYSGAGAVTWLSPLGPMKFRYAVPLKKKPEDEIQRFOQLGTTTF 797
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
750 ---SSRIRASTGCGFQWSPGPIGLVFSYAKPIKKYENDVDEQFQFSIGGSF 797
```

Search completed: July 6, 2005, 15:20:39
Job time : 68.3077 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:53:24 ; Search time 235.676 Seconds
(without alignments)
1307.930 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 4152

Sequence: 1 MKLKQIASALMMLGISLAP.....LKKKPEDEIQRFOQLGTTTF 797

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Geneseqp16Dec04:*
- 2: Geneseqp1980s:*
- 3: Geneseqp1990s:*
- 4: Geneseqp2000s:*
- 5: Geneseqp2001s:*
- 6: Geneseqp2002s:*
- 7: Geneseqp2003as:*
- 8: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4152	100.0	797	3	AAy84947 Amino aci
2	4152	100.0	797	5	ABb79802 Neisseria
3	4140	99.7	797	4	AAu03957 Neisseria
4	4140	99.7	797	4	AAb23784 Neisseria
5	4140	99.7	797	4	AAb84744 Amino aci
6	4136	99.6	797	4	AAu03959 Neisseria
7	4136	99.6	797	4	AAu04451 Neisseria
8	4136	99.6	797	4	AAb23788 Neisseria
9	4136	99.6	797	4	AAb84746 Amino aci
10	3956.5	95.3	792	4	AAu03958 Neisseria
11	3956.5	95.3	792	4	AAb23786 Neisseria
12	3956.5	95.3	792	4	AAb84745 Amino aci
13	3956.5	95.3	792	6	ABP80499 N. gonorr
14	3956.5	95.3	792	6	ABP79748 N. gonorr
15	3937.5	94.8	792	3	AAy84946 Amino aci
16	3937.5	94.8	792	5	ABg91064 Neisseria
17	3937.5	94.8	792	5	ABb79801 Neisseria
18	1286.5	31.0	821	7	ABO72267 Pseudomon
19	1266.5	30.5	865	6	ADA36211 Acinetoba
20	1259	30.3	827	7	ADF06140 Bacterial
21	1240	29.9	798	6	ABm67563 Phototrab
22	1213.5	29.2	815	7	ABO65952 Klebsiell
23	1187.5	28.6	825	7	ABO61952 Klebsiell
24	1136	27.4	797	2	AAr53755 H. influe
25	1134	27.3	797	2	AAr53756 H. influe

26	1131	27.2	797	2	AAr53754 H. influe
27	1114	26.8	793	2	AAr53758 H. influe
28	1112	26.8	813	8	ADL05786 M. catarr
29	1109.5	26.7	792	2	AAr53757 H. influe
30	1109	26.7	813	3	AAy44390 M. catarr
31	1109	26.7	813	3	AAy44391 M. catarr
32	990.5	23.9	792	8	ADH12911 Francisel
33	870.5	21.0	639	4	ABG17654 Novel hum
34	703	16.9	896	4	AAg78603 Lawsonia
35	703	16.9	896	6	ABU92009 Omp100 po
36	703	16.9	896	7	ADG33885 L. intrac
37	703	16.9	896	7	ADJ66790 Lawsonia
38	703	16.9	896	8	ADR72942 Lawsonia
39	533	12.8	916	4	ABa46311 H. pylori
40	532	12.8	847	2	AAW71477 Helicobac
41	526	12.7	925	2	AAW55729 H. pylori
42	526	12.7	925	2	AAy17183 H. pylori
43	454.5	10.9	795	2	AAy34896 Chlamydia
44	453	10.9	706	5	ABU51298 Helicobac
45	452.5	10.9	790	5	ABb90599 Chlamydia

ALIGNMENTS

RESULT 1
AAy84947
ID AAy84947 standard; protein; 797 AA.
XX
AC AAy84947;
XX
DT 21-AUG-2000 (first entry)
XX
DB Amino acid sequence of outer membrane protein (omp) 85.
XX
KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
KW meningococcal infection; protective immune response; vaccine.
XX
OS Neisseria meningitidis.
XX
PN WO200023595-A1.
XX
PD 27-APR-2000.
XX
PF 22-OCT-1998; 98WO-US022352.
XX
PR 22-OCT-1998; 98WO-US022352.
XX
(UYMO-) UNIV MONTANA.
PA Judd RC, Manning SD;
XX
DR WPI; 2000-339694/29.
DR N-PSDB; AAA15156.
XX
PT New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
PT meningitidis useful for vaccine, therapeutic and diagnostic compositions
PT for gonococcal or meningococcal infections.
PS Claim 41; Page 89-92; 98pp; English.
XX
CC The present sequence represents an outer membrane protein (omp) 85 of
CC Neisseria meningitidis. The omp polypeptides and polynucleotides are
CC useful in compositions for use in the prevention, treatment and diagnosis
CC of non-symptomatic gonococcal infection or meningococcal infection and
CC symptomatic disease. They are also useful for the detection of
CC hybridisation complexes. Antigens and antibodies specific omp proteins
CC also provide diagnostic, therapeutic and prophylactic compositions for
CC the treatment or prevention of the infections described above. The
CC antibodies are useful for inducing a protective immune response in humans
CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC species. The proteins, antibodies and polynucleotide sequences of the
CC present invention may also be used in the screening and development of

CC chemical compounds such as drugs or vaccines

XX Sequence 797 AA;

Query Match 100.0%; Score 4152; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 9e-281;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SOYFNOATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Qy 181 FEGNQVYSRDKLRQMSLTGGIWTWLTTRSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Db 181 FEGNQVYSRDKLRQMSLTGGIWTWLTTRSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Qy 241 DTDIQTNEDKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
Db 241 DTDIQTNEDKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
Qy 301 MTAVLGSIONRMSGAGYAYSEISVQIPNAETKTVDVFLHIEPRKLYVNEIHTGNKKT 360
Db 301 MTAVLGSIONRMSGAGYAYSEISVQIPNAETKTVDVFLHIEPRKLYVNEIHTGNKKT 360
Qy 361 RDEVVRRELROMESAPYDTSKLORSKERVVELLGYFDNVQFDPVPLAGTDPKVDLNLMLTE 420
Db 361 RDEVVRRELROMESAPYDTSKLORSKERVVELLGYFDNVQFDPVPLAGTDPKVDLNLMLTE 420
Qy 421 RSTGSLDLGAGWQDTGLVMSAGVSDNLFQGTGKSAALRASRKTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDLGAGWQDTGLVMSAGVSDNLFQGTGKSAALRASRKTTLNGSLSFDPYFTA 480
Qy 481 DGVSGLGYDVYKAFDPKASTSIKOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAFDPKASTSIKOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHAYDFIKYKGTGDTGDSFGKWLKGTGWRNKTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHAYDFIKYKGTGDTGDSFGKWLKGTGWRNKTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPSGKLOYSATHNQTWFFPLSKTFTLMLGGEVGIAGGYGRTKIIPPFFENFYGGGLGSVR 660
Db 601 LPSGKLOYSATHNQTWFFPLSKTFTLMLGGEVGIAGGYGRTKIIPPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFQGLGTTTF 797
Db 781 KPEDEIQRFQGLGTTTF 797

RESULT 2

ID ABB79802

XX ABB79802 standard; protein; 797 AA.

XX AC ABB79802;

XX 15-NOV-2002 (first entry)

DT 15-NOV-2002 (first entry)

XX 15-NOV-2002 (first entry)

DE Neisseria meningitidis outer membrane protein Omp85.
XX Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
KW antibacterial.
XX Neisseria meningitidis.

OS Neisseria meningitidis.
XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= signal_peptide
FT Protein 22..797
FT /label= Mature_protein

XX US2002086028-A1.

XX 04-JUL-2002.

XX 26-NOV-2001; 2001US-00994192.

XX 22-OCT-1998; 98US-00177039.

XX (JUDD/) JUDD R C.

XX (MANN/) MANNING D S.

XX Judd RC, Manning DS;

XX WPI; 2002-642234/69.

XX Novel immunogenic composition for vaccinating against meningococcal or gonococcal infection, comprises Omp85 protein of Neisseria meningitidis or Neisseria gonorrhoeae, or nucleic acid encoding the protein.

XX Claim 13; Fig 5; 30pp; English.

XX The present sequence is that of the Neisseria meningitidis strain HH outer membrane protein 85 (Omp85), as predicted from a gene that was obtained from a genomic DNA by PCR amplification using primers based on the gonococcal omp85 gene. The meningococcal Omp85 protein is 95% identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed immunogenic compositions comprise N. meningitidis Omp85, its fragments, fusion proteins including the Omp85, or nucleic acids encoding them, which induce a protective immune response in a subject. The immunogenic compositions may also include an antigen from a heterologous or homologous pathogen, or a nucleic acid encoding it. They are used in a claimed method of vaccinating a human or animal against non-symptomatic meningococcal infection or symptomatic disease. A kit for diagnosing infection with N. meningitidis comprising labelled Omp85 is also claimed. The Omp85 polypeptides and polynucleotides are also useful in drug screening and development

XX Sequence 797 AA;

Query Match 100.0%; Score 4152; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 9e-281;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SOYFNOATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Qy 181 FEGNQVYSRDKLRQMSLTGGIWTWLTTRSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Db 181 FEGNQVYSRDKLRQMSLTGGIWTWLTTRSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Qy 241 DTDIQTNEDKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300

Db 241 DTDIQTNEDEKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQ 300
Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLVHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLVHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFDPVAVPLAGTDPKVDLNNLSL 420
Db 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFDPVAVPLAGTDPKVDLNNLSL 420
Qy 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
Db 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
Qy 481 DGVSGLGYDVGKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVGKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHVADFIKKYKGTGDSGFKGWLKGTGWRGNKTTDSALWPTRGVLTGVNAEIA 600
Db 541 YNKAPKHVADFIKKYKGTGDSGFKGWLKGTGWRGNKTTDSALWPTRGVLTGVNAEIA 600
Qy 601 LPSGKLOYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
Db 601 LPSGKLOYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDYGKISYGGNKKANVASALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDYGKISYGGNKKANVASALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGVQVNIYAGANTHKTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGVQVNIYAGANTHKTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFQGLGTTFF 797
Db 781 KPEDEIQRFQGLGTTFF 797

RESULT 3
AAU03957
ID AAU03957 standard; protein; 797 AA.
AC AAU03957;
AC AAU03957;
XX 23-OCT-2001 (first entry)
DT
DE Neisseria meningitidis serogroup B antigenic protein.
DE Serogroup B antigen; pharynx; meningitis; septicemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.
XX Neisseria meningitidis.
OS
FH Key Location/Qualifiers
FT Peptide 1..221
FT Protein /note= "Signal peptide"
FT Protein 22..797
FT Binding-site /note= "Mature N. meningitidis serogroup B antigen"
FT Binding-site 715..722
FT Binding-site /note= "ATP/GTP-binding site motif A (P-loop)"
XX W0200138350-A2.
PN 31-MAY-2001.
XX 28-NOV-2000; 2000WO-IB001851.
XX 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX (CHIR-) CHIRON SPA.
PA

PA (STAT-) STATENS INST FOLKEHELSE.
XX Giuliani MM, Pizsa M, Rappuoli R, Holst J;
XX WPI; 2001-381289/40.
DR N-PSDE; AAS07277.
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX Claim 1; Fig 1; 92pp; English.
XX The sequence represents a Neisseria meningitidis serogroup B 85 kDa
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicemia in the absence of meningitis.
CC This antigenic protein is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast
XX
SQ Sequence 797 AA;

Query Match 99.7%; Score 4140; DB 4; Length 797;
Best Local Similarity 99.7%; Pred. No. 6.2e-280;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFVPLVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFVPLVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNOAVAGLKEEYGRGKLNIIQITPKVTKLARNRVDIITIDEGSKAKITDIE 180
Db 121 SQYFNQATLNOAVAGLKEEYGRGKLNIIQITPKVTKLARNRVDIITIDEGSKAKITDIE 180
Qy 181 FEGNQVYSRKLQRQMSLTEGGIWTWLTNSQNFQEQFADMEKVTDFYQNGYFDFRIL 240
Db 181 FEGNQVYSRKLQRQMSLTEGGIWTWLTNSQNFQEQFADMEKVTDFYQNGYFDFRIL 240
Qy 241 DTDIQTNEDEKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQ 300
Db 241 DTDIQTNEDEKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQ 300
Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLVHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLVHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFDPVAVPLAGTDPKVDLNNLSL 420
Db 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFDPVAVPLAGTDPKVDLNNLSL 420
Qy 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
Db 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
Qy 481 DGVSGLGYDVGKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVGKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHVADFIKKYKGTGDSGFKGWLKGTGWRGNKTTDSALWPTRGVLTGVNAEIA 600
Db 541 YNKAPKHVADFIKKYKGTGDSGFKGWLKGTGWRGNKTTDSALWPTRGVLTGVNAEIA 600
Qy 601 LPSGKLOYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660

Db 601 LPGSKLOYYSATHNQTFWFFPLSKTFTTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Qy 781 KPEDEIORFQFOLGTTTF 797
Db 781 KPEDEIORFQFOLGTTTF 797
RESULT 4
AAB23784
ID AAB23784 standard; protein; 797 AA.
XX AAB23784;
XX 12-JAN-2001 (first entry)
DT 12-JAN-2001 (first entry)
XX Neisseria meningitidis serogroup B amino acid sequence.
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX Neisseria meningitidis.
OS Neisseria meningitidis.
XX WO200050075-A2.
XX 31-AUG-2000.
XX 09-FEB-2000; 2000WO-IB000176.
XX 26-FEB-1999; 99US-0121792P.
XX (CHIR-) CHIRON SPA.
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX WPI; 2001-015529/02.
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX Claim 22; Page 32; 39pp; English.
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup B amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention
XX
XX Sequence 797 AA;
Query Match 99.7%; Score 4140; DB 4; Length 797;
Best Local Similarity 99.7%; Pred. No. 6.2e-280;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAPADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLVIERPTTIGSLNITGAKMLQNDALIKONLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLVIERPTTIGSLNITGAKMLQNDALIKONLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLRGKLNITQTPKVTYKLARNRVDITIDITDEGSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLRGKLNITQTPKVTYKLARNRVDITIDITDEGSAKITDIE 180
Qy 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLRNSQNEQKFAQDMKVTDFYQNNYGFDFRIL 240
Db 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLRNSQNEQKFAQDMKVTDFYQNNYGFDFRIL 240
Qy 241 DTDIOTNEDKTQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQ 300
Db 241 DTDIOTNEDKTQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQ 300
Qy 301 MTAVLGEIQNRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
Db 301 MTAVLGEIQNRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
Qy 361 RDEVVRRELQWESAPYDTSKLQSRKERVLLGYFDNVQFDVAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQWESAPYDTSKLQSRKERVLLGYFDNVQFDVAVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGSLSTDPDYFTA 480
Db 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGSLSTDPDYFTA 480
Qy 481 DGVS LGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVS LGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPHYADFIKKYKTDGTGSGFKGMYLYKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPHYADFIKKYKTDGTGSGFKGMYLYKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPGSKLOYYSATHNQTFWFFPLSKTFTTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQTFWFFPLSKTFTTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Qy 781 KPEDEIORFQFOLGTTTF 797
Db 781 KPEDEIORFQFOLGTTTF 797
RESULT 5
AAB84744
ID AAB84744 standard; protein; 797 AA.
XX AAB84744;
XX 17-SEP-2001 (first entry)
DT 17-SEP-2001 (first entry)
XX Amino acid sequence of a Neisseria serogroup B protein.
XX Serogroup B protein; outer membrane protein; Neisserial infection;
KW vaccine.
XX Neisseria meningitidis.
XX Key Location/Qualifiers
FH

FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
XX /note= "mature protein"
FN WO200152885-A1.
XX
XX 26-JUL-2001.
XX
XX 17-JAN-2001; 2001WO-IB000166.
XX
XX 17-JAN-2000; 2000GB-00001067.
PR 09-MAR-2000; 2000GB-00005699.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Pizza M, Rappuoli R, Giuliani M;
XX
XX WPI; 2001-451895/48.
DR N-PSDB; AAH42128.
XX
XX Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisseria bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX
XX Disclosure; Page 59-61; 83pp; English.
XX
XX The present sequence represents a Neisseria serogroup B protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria; a diagnostic reagent for detecting the presence of Neisseria
CC bacteria or of antibodies raised against Neisseria bacteria; and/or a
CC reagent which can raise antibodies against Neisseria bacteria. It may
CC also be used as a vaccine
XX
XX Sequence 797 AA;
XX
XX Query Match 99.7%; Score 4140; DB 4; Length 797;
XX Best Local Similarity 99.7%; Pred. No. 6.2e-280;
XX Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLQIASALMLGLGISPLAFADFTIQDIRVEGLQRTPESTVFNLPVKVGTNDTHGSA 60
DB 1 MKLQIASALMLGLGISPLAFADFTIQDIRVEGLQRTPESTVFNLPVKVGTNDTHGSA 60
QY 61 IISLYATGFFDDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLSEFGLAQ 120
DB 61 IISLYATGFFDDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLSEFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEHLGRKLNQITPQVTKLARNRVDITIDEGKSAKITDIE 180
DB 121 SQYFNQATLNQAVAGLKEEHLGRKLNQITPQVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 PEGNQVSDRLKMQMSLTGEGITWLTTRSNQFNEQKFAODMEKVTDFYQNNGYDFPRIL 240
DB 181 PEGNQVSDRLKMQMSLTGEGITWLTTRSNQFNEQKFAODMEKVTDFYQNNGYDFPRIL 240
QY 241 DTDITQNETDKTQIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
DB 241 DTDITQNETDKTQIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
QY 301 MTAVLGEIQNRMSGAGYAYSEISVQPLNPAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
DB 301 MTAVLGEIQNRMSGAGYAYSEISVQPLNPAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
QY 361 RDEVVRELQMESAPYDTSKLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNMSLTE 420

DB 361 RDEVVRELQMESAPYDTSKLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNMSLTE 420
QY 421 RSTGSLDLASAGVQDTGLVMSAGVSDNLPCTGKSAALRASRSKTTILNGSLSTDPDFFTA 480
DB 421 RSTGSLDLASAGVQDTGLVMSAGVSDNLPCTGKSAALRASRSKTTILNGSLSTDPDFFTA 480
QY 481 DGVSGLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSGLGYDVYKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKTKDGTGDSFKGWLKYGTVGMRNKTDSALMPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKTKDGTGDSFKGWLKYGTVGMRNKTDSALMPTRGYLTGVNAEIA 600
QY 601 LPSKLOYYSATNQTWFFPLSKTFTILMLGGEVGIAGGYGTKEIIPPENFYGGGLGSVR 660
DB 601 LPSKLOYYSATNQTWFFPLSKTFTILMLGGEVGIAGGYGTKEIIPPENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSARELLFPMPGAKDARTVLSLPADAGSVWDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSARELLFPMPGAKDARTVLSLPADAGSVWDG 720
QY 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVAVTWLSPGLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVAVTWLSPGLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQGLGTTTF 797
DB 781 KPEDEIQRFQFQGLGTTTF 797
RESULT 6
AAU03959
ID AAU03959 standard; protein; 797 AA.
AC AAU03959;
XX
XX 23-OCT-2001 (first entry)
XX
XX Neisseria gonorrhoeae antigenic protein.
XX
XX Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
XX bacterial infection; baculovirus; yeast; Neisseria meningitidis.
XX
XX Neisseria gonorrhoeae.
XX
XX Key Location/Qualifiers
XX Peptide 1..21 "Signal peptide"
XX Protein 22..797
XX /note= "Mature N. gonorrhoeae antigen"
XX WO200138350-A2.
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WC-IB001851.
XX
XX 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX
XX (CHIR-) CHIRON SPA.
XX (STAT-) STATENS INST FOLKEHELSE.
XX
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX WPI; 2001-381289/40.
DR N-PSDB; AAS07279.
XX
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisseria bacterial infection.

XX PS Claim 1; Page 37-39; 92pp; English.

CC The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.

CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the

CC pharynx, causing meningitis and, occasionally, septicaemia in the absence

CC of meningitis. This antigenic protein is useful in the manufacture of a

CC medicament for treating or preventing infection due to Neisseria

CC bacteria, such as meningitis and septicaemia. It is also useful as a

CC diagnostic reagent for detecting the presence of Neisseria bacteria or

CC antibodies raised against Neisseria, and as a reagent for raising the

CC antibodies. The Neisseria nucleotide sequences can be expressed in a

CC variety of different expression systems, for example, mammalian cells,

CC baculoviruses, plants, bacteria and yeast

XX SQ Sequence 797 AA;

Query Match 99.6%; Score 4136; DB 4; Length 797;

Best Local Similarity 99.6%; Pred. No. 1.2e-279;

Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKOIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Db 1 MKLKOIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Qy 121 SOYFNOATNQAVAGLKEEYVGRGLNIQITPKVKTLARNRVDITIDEGSAKITDIE 180

Db 121 SOYFNOATNQAVAGLKEEYVGRGLNIQITPKVKTLARNRVDITIDEGSAKITDIE 180

Qy 181 FEGNOVYSRDLKRMQSLTEGGIWTLTRSNQFNEQFAQDMKVTDYQNGVYDFRIL 240

Db 181 FEGNOVYSRDLKRMQSLTEGGIWTLTRSNQFNEQFAQDMKVTDYQNGVYDFRIL 240

Qy 241 DTIDQTNEDTKTQIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300

Db 241 DTIDQTNEDTKTQIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300

Qy 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPRKTIYNEIHTGNKT 360

Db 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPRKTIYNEIHTGNKT 360

Qy 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLGVDFNDVQFVDAVPLAGTPDKVDLNMSLTE 420

Db 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLGVDFNDVQFVDAVPLAGTPDKVDLNMSLTE 420

Qy 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSFDPYFTA 480

Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSFDPYFTA 480

Qy 481 DGVSLGVDYVTKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFVGLVAEHLTVNT 540

Db 481 DGVSLGVDYVTKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFVGLVAEHLTVNT 540

Qy 541 YNKAPKHVADFIKYGKTDGDSFGKWLKYGTVGWRNKTTDSALMPTRCYLGVNAEIA 600

Db 541 YNKAPKHVADFIKYGKTDGDSFGKWLKYGTVGWRNKTTDSALMPTRCYLGVNAEIA 600

Qy 601 LPGSKLQYYSATHNQTFWFFPLSKFTTLLMGEVGIAGGYGRKEIIPFFENFYGGGLGSVR 660

Db 601 LPGSKLQYYSATHNQTFWFFPLSKFTTLLMGEVGIAGGYGRKEIIPFFENFYGGGLGSVR 660

Qy 661 GYESGTLGPKVYDYGKISYGGNKKANVAEALLFPMFGAKDARTVRLSLFADAGSVWDG 720

Db 661 GYESGTLGPKVYDYGKISYGGNKKANVAEALLFPMFGAKDARTVRLSLFADAGSVWDG 720

Qy 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLGPMKFRYAYPLKK 780

Db 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLGPMKFRYAYPLKK 780

Qy 781 KPEDIQRFQFQLGTTTF 797

Db 781 KPEDIQRFQFQLGTTTF 797

RESULT 7

ID AAU04451

XX AAU04451 standard; protein; 797 AA.

AC AAU04451;

XX 23-OCT-2001 (first entry)

DE Neisseria meningitidis serogroup A antigenic protein #2.

XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;

XX bacterial infection; baculovirus; yeast.

OS Neisseria meningitidis.

EH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "Signal peptide"

FT /note= "Mature N. meningitidis serogroup A antigen"

XX WO200138350-A2.

PN 31-MAY-2001.

PD 28-NOV-2000; 2000WO-IB001851.

XX 29-NOV-1999; 99GB-00028197.

PR 09-MAR-2000; 2000GB-00005698.

XX (CHIR-) CHIRON SPA.

PA (STAT-) STATENS INST FOLKEHELS.

XX Giuliani MM, Pizza M, Rappuoli R, Holst J;

XX WPI; 2001-381289/40.

XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria

PT gonorrhoeae, useful in the manufacture of a medicament for treating and

PT preventing Neisserial bacteria infection.

XX Claim 1; Page 39-40; 92pp; English.

CC The sequence represents a Neisseria meningitidis serogroup A 85 kDa

CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing

CC meningitis and, occasionally, septicaemia in the absence of meningitis.

CC This antigenic protein is useful in the manufacture of a medicament for

CC treating or preventing infection due to Neisseria bacteria, such as

CC meningitis and septicaemia. It is also useful as a diagnostic reagent for

CC detecting the presence of Neisseria bacteria or antibodies raised against

CC Neisseria, and as a reagent for raising the antibodies. The Neisserial

CC nucleotide sequences can be expressed in a variety of different

CC expression systems, for example, mammalian cells, baculoviruses, plants,

CC bacteria and yeast. Note: There are two versions of this sequence

CC displayed in the specification (see AAU03958)

XX SQ Sequence 797 AA;

Query Match 99.6%; Score 4136; DB 4; Length 797;

Best Local Similarity 99.6%; Pred. No. 1.2e-279;

Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKOIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Db 1 MKLKOIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Db 61 I I K S L Y A T G F P D D V R V E T A D Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K N L E S F G L A Q 120
 QY 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G K S A K I T D I E 180
 Db 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G K S A K I T D I E 180
 QY 181 F E G N Q V Y S D R K L M Q M S L T E G G I W T L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L 240
 Db 181 F E G N Q V Y S D R K L M Q M S L T E G G I W T L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L 240
 QY 241 D T D I Q T N E D K T K Q I K I T V H E G G R F R G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
 Db 241 D T D I Q T N E D K T K Q I K I T V H E G G R F R G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
 QY 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N K T 360
 Db 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N K T 360
 QY 361 R D E V V R E L R O M E S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
 Db 361 R D E V V R E L R O M E S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
 QY 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
 Db 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
 QY 481 D G V S L G Y D V Y G K A F D P R K A S T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
 Db 481 D G V S L G Y D V Y G K A F D P R K A S T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
 QY 541 Y N K A P H Y A D F I K Y K Y T D G T D G S F G K W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600
 Db 541 Y N K A P H Y A D F I K Y K Y T D G T D G S F G K W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600
 QY 601 L P G S K L Q Y S A T H N Q T W F F P L S K T F T L M L G E V G I A G Y G R T K E I P F F E N F Y G G L G S V R 660
 Db 601 L P G S K L Q Y S A T H N Q T W F F P L S K T F T L M L G E V G I A G Y G R T K E I P F F E N F Y G G L G S V R 660
 QY 661 G Y E S G T L G P K Y D Y G E K I S Y G G N K A N V S A E L L F P M P G A K A D A R T V R L S L F A D A G S V W D G 720
 Db 661 G Y E S G T L G P K Y D Y G E K I S Y G G N K A N V S A E L L F P M P G A K A D A R T V R L S L F A D A G S V W D G 720
 QY 721 K T Y D D N S S A T G G R V Q N I Y G A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K R Y A Y P L K K 780
 Db 721 K T Y D D N S S A T G G R V Q N I Y G A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K R Y A Y P L K K 780
 QY 781 K P E D E I O R F O L G T T F 797
 Db 781 K P E D E I O R F O L G T T F 797

RESULT 8
 AAB23788 standard; protein; 797 AA.
 ID AAB23788
 AC AAB23788;
 XX 12-JAN-2001 (first entry)
 DT Neisseria meningitidis serogroup A amino acid sequence.
 DE CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
 XX Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
 KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
 KW immune response.
 XX Neisseria meningitidis.
 OS WO200050075-A2.
 FN 31-AUG-2000.
 PD 09-FEB-2000; 2000WO-IB000176.
 PF

XX 26-FEB-1999; 99US-0121792P.
 PR (CHIR-) CHIRON SPA.
 PA Grandi G, Rappuoli R, Giuliani MM, Pizza M;
 PI WPI; 2001-015529/02.
 DR Immunogenic composition useful for stimulating an immune response in a
 XX mammal against Neisseria infection, comprises Neisseria antigen and an
 PT adjuvant composition comprising an oligonucleotide with a CG motif.
 PR Claim 22; Page 33; 39pp; English.
 PS The present invention describes an immunogenic composition (I) comprising
 XX a Neisseria antigen and an adjuvant composition comprising an
 CC oligonucleotide comprising at least 1 CG motif. Also described is an
 CC adjuvant composition (II) comprising an oligonucleotide which comprises
 CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
 CC oligonucleotide preferably comprises at least one phosphorothioate bond.
 CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
 CC the present invention. (i) is useful for stimulating an immune response
 CC in a mammal, preferably a human, against Neisseria infection, preferably
 CC Neisseria meningitidis infection and in the manufacture of a medicament
 CC for inducing a protective immune response in a mammal. The present
 CC sequence represents the claimed Neisseria meningitidis serogroup A amino
 CC acid sequence disclosed in GB-9928197.4, which is given in the present
 CC invention
 XX SQ Sequence 797 AA;
 Query Match 99.8%; Score 4136; DB 4; Length 797;
 Best Local Similarity 99.6%; Pred. No. 1.2e-279;
 Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 M K L K O T A S A L M L G I S P L A F A D E T I O D I R V E G Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
 Db 1 M K L K O T A S A L M L G I S P L A D A D F T I O D I R V E G Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
 QY 61 I I K S L Y A T G F D D V R V E T A D Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K N L E S F G L A Q 120
 Db 61 I I K S L Y A T G F D D V R V E T A D Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K N L E S F G L A Q 120
 QY 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G K S A K I T D I E 180
 Db 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G K S A K I T D I E 180
 QY 181 F E G N Q V Y S D R K L M Q M S L T E G G I W T L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L 240
 Db 181 F E G N Q V Y S D R K L M Q M S L T E G G I W T L T R S N Q F N E Q K F A Q D M E K V T D F Y Q N N G Y F D F R I L 240
 QY 241 D T D I Q T N E D K T K Q I K I T V H E G G R F R G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
 Db 241 D T D I Q T N E D K T K Q I K I T V H E G G R F R G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
 QY 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N K T 360
 Db 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y V N E I H I T G N K T 360
 QY 361 R D E V V R E L R O M E S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
 Db 361 R D E V V R E L R O M E S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
 QY 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
 Db 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
 QY 481 D G V S L G Y D V Y G K A F D P R K A S T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
 Db 481 D G V S L G Y D V Y G K A F D P R K A S T S I K Q Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
 QY 541 Y N K A P H Y A D F I K Y K Y T D G T D G S F G K W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600

||||| 541 YNKAPHYADFIKKYKTDGDFGSKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
||||| 601 LPSGKLOYSATHNQTFWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
||||| 601 LPSGKLOYSATHNQTFWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
661 GYESGTLGPKVYDYGKISYGGNKKANVSAELLFPMFGAKDARTVRLSLFADAGSVWDG 720
661 GYESGTLGPKVYDYGKISYGGNKKANVSAELLFPMFGAKDARTVRLSLFADAGSVWDG 720
721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
781 KPEDEIQRFQFQLGTTTF 797
781 KPEDEIQRFQFQLGTTTF 797
RESULT 9
AAB84746
ID AAB84746 standard; protein; 797 AA.
XX AAB84746;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a Neisseria serogroup A protein.
XX
KW Serogroup A protein; outer membrane protein; Neisserial infection;
XX vaccine.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
FT Protein 22..797
FT Protein /note= "mature protein"
XX WO200152885-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-IB000166.
XX
PR 17-JAN-2000; 2000GB-00001067.
PR 09-MAR-2000; 2000GB-00005699.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Pizza M, Rappuoli R, Giuliani M;
XX
DR WPI; 2001-451895/48.
DR N-PSDB; AAH42130.
XX
PT Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisserial bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX
PS Disclosure; Page 71-74; 83pp; English.
XX
CC The present sequence represents a Neisseria serogroup A protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisserial

CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX
SQ Sequence 797 AA;
Query Match 99.6%; Score 4136; DB 4; Length 797;
Best Local Similarity 99.6%; Pred. No. 1.2e-279;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLKQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDITNDTHGSA 60
DB 1 MKLKQIASALMWLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDITNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 FEGNQVYSDRKLMRQMSLTGEGGIWTLTRSNQNEQKFAQDMKVKTDFTQNNNGYFDFRIL 240
DB 181 FEGNQVYSDRKLMRQMSLTGEGGIWTLTRSNQNEQKFAQDMKVKTDFTQNNNGYFDFRIL 240
QY 241 DTDIQTNEDKTKQTIKITVHEGGRFRWGVSTEGDTNEVPKAELEKLLTWKPKWVERQQ 300
DB 241 DTDIQTNEDKTKQTIKITVHEGGRFRWGVSTEGDTNEVPKAELEKLLTWKPKWVERQQ 300
QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVLHIEBGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVLHIEBGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFNVQFQFVPLAGTDPKVDLNNSLTE 420
DB 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFNVQFQFVPLAGTDPKVDLNNSLTE 420
QY 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQTKSAALRASRKTTLNGLSFTDPYETA 480
DB 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQTKSAALRASRKTTLNGLSFTDPYETA 480
QY 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPHYADFIKKYKTDGDFGSKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPHYADFIKKYKTDGDFGSKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
QY 601 LPSGKLOYSATHNQTFWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
DB 601 LPSGKLOYSATHNQTFWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDYGKISYGGNKKANVSAELLFPMFGAKDARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDYGKISYGGNKKANVSAELLFPMFGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQLGTTTF 797
DB 781 KPEDEIQRFQFQLGTTTF 797
RESULT 10
AAU03958
ID AAU03958 standard; protein; 792 AA.
XX
AC AAU03958;

XX 23-Oct-2001 (first entry)
 XX Neisseria meningitidis serogroup A antigenic protein #1.
 XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX Neisseria meningitidis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein /note= "Signal peptide"
 FT Protein 22..792
 FT /note= "Mature N. meningitidis serogroup A antigen"
 XX WO200138350-A2.
 FN
 XX
 PD 31-MAY-2001.
 XX
 PF 28-NOV-2000; 2000WO-IB001851.
 XX
 PR 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 XX
 XX (CHIR-) CHIRON SPA.
 PA (STAT-) STATENS INST FOLKEHELSE.
 XX
 PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX
 DR WPI; 2001-381289/40.
 DR N-PSDB; AAS07278.
 XX
 XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX
 PS Claim 1; Page 66-68; 92pp; English.
 XX
 CC The sequence represents a Neisseria meningitidis serogroup A 85 kDa
 CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
 CC meningitis and, occasionally, septicaemia in the absence of meningitis.
 CC This antigenic protein is useful in the manufacture of a medicament for
 CC treating or preventing infection due to Neisseria bacteria, such as
 CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
 CC detecting the presence of Neisseria bacteria or antibodies raised against
 CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
 CC nucleotide sequences can be expressed in a variety of different
 CC expression systems, for example, mammalian cells, baculoviruses, plants,
 CC bacteria and yeast. Note: There are two versions of this sequence
 CC displayed in the specification (see AAU04451)
 XX
 SQ Sequence 792 AA;
 Query Match 95.38; Score 3956.5; DB 4; Length 792;
 Best Local Similarity 95.48; Pred. No. 3.9e-267;
 Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;
 QY 1 MKLKQIASALMMLGISPLAFADFTIQIRVEGLQRTPEPTVFVYLPVKVGDYNDTHGSA 60
 DB 1 MKLKQIASALMMLGISPLAFADFTIQIRVEGLQRTPEPTVFVYLPVKVGDYNDTHGSA 60
 QY 61 IISLSYATGFFDDVRVTADQQLLTIVERTPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IISLSYATGFFDDVRVTADQQLLTIVERTPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SOYFNOATLQNAVAGLKEEYLGKGLNIQITPKVKTLARNRVDITIDEGKSAKITDIE 180
 DB 121 SOYFNOATLQNAVAGLKEEYLGKGLNIQITPKVKTLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNQVYSRDKLMQMSLTGGIWTWLTNRNQNEOKFAODMEKVTDFYQNNGYFDFRIL 240
 DB 181 FEGNQVYSRDKLMQMSLTGGIWTWLTNRSDRDFRQKFAODMEKVTDFYQNNGYFDFRIL 240

QY 241 DTDIOTNEDKTKOTIKITVHEGGRFRWGVKVSIRGDTNEVPKAELEKLLTMKPGKMYERQQ 300
 DB 241 DTDIOTNEDKTKOTIKITVHEGGRFRWGVKVSIRGDTNEVPKAELEKLLTMKPGKMYERQQ 300
 QY 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 DB 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 QY 361 RDEVRRRELQRMESAPYDTSKLORSKERVVELLYGFDNVQPDVPLAGTDPKVDLNNSLTE 420
 DB 361 RDEVRRRELQRMESAPYDTSKLORSKERVVELLYGFDNVQPDVPLAGTDPKVDLNNSLTE 420
 QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTCKSAALRASRSKTLTNGSLSTFDPVFTA 480
 DB 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTCKSAALRASRSKTLTNGSLSTFDPVFTA 480
 QY 481 DGVSGLGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 DB 481 DGVSGLGYDVYVGKAFDPRKASTSVKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPKHYADFIKKYOKTDTGDSFGKGLYKGTGVRGNKNTDSALMPTRGYLTGCVNAEIA 600
 DB 541 YNKAPKRYADFIKKYOKTDTGDSFGKGLYKGTGVRGNKNTDSASWPTRGYLTGCVNAEIA 600
 QY 601 LPGSKLOYYSATHNOTWTFPLSKTFTMLGSGEYGIAGGYGRTKEIIPFFENFYGGGLGVS 660
 DB 601 LPGSKLOYYSATHNOTWTFPLSKTFTMLGSGEYGIAGGYGRTKEIIPFFENFYGGGLGVS 660
 QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMGAKADARTVRLSLFADAGSVWDG 720
 DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMGAKADARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKPFYAYPLKK 780
 DB 721 RTY- ---TAAENGNNKSVY- SENAHKSTFTNELRYSGAGVATWLSPLGPMKPFYAYPLKK 775
 QY 781 KPEDEIQRFQQLGTTTF 797
 DB 776 KPEDEIQRFQQLGTTTF 792
 RESULT 11
 AAB23786
 ID AAB23786 standard; protein; 792 AA.
 XX AAB23786;
 XX 11-SEP-2003 (revised)
 DT 12-JAN-2001 (first entry)
 XX
 DE Neisseria gonorrhoeae amino acid sequence.
 XX
 KW CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
 KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
 KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
 KW immune response.
 XX
 OS Neisseria gonorrhoeae.
 XX
 PN WO200050075-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 09-FEB-2000; 2000WO-IB000176.
 XX
 PR 26-FEB-1999; 99US-0121792P.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
 XX WPI; 2001-015529/02.
 DR

XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
PS Claim 22; Page 32; 39pp; English.
XX
CC The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA2359 to AAA2385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria gonorrhoea amino acid sequence
CC disclosed in GB-9928197.4, which is given in the present invention.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 792 AA;
SQ
Query Match 95.3%; Score 3956.5; DB 4; Length 792;
Best Local Similarity 95.4%; Pred. No. 3.9e-267;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;
QY 1 MKLKOIASALMLGIGSLAPADFIIQDIRVEGQRTPESTFVFNYPVKVGDYNDTHGSA 60
DB 1 MKLKOIASALMLGIGSLAPADFIIQDIRVEGQRTPESTFVFNYPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120
DB 61 IIKSLYATGFFDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120
QY 121 SQYFNQATLQNAVAGLKEEYVGRGKUNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
DB 121 SQYFNQATLQNAVAGLKEEYVGRGKUNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
QY 181 FEGNQVSDRKLMQMSLTGGITWLTTRSNQFNEQKFAQMEKVTDFYQNNGYEOPRIL 240
DB 181 FEGNQVSDRKLMQMSLTGGITWLTTRSDRDFQRKFAQMEKVTDFYQNNGYEOPRIL 240
QY 241 DTDITQWEDTKTQITKIVTVEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQ 300
DB 241 DTDITQWEDTKTQITKIVTVEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQ 300
QY 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRELQMESAPYDTSKLOBSKERVLLGYFDNVQFQDAVPLAGTPDKVNLNLSLITE 420
DB 361 RDEVVRELQMESAPYDTSKLOBSKERVLLGYFDNVQFQDAVPLAGTPDKVNLNLSLITE 420
QY 421 RSTGSLDLSAGWQDVTGLNVSAGVSDONLFGTGSAALRASRKTTLNGLSFTDPYFTA 480
DB 421 RSTGSLDLSAGWQDVTGLNVSAGVSDONLFGTGSAALRASRKTTLNGLSFTDPYFTA 480
QY 481 DGVSLGYDVTGKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGYDVTGKAPDPKASTSVKQYKTTTAGGGVRMGIPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGDSFKGLYKGTGNGENKTDNALWTRCYLGVNVAEIA 600
DB 541 YNKAPKHYADFIKKYKGTGDTGDSFKGLYKGTGNGENKTDNALWTRCYLGVNVAEIA 600
QY 601 LPGSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
DB 601 LPGSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVAELLFPMPGAKDARTVRLSLFADAGSVWDG 720

DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANVAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
QY 721 KYTDDNSSATGRGVONIVYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
DB 721 RTY----TAENGNNKSVY-SENAHKSTFTNELRYSAGGAVTWLSPLGPMKFSYAYPLKK 775
QY 781 KPDEIQRFQFQGLGTTTF 797
DB 776 KPDEIQRFQFQGLGTTTF 792
RESULT 12
AAB84745
ID AAB84745 standard; protein; 792 AA.
XX AAB84745;
XX AC
DT 11-SEP-2003 (revised)
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a Neisseria gonorrhoea protein.
XX
XX Serogroup B protein; outer membrane protein; Neisserial infection;
KW vaccine.
XX
OS Neisseria gonorrhoeae.
XX
FH Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Protein 22..792 /note= "mature protein"
FT
XX
PN WC200152885-A1.
XX
PD 26-JUL-2001.
XX
XX 17-JAN-2001; 2001WO-1B000166.
XX
PR 17-JAN-2000; 2000GB-00001067.
PR 09-MAR-2000; 2000GB-00005699.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Pizza M, Rappuoli R, Giuliani M;
XX
XX WPI; 2001-451895/48.
DR N-PSDB; AAH42129.
XX
PT Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisserial bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX
PS Disclosure; Page 65-67; 83pp; English.
XX
XX The present sequence represents a Neisseria gonorrhoea protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisserial
CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria; or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX Sequence 792 AA;

Query Match		95.3%; Score 3956.5; DB 4; Length 792;
Best Local Similarity		95.4%; Pred. No. 3.9e-267;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;		
Qy	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Dd	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy	61	IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
Dd	61	IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
Qy	121	SOYFNOATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Dd	121	SOYFNOATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Qy	181	FEQNQVYSRDKLRQMSLTGEGGIWTLTRSNQFNQKFAQDMKVTDYQNNGYFDFRIL 240
Dd	181	FEQNQVYSRDKLRQMSLTGEGGIWTLTRSDRFDQKFAQDMKVTDYQNNGYFDFRIL 240
Qy	241	DTDIQTNEDEKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQ 300
Dd	241	DTDIQTNEDEKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQ 300
Qy	301	MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Dd	301	MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Qy	361	RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFQNVQFQDAVPLAGTDPKVDLNNSLTE 420
Dd	361	RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFQNVQFQDAVPLAGTDPKVDLNNSLTE 420
Qy	421	RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTFDYFETA 480
Dd	421	RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTFDYFETA 480
Qy	481	DGVSLSGVDYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Dd	481	DGVSLSGVDYVGKAFDPRKASTSVKQYKTTTAGGGVRMGIPVTEYDRVNFGLAAEHLTVNT 540
Query Match		95.3%; Score 3956.5; DB 6; Length 792;
Best Local Similarity		95.4%; Pred. No. 3.9e-267;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;		
Qy	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Dd	1	MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy	61	IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
Dd	61	IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
Qy	121	SOYFNOATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Dd	121	SOYFNOATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Qy	181	FEQNQVYSRDKLRQMSLTGEGGIWTLTRSNQFNQKFAQDMKVTDYQNNGYFDFRIL 240
Dd	181	FEQNQVYSRDKLRQMSLTGEGGIWTLTRSDRFDQKFAQDMKVTDYQNNGYFDFRIL 240
Qy	241	DTDIQTNEDEKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQ 300
Dd	241	DTDIQTNEDEKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQ 300
Qy	301	MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Dd	301	MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Qy	361	RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFQNVQFQDAVPLAGTDPKVDLNNSLTE 420
Dd	361	RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFQNVQFQDAVPLAGTDPKVDLNNSLTE 420
Qy	421	RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTFDYFETA 480
Dd	421	RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTFDYFETA 480
Qy	481	DGVSLSGVDYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Dd	481	DGVSLSGVDYVGKAFDPRKASTSVKQYKTTTAGGGVRMGIPVTEYDRVNFGLAAEHLTVNT 540
Qy	541	YNKAPKHYADFIKKYKGTGDTGDSFGKWLKGTGWRNKNTDSALMPTRGILYGVNAEIA 600
Dd	541	YNKAPKHYADFIKKYKGTGDTGDSFGKLLYKGTGWRNKNTDSASWPTRGILYGVNAEIA 600
Qy	601	LPQSKLYYSATHNQTFWPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
Dd	601	LPQSKLYYSATHNQTFWPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
Qy	661	GYESGTLGPKVDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Dd	661	GYESGTLGPKVDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy	721	KTYDDNSSSATGGRVQNIYAGNTHKSTFNEILRYSAGGAVTWLSPLGPMKFFYAYPLKK 780
Dd	721	RTY----TAENGNNKSVY-SENAHKSTFNEILRYSAGGAVTWLSPLGPMKFFYAYPLKK 775
Qy	781	KPEDEIQRFQFQGTTF 797
Dd	776	KPEDEIQRFQFQGTTF 792
RESULT 13		
ABP80499		
ID ABP80499 standard; protein; Indel 7528.		
XX		
AC ABP80499;		
XX		
DT 07-MAR-2003 (first entry)		
XX		
DE N. gonorrhoeae amino acid sequence SEQ ID 7528.		
XX		
KW Antibacterial; infection; vaccine; gene therapy.		

XX Neisseria gonorrhoeae.
OS WO200279243-A2.
PN 10-OCT-2002.
XX 12-FEB-2002; 2002WO-IB002069.
XX 12-FEB-2001; 2001GB-00003424.
XX (CHIR-) CHIRON SPA.
XX Fontana MR, Pizza M, Masignani V, Monaci E;
XX WPI; 2003-058415/05.
XX N-PSDB; ABZ41469.
XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX medicament for treating or preventing N. gonorrhoeae infection.
XX Disclosure; Page 736; 815pp; English.
XX The present invention relates to proteins from Neisseria gonorrhoeae.
XX Also disclosed are the nucleic acid molecules encoding the proteins and
XX antibodies that specifically bind to the proteins. The composition
XX comprising the protein, nucleic acid or antibody is useful for the
XX manufacture of a medicament for treating or preventing N. gonorrhoeae
XX infection, this may be in the form of a vaccine or gene therapy.
XX Sequences given in records ABP76736-ABP81046 represent nucleic acid
XX molecules of the invention
XX Sequence 792 AA;

Query Match 95.3%; Score 3956.5; DB 6; Length 792;
Best Local Similarity 95.4%; Pred. No. 3.9e-267;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;
Qy 1 MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Dd 1 MLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
Dd 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Dd 121 SOYFNOATLNQAVAGLKEEYLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Qy 181 FEQNQVYSRDKLRQMSLTGEGGIWTLTRSNQFNQKFAQDMKVTDYQNNGYFDFRIL 240
Dd 181 FEQNQVYSRDKLRQMSLTGEGGIWTLTRSDRFDQKFAQDMKVTDYQNNGYFDFRIL 240
Qy 241 DTDIQTNEDEKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQ 300
Dd 241 DTDIQTNEDEKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQ 300
Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Dd 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFQNVQFQDAVPLAGTDPKVDLNNSLTE 420
Dd 361 RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFQNVQFQDAVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTFDYFETA 480
Dd 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFQGTCKSAALRASRSKTTLNGSLSTFDYFETA 480
Qy 481 DGVSLSGVDYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Dd 481 DGVSLSGVDYVGKAFDPRKASTSVKQYKTTTAGGGVRMGIPVTEYDRVNFGLAAEHLTVNT 540

PT WO200023595-A1. /note= "signal peptide"

XX 27-APR-2000.

XX 22-OCT-1998; 98WO-US022352.

XX 22-OCT-1998; 98WO-US022352.

XX (UYMO-) UNIV MONTANA.

XX Judd RC, Manning SD;

XX WPI; 2000-339694/29.

XX N-PSDB; AAA15155.

PT New isolated outer membrane protein 85 of *Neisseria gonorrhoeae* and *N. meningitidis* useful for vaccine, therapeutic and diagnostic compositions

PT for gonococcal or meningococcal infections.

XX Claim 1; Fig 2; 98pp; English.

XX The present sequence represents an outer membrane protein (omp) 85 of *Neisseria gonorrhoeae*. The omp polypeptides and polynucleotides are useful in compositions for use in the prevention, treatment and diagnosis of non-symptomatic gonococcal infection or meningococcal infection and of symptomatic disease. They are also useful for the detection of hybridisation complexes. Antigens and antibodies specific omp proteins also provide diagnostic, therapeutic and prophylactic compositions for the treatment or prevention of the infections described above. The antibodies are useful for inducing a protective immune response in humans or animals with *N. gonorrhoeae*, *N. meningitidis*, or other *Neisseria* species. The proteins, antibodies and polynucleotide sequences of the present invention may also be used in the screening and development of chemical compounds such as drugs or vaccines. (Updated on 12-SEP-2003 to standardise OS field)

XX Sequence 792 AA;

Query Match 94.8%; Score 3937.5; DB 3; Length 792;

Best Local Similarity 95.1%; Pred. No. 8.3e-266;

Matches 758; Conservative 16; Mismatches 18; Indels 5; Gaps 2;

QY 1 MKLQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDTYNDTHGSA 60

DB 1 MKLQIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDTYNDTHGSA 60

QY 61 IISLYATGFFDVRVETADGQLLLTVIERPTGSLNITGAKMLONDAIKKNLESFGLAQ 120

DB 61 IISLYATGFFDVRVETADGQLLLTVIVCPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNOAVAGLKEEYLGRKLNQITPKVTKLARNRVDITIDEGSKAKITDIE 180

DB 121 SQYFNQATLNOAVAGLKEEYLGRKLNQITPKVTKLARNRVDITIDEGSKAKITDIE 180

QY 181 FEGNQVYSRDLKRMQSLTEGGIWTWLTDRSDRQFAQDMKVTDFYQNGGYDFDFRIL 240

DB 181 FEGNQVYSRDLKRMQSLTEGGIWTWLTDRSDRQFAQDMKVTDFYQNGGYDFDFRIL 240

QY 241 DTDIQTNEDKTKITITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQ 300

DB 241 DTDIQTNEDKTKITITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQ 300

QY 301 MTAVLGEIQRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEGRKIYVNEIHTGNKKT 360

DB 301 MTAVLGEIQRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEGRKIYVNEIHTGNKKT 360

QY 361 RDEVVRELQRMESAPYDTSKLQSKERVELLYGFDVNFQVDAVPLAGTDPKVDLNMSLTE 420

DB 361 RDEVVRELQRMESAPYDTSKLQSKERVELLYGFDVNFQVDAVPLAGTDPKVDLNMSLTE 420

QY 421 RSTGSLDLSAGVQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480

DB 421 RSTGSLDLSAGVQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480

QY 481 DGVSGLGYDVYVGKAFDPRKASTSIKQYKTTTATAGIRMSVPTVEYDRVNFGLVAEHLTVNT 540

DB 481 DGVSGLGYDVYVGKAFDPRKASTSVKQYKTTTATAGGVRMGIPTVEYDRVNFGLAAEHLTVNT 540

QY 541 YNKAPKHYADFIKKYKTKTGTGDSFGKWLKYGTVGGRNKTDLSALMPTRGYLTGVNAEIA 600

DB 541 YNKAPKRYADFIKQYKTKGTGADGSPKGLLYKYGTVGGRNKTDLSALMPTRGYLTGVNAEIA 600

QY 601 LPSGKLOYYSATHNQTFWFFPLSKTFTMLGCEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660

DB 601 LPSGKLOYYSATHNQTFWFFPLSKTFTMLGCEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660

QY 661 GYESGTLGPKVYDEYGEKISYGCNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720

DB 661 GYESGTLGPKVYDEYGEKISYGCNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720

QY 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGGAVTWLSPGLGPMKFRYAYPLKK 780

DB 721 RTY----TAAENGNNKSVY--SENAHKSTFTNELRYSGAGGAVTWLSPGLGPMKFRYAYPLKK 775

QY 781 KPEDEIQRFQFQGLGTTTF 797

DB 776 KPEDEIQRFQFQGLGTTTF 792

Search completed: July 6, 2005, 15:13:13

Job time : 239.676 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:19:22 ; Search time 49 Seconds
(without alignments)
1214.190 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLGISPLAF.....LKKKPEDEIQFQFLGTTT 797

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- Issued Patents AA:*
- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
 - 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
 - 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
 - 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
 - 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
 - 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	4	US-09-994-192-4
2	157	19.7	792	4	US-09-994-192-2
3	8	1.0	94	4	US-09-489-039A-8163
4	8	1.0	97	4	US-09-205-258-1092
5	8	1.0	230	4	US-09-270-767-45805
6	8	1.0	274	4	US-09-902-540-15552
7	8	1.0	648	4	US-09-252-991A-24628
8	8	1.0	1589	4	US-09-543-681A-4998
9	7	0.9	23	4	US-09-674-973A-147
10	7	0.9	58	3	US-08-971-089-10
11	7	0.9	60	4	US-09-513-999C-7231
12	7	0.9	86	4	US-09-328-352-6252
13	7	0.9	86	4	US-09-489-039A-10485
14	7	0.9	88	4	US-09-461-325-325
15	7	0.9	88	4	US-10-012-542-325
16	7	0.9	88	4	US-10-115-123-325
17	7	0.9	97	4	US-09-252-991A-18360
18	7	0.9	106	4	US-09-270-767-62368
19	7	0.9	110	4	US-09-513-999C-6601
20	7	0.9	129	4	US-09-543-681A-5037
21	7	0.9	147	2	US-08-942-819-13
22	7	0.9	147	4	US-09-522-955A-21
23	7	0.9	157	4	US-09-543-681A-7658
24	7	0.9	157	4	US-09-270-767-39460
25	7	0.9	157	4	US-09-270-767-54677
26	7	0.9	159	4	US-09-270-767-38687
27	7	0.9	159	4	US-09-270-767-53904

165	4	US-09-270-767-46749	Sequence 46749, A
176	4	US-09-902-540-16369	Sequence 16369, A
178	4	US-09-716-129-55	Sequence 55, Appl
179	4	US-09-252-991A-24524	Sequence 24524, A
193	4	US-09-252-991A-17828	Sequence 17828, A
213	4	US-09-252-991A-17280	Sequence 17280, A
218	4	US-09-270-767-31864	Sequence 31864, A
228	4	US-09-270-767-47081	Sequence 47081, A
228	4	US-09-270-767-61520	Sequence 61520, A
239	4	US-09-248-796A-18574	Sequence 18574, A
244	4	US-09-489-039A-14079	Sequence 14079, A
253	4	US-09-540-236-2592	Sequence 2592, Ap
254	4	US-09-586-106D-127	Sequence 127, App
257	4	US-09-352-991A-31224	Sequence 31224, A
260	4	US-09-902-540-15829	Sequence 15829, A
263	4	US-09-252-991A-26300	Sequence 26300, A
267	4	US-09-634-238-360	Sequence 360, App
268	4	US-09-252-991A-23138	Sequence 23138, A
268	4	US-09-252-991A-23139	Sequence 23139, A
270	4	US-09-252-991A-31998	Sequence 31998, A
282	4	US-09-252-991A-23186	Sequence 23186, A
288	4	US-09-107-532A-5538	Sequence 5538, Ap
291	4	US-09-538-092-764	Sequence 764, App
294	4	US-09-352-991A-28354	Sequence 28354, A
294	4	US-09-107-532A-4247	Sequence 4247, Ap
300	4	US-09-489-039A-9673	Sequence 9673, Ap
310	4	US-09-902-540-15612	Sequence 15612, A
316	4	US-09-248-796A-19882	Sequence 19882, A
327	4	US-09-252-991A-30618	Sequence 30618, A
351	4	US-09-489-039A-9415	Sequence 9415, Ap
355	4	US-08-178-257-4	Sequence 4, Appli
355	4	US-09-328-352-5414	Sequence 5414, Ap
357	4	US-09-252-991A-33139	Sequence 33139, A
357	4	US-09-902-540-13021	Sequence 13021, A
363	4	US-09-902-540-16014	Sequence 16014, A
366	3	US-09-040-681A-6	Sequence 6, Appli
366	3	US-09-497-897-6	Sequence 6, Appli
366	4	US-09-270-767-45981	Sequence 45981, A
389	4	US-09-248-796A-23182	Sequence 23182, A
393	4	US-09-252-991A-16771	Sequence 16771, A
399	4	US-09-252-991A-18432	Sequence 18432, A
413	4	US-09-902-540-13562	Sequence 13562, A
425	3	US-09-310-363C-8	Sequence 8, Appli
425	4	US-10-117-015-8	Sequence 8, Appli
434	4	US-09-252-991A-27235	Sequence 27235, A
441	4	US-09-134-000C-4521	Sequence 4521, Ap
444	4	US-09-721-870-42	Sequence 42, Appl
458	4	US-09-435-956A-1	Sequence 1, Appli
459	4	US-09-252-991A-25839	Sequence 25839, A
464	4	US-09-711-164-441	Sequence 441, App
464	4	US-09-492-709A-281	Sequence 281, App
465	4	US-09-252-991A-29387	Sequence 29387, A
472	3	US-09-516-914-3	Sequence 3, Appli
473	4	US-09-328-352-5279	Sequence 5279, Ap
480	3	US-09-252-149B-26	Sequence 26, Appl
480	4	US-09-583-110-5088	Sequence 5088, Ap
497	4	US-09-107-433-3732	Sequence 3732, Ap
504	4	US-09-949-016-11380	Sequence 11380, A
514	4	US-09-723-368-4	Sequence 4, Appli
517	4	US-09-919-172-20	Sequence 20, Appl
518	4	US-09-504-358-22	Sequence 22, Appl
529	3	US-09-354-314-22	Sequence 22, Appl
529	4	US-10-230-562-22	Sequence 22, Appl
536	4	US-09-370-767-46294	Sequence 46294, A
544	1	US-08-387-156-10	Sequence 10, Appl
544	2	US-08-694-865-10	Sequence 10, Appl
544	2	US-08-878-748-10	Sequence 10, Appl
544	3	US-09-124-491-10	Sequence 10, Appl
544	4	US-09-383-912-10	Sequence 10, Appl
559	4	US-09-252-991A-24692	Sequence 24692, A
568	4	US-09-949-016-10896	Sequence 10896, A
576	4	US-09-252-991A-23246	Sequence 23246, A
587	4	US-09-538-092-1130	Sequence 1130, Ap

101	7	0.9	604	4	US-09-345-473E-17	Sequence 17, Appl	174	7	0.9	1447	3	US-08-954-668-19	Sequence 19, Appl
102	7	0.9	609	4	US-09-311-021-196	Sequence 196, App	175	7	0.9	1447	3	US-09-268-140-5	Sequence 5, Appli
103	7	0.9	614	4	US-09-328-352-4504	Sequence 4504, Ap	176	7	0.9	1447	4	US-08-918-658-19	Sequence 19, Appl
104	7	0.9	620	1	US-08-484-105-4	Sequence 4, Appli	177	7	0.9	1447	4	US-09-724-631-19	Sequence 19, Appl
105	7	0.9	620	1	US-08-484-106-4	Sequence 4, Appli	178	7	0.9	1447	4	US-08-954-701A-19	Sequence 19, Appl
106	7	0.9	621	4	US-09-232-991A-19125	Sequence 19125, A	179	7	0.9	1447	5	PCT-US95-13233-19	Sequence 19, Appl
107	7	0.9	671	3	US-08-858-207A-301	Sequence 301, App	180	7	0.9	1454	4	US-09-673-896-2	Sequence 2, Appli
108	7	0.9	671	4	US-09-583-110-3642	Sequence 4098, Ap	181	7	0.9	1457	4	US-09-673-896-4	Sequence 4, Appli
109	7	0.9	676	4	US-09-107-433-4098	Sequence 16, Appl	182	7	0.9	1633	4	US-09-502-540-12892	Sequence 12892, A
110	7	0.9	699	2	US-08-694-865-16	Sequence 16, Appl	183	7	0.9	1636	4	US-09-355-160D-2	Sequence 2, Appli
111	7	0.9	699	3	US-09-124-491-16	Sequence 16, Appl	184	7	0.9	1686	4	US-10-092-219-2	Sequence 2, Appli
112	7	0.9	699	4	US-09-383-912-16	Sequence 16, Appl	185	7	0.9	2431	1	US-07-520-281C-2	Sequence 2, Appli
113	7	0.9	699	4	US-09-232-991A-17073	Sequence 17073, A	186	7	0.9	2431	3	US-08-466-277-2	Sequence 2, Appli
114	7	0.9	781	4	US-09-248-796A-15502	Sequence 15502, A	187	7	0.9	2431	4	US-09-688-842-2	Sequence 2, Appli
115	7	0.9	823	4	US-09-252-991A-21013	Sequence 21013, A	188	7	0.9	3122	4	US-10-237-551-201	Sequence 201, App
116	7	0.9	827	4	US-09-543-681A-6425	Sequence 6425, Ap	189	7	0.9	3122	4	US-10-237-551-250	Sequence 250, App
117	7	0.9	901	4	US-09-270-767-45367	Sequence 45367, A	190	6	0.8	7	1	US-08-384-680-2	Sequence 2, Appli
118	7	0.9	908	4	US-08-714-741-44	Sequence 44, Appl	191	6	0.8	7	1	US-08-384-680-12	Sequence 12, Appl
119	7	0.9	924	3	US-08-619-812-8	Sequence 8, Appli	192	6	0.8	9	2	US-08-986-234-84	Sequence 84, Appl
120	7	0.9	926	1	US-07-908-253-2	Sequence 2, Appli	193	6	0.8	10	1	US-08-397-101-7	Sequence 7, Appli
121	7	0.9	926	1	US-08-455-970A-2	Sequence 2, Appli	194	6	0.8	10	4	US-08-135-319A-4	Sequence 4, Appli
122	7	0.9	926	1	US-08-387-156-6	Sequence 6, Appli	195	6	0.8	10	4	US-08-135-319A-5	Sequence 5, Appli
123	7	0.9	926	2	US-08-694-865-6	Sequence 6, Appli	196	6	0.8	10	4	US-08-135-319A-6	Sequence 6, Appli
124	7	0.9	926	2	US-08-878-748-6	Sequence 6, Appli	197	6	0.8	10	4	US-08-135-319A-19	Sequence 19, Appl
125	7	0.9	926	2	US-08-535-837-2	Sequence 2, Appli	198	6	0.8	10	5	PCT-US93-08436-7	Sequence 7, Appli
126	7	0.9	926	3	US-09-124-491-6	Sequence 6, Appli	199	6	0.8	13	2	US-08-803-899-13	Sequence 13, Appl
127	7	0.9	926	4	US-09-383-912-6	Sequence 6, Appli	200	6	0.8	18	1	US-08-279-058B-20	Sequence 20, Appl
128	7	0.9	926	4	US-08-976-566-2	Sequence 2, Appli	201	6	0.8	18	4	US-08-828-323-20	Sequence 20, Appl
129	7	0.9	926	6	5476657-3	Patent No. 5476657	202	6	0.8	19	1	US-08-634-060-42	Sequence 42, Appl
130	7	0.9	926	6	5476657-3	Patent No. 5476657	203	6	0.8	19	3	US-08-676-186-1	Sequence 1, Appli
131	7	0.9	934	1	US-08-215-805A-80	Sequence 80, Appl	204	6	0.8	19	4	US-09-932-923-1	Sequence 1, Appli
132	7	0.9	936	1	US-08-455-970A-12	Sequence 12, Appl	205	6	0.8	20	1	US-08-279-906A-22	Sequence 22, Appl
133	7	0.9	936	4	US-08-976-566-12	Sequence 12, Appl	206	6	0.8	24	4	US-09-843-221A-129	Sequence 129, App
134	7	0.9	943	1	US-08-455-970A-10	Sequence 10, Appl	207	6	0.8	24	4	US-09-843-221A-130	Sequence 130, App
135	7	0.9	943	1	US-08-976-566-10	Sequence 10, Appl	208	6	0.8	25	4	US-09-911-927-35	Sequence 35, Appl
136	7	0.9	951	1	US-08-455-970A-14	Sequence 14, Appl	209	6	0.8	25	4	US-09-911-882-35	Sequence 35, Appl
137	7	0.9	951	4	US-08-976-566-14	Sequence 14, Appl	210	6	0.8	25	4	US-09-911-888-35	Sequence 35, Appl
138	7	0.9	963	4	US-09-914-259-20	Sequence 20, Appl	211	6	0.8	26	3	US-08-965-762-35	Sequence 35, Appl
139	7	0.9	963	4	US-09-914-259-22	Sequence 22, Appl	212	6	0.8	27	3	US-08-433-522A-35	Sequence 35, Appl
140	7	0.9	963	4	US-09-538-092-1060	Sequence 1060, Ap	213	6	0.8	27	3	US-09-135-166-35	Sequence 35, Appl
141	7	0.9	970	4	US-09-248-796A-16191	Sequence 16191, A	214	6	0.8	27	3	US-08-942-046-35	Sequence 35, Appl
142	7	0.9	977	1	US-08-387-156-8	Sequence 8, Appli	215	6	0.8	28	2	US-08-724-774B-4	Sequence 4, Appli
143	7	0.9	977	2	US-08-694-865-8	Sequence 8, Appli	216	6	0.8	28	3	US-09-089-595-4	Sequence 4, Appli
144	7	0.9	977	2	US-08-878-748-8	Sequence 8, Appli	217	6	0.8	28	3	US-09-382-855-4	Sequence 4, Appli
145	7	0.9	977	4	US-09-124-491-8	Sequence 8, Appli	218	6	0.8	28	3	US-09-183-714B-4	Sequence 4, Appli
146	7	0.9	977	4	US-09-383-912-8	Sequence 8, Appli	219	6	0.8	28	3	US-09-642-281-4	Sequence 4, Appli
147	7	0.9	978	4	US-09-949-016-10196	Sequence 10196, A	220	6	0.8	28	4	US-09-589-717-4	Sequence 4, Appli
148	7	0.9	1022	4	US-09-949-016-10242	Sequence 10242, A	221	6	0.8	28	4	US-09-843-221A-93	Sequence 93, Appl
149	7	0.9	1069	1	US-07-777-715-9	Sequence 9, Appli	222	6	0.8	28	4	US-09-843-221A-94	Sequence 94, Appl
150	7	0.9	1069	1	US-08-170-126-4	Sequence 4, Appli	223	6	0.8	28	4	US-09-471-276-1203	Sequence 1203, Ap
151	7	0.9	1069	3	US-08-954-418-4	Sequence 4, Appli	224	6	0.8	30	4	US-09-843-221A-124	Sequence 124, App
152	7	0.9	1098	1	US-07-777-715-7	Sequence 7, Appli	225	6	0.8	30	4	US-09-843-221A-125	Sequence 125, App
153	7	0.9	1098	1	US-08-170-126-2	Sequence 2, Appli	226	6	0.8	30	4	US-09-843-221A-158	Sequence 158, App
154	7	0.9	1098	3	US-08-554-418-2	Sequence 2, Appli	227	6	0.8	31	4	US-09-228-990-50	Sequence 50, Appl
155	7	0.9	1121	4	US-08-915-048A-2	Sequence 2, Appli	228	6	0.8	33	1	US-08-209-747-19	Sequence 19, Appl
156	7	0.9	1129	4	US-09-252-991A-28552	Sequence 28552, A	229	6	0.8	33	1	US-08-458-298-19	Sequence 19, Appl
157	7	0.9	1296	4	US-08-857-636-60	Sequence 60, Appl	230	6	0.8	34	1	US-07-915-247A-23	Sequence 23, Appl
158	7	0.9	1334	6	5476657-1	Patent No. 5476657	231	6	0.8	34	1	US-08-443-863-23	Sequence 23, Appl
159	7	0.9	1334	6	5476657-1	Patent No. 5476657	232	6	0.8	34	1	US-08-448-070-23	Sequence 23, Appl
160	7	0.9	1403	1	US-07-908-253-3	Sequence 3, Appli	233	6	0.8	34	1	US-08-449-500-23	Sequence 23, Appl
161	7	0.9	1403	2	US-08-694-865-17	Sequence 17, Appl	234	6	0.8	34	1	US-08-449-317A-23	Sequence 23, Appl
162	7	0.9	1403	2	US-08-535-837-3	Sequence 3, Appli	235	6	0.8	34	2	US-08-477-022-23	Sequence 23, Appl
163	7	0.9	1403	3	US-09-124-491-17	Sequence 17, Appl	236	6	0.8	34	2	US-08-449-447-23	Sequence 23, Appl
164	7	0.9	1403	4	US-09-383-912-17	Sequence 17, Appl	237	6	0.8	34	2	US-08-184-328-23	Sequence 23, Appl
165	7	0.9	1434	2	US-08-540-406-10	Sequence 10, Appl	238	6	0.8	34	2	US-08-521-097-23	Sequence 23, Appl
166	7	0.9	1434	3	US-08-556-055-10	Sequence 10, Appl	239	6	0.8	34	4	US-09-843-221A-88	Sequence 88, Appl
167	7	0.9	1434	3	US-08-954-668-10	Sequence 10, Appl	240	6	0.8	34	4	US-09-843-221A-89	Sequence 89, Appl
168	7	0.9	1434	4	US-08-918-658-10	Sequence 10, Appl	241	6	0.8	34	4	US-09-843-221A-122	Sequence 122, App
169	7	0.9	1434	4	US-09-724-631-10	Sequence 10, Appl	242	6	0.8	36	4	US-09-902-540-14017	Sequence 14017, A
170	7	0.9	1434	4	US-08-954-701A-10	Sequence 10, Appl	243	6	0.8	37	3	US-08-751-344B-18	Sequence 18, Appl
171	7	0.9	1434	5	PCT-US95-13233-10	Sequence 10, Appl	244	6	0.8	39	1	US-08-209-747-23	Sequence 23, Appl
172	7	0.9	1447	2	US-08-540-406-19	Sequence 19, Appl	245	6	0.8	39	1	US-08-458-298-23	Sequence 23, Appl
173	7	0.9	1447	3	US-08-656-055-19	Sequence 19, Appl	246	6	0.8	39	4	US-09-270-767-31845	Sequence 31845, A

247	6	0.8	39	4	US-09-270-767-47062	Sequence 47062, A	320	80	4	US-09-640-211A-905	Sequence 905, App
248	6	0.8	40	3	US-07-741-453A-4	Sequence 4, Appli	321	82	3	US-09-134-001C-2351	Sequence 2351, Ap
249	6	0.8	42	5	PCT-US96-10043-13	Sequence 13, Appl	322	84	4	US-09-621-976-5976	Sequence 5976, Ap
250	6	0.8	47	1	US-08-209-747-24	Sequence 24, Appl	323	84	4	US-09-270-767-32345	Sequence 32345, A
251	6	0.8	47	1	US-08-209-747-26	Sequence 26, Appl	324	84	4	US-09-270-767-46371	Sequence 46371, A
252	6	0.8	47	1	US-08-458-298-24	Sequence 24, Appl	325	84	4	US-09-270-767-47562	Sequence 47562, A
253	6	0.8	47	1	US-08-458-298-26	Sequence 26, Appl	326	84	4	US-09-311-021-100	Sequence 100, App
254	6	0.8	48	1	US-08-209-747-21	Sequence 21, Appl	327	84	4	US-09-513-999C-5815	Sequence 5815, Ap
255	6	0.8	48	1	US-08-458-298-21	Sequence 21, Appl	328	86	1	US-08-680-726A-82	Sequence 82, Appl
256	6	0.8	49	1	US-08-209-747-22	Sequence 22, Appl	329	86	3	US-09-092-409-82	Sequence 82, Appl
257	6	0.8	49	1	US-08-458-298-20	Sequence 20, Appl	330	86	4	US-09-270-767-34956	Sequence 34956, A
258	6	0.8	50	1	US-08-458-298-22	Sequence 22, Appl	331	86	4	US-09-270-767-50173	Sequence 50173, A
259	6	0.8	50	1	US-08-209-747-27	Sequence 27, Appl	332	86	4	US-09-543-681A-7373	Sequence 7373, Ap
260	6	0.8	51	1	US-08-458-298-27	Sequence 27, Appl	333	87	4	US-09-270-767-32832	Sequence 32832, A
261	6	0.8	51	1	US-08-209-747-30	Sequence 30, Appl	334	87	4	US-09-270-767-48049	Sequence 48049, A
262	6	0.8	51	1	US-08-458-298-20	Sequence 20, Appl	335	88	4	US-09-489-039A-10714	Sequence 10714, A
263	6	0.8	51	1	US-08-458-298-30	Sequence 30, Appl	336	88	4	US-09-687-637B-29	Sequence 29, Appl
264	6	0.8	52	3	US-09-277-078-46	Sequence 46, Appl	337	89	4	US-09-687-637B-30	Sequence 30, Appl
265	6	0.8	55	1	US-08-209-747-25	Sequence 25, Appl	338	90	1	US-08-209-747-16	Sequence 16, Appl
266	6	0.8	55	1	US-08-458-298-25	Sequence 25, Appl	339	90	1	US-08-458-298-16	Sequence 16, Appl
267	6	0.8	56	3	US-08-936-165A-332	Sequence 332, App	340	90	4	US-09-621-976-4742	Sequence 4742, Ap
268	6	0.8	56	4	US-09-621-976-5925	Sequence 5925, Ap	341	96	4	US-09-107-532A-6122	Sequence 6122, Ap
269	6	0.8	56	4	US-09-270-767-57982	Sequence 57982, A	342	96	4	US-09-147-875A-1	Sequence 1, Appli
270	6	0.8	57	4	US-09-006-428A-5	Sequence 5, Appli	343	98	2	US-08-710-749-9	Sequence 9, Appli
271	6	0.8	57	4	US-09-615-387C-5	Sequence 5, Appli	344	99	2	US-08-710-749-10	Sequence 10, Appl
272	6	0.8	58	4	US-09-270-767-57771	Sequence 57771, A	345	99	2	US-08-710-749-11	Sequence 11, Appl
273	6	0.8	59	4	US-09-621-976-6937	Sequence 6937, Ap	346	99	4	US-09-732-210-1583	Sequence 1583, Ap
274	6	0.8	59	4	US-09-270-767-61138	Sequence 61138, A	347	99	4	US-09-147-875A-11	Sequence 11, Appl
275	6	0.8	60	3	US-08-928-213B-70	Sequence 70, Appl	348	99	4	US-09-147-875A-14	Sequence 14, Appl
276	6	0.8	61	4	US-09-248-796A-25960	Sequence 25960, A	349	99	4	US-09-147-875A-15	Sequence 15, Appl
277	6	0.8	61	4	US-09-248-796A-24801	Sequence 24801, A	350	99	4	US-09-147-875A-16	Sequence 16, Appl
278	6	0.8	61	4	US-09-248-796A-26402	Sequence 26402, A	351	100	2	US-08-308-494A-19	Sequence 19, Appl
279	6	0.8	63	4	US-09-673-395A-403	Sequence 403, App	352	100	4	US-09-147-875A-4	Sequence 4, Appli
280	6	0.8	64	2	US-08-209-521-20	Sequence 20, Appl	353	100	4	US-09-147-875A-8	Sequence 8, Appli
281	6	0.8	64	3	US-08-961-810D-130	Sequence 130, App	354	100	4	US-09-147-875A-10	Sequence 10, Appl
282	6	0.8	64	3	US-08-352-902D-130	Sequence 130, App	355	100	4	US-09-147-875A-12	Sequence 12, Appl
283	6	0.8	64	4	US-09-265-503B-130	Sequence 130, App	356	101	2	US-08-710-749-3	Sequence 3, Appli
284	6	0.8	64	4	US-09-270-767-61944	Sequence 61944, A	357	101	2	US-08-710-749-7	Sequence 7, Appli
285	6	0.8	65	4	US-09-248-796A-25471	Sequence 25471, A	358	101	4	US-09-147-875A-9	Sequence 9, Appli
286	6	0.8	65	4	US-09-640-211A-604	Sequence 604, App	359	102	1	US-08-169-701-1	Sequence 1, Appli
287	6	0.8	66	4	US-09-621-976-4488	Sequence 4488, App	360	102	2	US-08-710-749-8	Sequence 8, Appli
288	6	0.8	66	4	US-09-270-767-60792	Sequence 60792, A	361	102	2	US-08-710-749-21	Sequence 21, Appl
289	6	0.8	67	4	US-09-248-796A-23279	Sequence 23279, A	362	102	2	US-08-760-903-1	Sequence 1, Appli
290	6	0.8	68	4	US-09-352-991A-30574	Sequence 30574, A	363	102	2	US-08-482-191-1	Sequence 1, Appli
291	6	0.8	68	4	US-09-489-039A-11466	Sequence 11466, A	364	102	4	US-09-147-875A-18	Sequence 18, Appl
292	6	0.8	68	4	US-09-902-540-11724	Sequence 11724, A	365	102	4	US-09-270-767-57873	Sequence 57873, A
293	6	0.8	69	4	US-09-732-210-1004	Sequence 1004, Ap	366	102	4	US-09-902-540-14676	Sequence 14676, A
294	6	0.8	70	2	US-08-691-814B-34	Sequence 34, Appl	367	102	5	PCT-US96-10237-1	Sequence 1, Appli
295	6	0.8	70	4	US-09-732-210-883	Sequence 883, App	368	103	1	US-08-467-393-4	Sequence 4, Appli
296	6	0.8	70	4	US-09-621-976-5508	Sequence 5508, App	369	103	1	US-08-209-747-4	Sequence 4, Appli
297	6	0.8	70	6	5453566-2	Patent No. 5453566	370	103	1	US-08-458-298-4	Sequence 4, Appli
298	6	0.8	70	6	5453566-2	Patent No. 5453566	371	104	2	US-08-710-749-19	Sequence 19, Appl
299	6	0.8	71	4	US-09-732-210-93	Sequence 93, Appl	372	104	2	US-08-710-749-20	Sequence 20, Appl
300	6	0.8	71	4	US-09-270-767-56690	Sequence 56690, A	373	104	3	US-08-479-089A-5	Sequence 5, Appli
301	6	0.8	71	4	US-09-949-016-8499	Sequence 8499, Ap	374	104	3	US-08-479-089A-6	Sequence 6, Appli
302	6	0.8	73	4	US-09-489-039A-12244	Sequence 12244, A	375	104	4	US-07-669-545B-5	Sequence 5, Appli
303	6	0.8	73	4	US-09-502-540-10352	Sequence 10352, A	376	104	4	US-07-669-545B-6	Sequence 6, Appli
304	6	0.8	74	4	US-09-543-681A-8341	Sequence 8341, Ap	377	104	4	US-09-147-875A-20	Sequence 20, Appl
305	6	0.8	74	4	US-09-248-796A-25832	Sequence 25832, A	378	104	4	US-09-147-875A-21	Sequence 21, Appl
306	6	0.8	74	4	US-09-513-999C-5011	Sequence 5011, Ap	379	105	2	US-08-889-013C-6	Sequence 6, Appli
307	6	0.8	75	4	US-09-352-991A-21927	Sequence 21927, A	380	105	4	US-09-205-258-1082	Sequence 1082, Ap
308	6	0.8	75	4	US-09-198-452A-1228	Sequence 1228, Ap	381	105	4	US-09-583-110-5144	Sequence 5144, Ap
309	6	0.8	75	4	US-09-270-767-33600	Sequence 33600, A	382	105	4	US-09-640-211A-924	Sequence 924, App
310	6	0.8	76	4	US-09-270-767-48817	Sequence 48817, A	383	106	1	US-07-640-211A-2239	Sequence 2239, Ap
311	6	0.8	76	4	US-09-621-976-6191	Sequence 6191, Ap	384	106	2	US-07-732-242C-2	Sequence 2, Appli
312	6	0.8	78	4	US-09-732-210-1591	Sequence 1591, Ap	385	106	2	US-08-290-592B-34	Sequence 34, Appl
313	6	0.8	79	4	US-09-270-767-39286	Sequence 39286, A	386	106	2	US-08-290-592B-35	Sequence 35, Appl
314	6	0.8	79	4	US-09-270-767-54503	Sequence 54503, A	387	106	2	US-08-956-047-33	Sequence 33, Appl
315	6	0.8	80	1	US-08-209-747-12	Sequence 12, Appl	388	106	3	US-08-397-411-8	Sequence 8, Appli
316	6	0.8	80	1	US-08-458-298-12	Sequence 12, Appl	389	106	3	US-08-397-411-9	Sequence 9, Appli
317	6	0.8	80	2	US-08-710-749-18	Sequence 18, Appl	390	106	4	US-09-771-415-1	Sequence 1, Appli
318	6	0.8	80	4	US-09-336-536-35	Sequence 35, Appl	391	106	4	US-09-771-415-17	Sequence 17, Appl
319	6	0.8	80	4	US-09-147-875A-19	Sequence 19, Appl	392	106	4	US-09-232-290-24	Sequence 24, Appl

393	6	0.8	106	4	US-09-996-288-8	Sequence 8, Appli	466	6	0.8	123	4	US-09-270-767-43402	Sequence 43402, A
394	6	0.8	106	4	US-09-996-288-11	Sequence 11, Appl	467	6	0.8	123	4	US-09-438-185A-585	Sequence 585, App
395	6	0.8	106	4	US-09-996-288-54	Sequence 54, Appl	468	6	0.8	124	4	US-09-509-738C-15	Sequence 15, Appl
396	6	0.8	106	5	PCT-US95-10053-31	Sequence 31, Appl	469	6	0.8	126	2	US-08-656-586-6	Sequence 6, Appli
397	6	0.8	106	5	PCT-US95-10053-32	Sequence 32, Appl	470	6	0.8	126	2	US-09-663-600A-102	Sequence 102, App
398	6	0.8	106	5	PCT-US96-09448-34	Sequence 34, Appl	471	6	0.8	126	4	US-09-270-767-41467	Sequence 41467, A
399	6	0.8	106	5	PCT-US96-09448-35	Sequence 35, Appl	472	6	0.8	126	4	US-09-270-767-58058	Sequence 58058, A
400	6	0.8	107	1	US-07-942-245-3	Sequence 3, Appli	473	6	0.8	128	2	US-08-656-586-2	Sequence 2, Appli
401	6	0.8	107	2	US-08-303-569B-25	Sequence 26, Appl	474	6	0.8	128	2	US-08-956-047-31	Sequence 31, Appl
402	6	0.8	107	2	US-08-303-569B-26	Sequence 27, Appl	475	6	0.8	128	3	US-08-444-644-25	Sequence 25, Appl
403	6	0.8	107	2	US-08-303-569B-27	Sequence 28, Appl	476	6	0.8	128	3	US-08-232-246A-25	Sequence 25, Appl
404	6	0.8	107	2	US-08-303-569B-28	Sequence 29, Appl	477	6	0.8	128	3	US-09-134-001C-4164	Sequence 4164, Ap
405	6	0.8	107	2	US-08-303-569B-29	Sequence 28, Appl	478	6	0.8	128	3	US-09-270-767-57599	Sequence 57599, A
406	6	0.8	107	2	US-08-070-116A-8	Sequence 6, Appli	479	6	0.8	129	4	US-09-134-000C-5429	Sequence 5429, Ap
407	6	0.8	107	2	US-08-070-116A-8	Sequence 8, Appli	480	6	0.8	129	4	US-09-513-999C-5540	Sequence 5540, Ap
408	6	0.8	107	2	US-08-070-116A-9	Sequence 9, Appli	481	6	0.8	129	4	US-09-513-999C-8080	Sequence 8080, Ap
409	6	0.8	107	2	US-08-070-116A-18	Sequence 18, Appl	482	6	0.8	129	4	US-09-902-540-12956	Sequence 12956, A
410	6	0.8	107	2	US-08-116-247-8	Sequence 8, Appli	483	6	0.8	131	4	US-09-270-767-38194	Sequence 38194, A
411	6	0.8	107	2	US-08-116-247-26	Sequence 26, Appl	484	6	0.8	131	4	US-09-270-767-53411	Sequence 53411, A
412	6	0.8	107	2	US-08-116-247-27	Sequence 27, Appl	485	6	0.8	131	4	US-09-621-976-6550	Sequence 6550, Ap
413	6	0.8	107	2	US-08-116-247-28	Sequence 28, Appl	486	6	0.8	134	4	US-08-529-055-65	Sequence 27186, A
414	6	0.8	107	2	US-08-116-247-29	Sequence 29, Appl	487	6	0.8	134	4	US-09-248-796A-27186	Sequence 27186, A
415	6	0.8	107	4	US-09-370-838-113	Sequence 113, App	488	6	0.8	135	4	US-09-252-991A-22092	Sequence 22092, A
416	6	0.8	107	4	US-08-557-050-6	Sequence 6, Appli	489	6	0.8	135	4	US-09-107-433-5156	Sequence 5156, Ap
417	6	0.8	107	4	US-08-557-050-8	Sequence 8, Appli	490	6	0.8	136	4	US-09-270-767-39814	Sequence 39814, A
418	6	0.8	107	4	US-08-557-050-9	Sequence 9, Appli	491	6	0.8	136	4	US-09-270-767-55031	Sequence 55031, A
419	6	0.8	107	4	US-09-795-515-25	Sequence 25, Appl	492	6	0.8	137	4	US-09-489-039A-7466	Sequence 7466, Ap
420	6	0.8	107	4	US-09-795-515-26	Sequence 26, Appl	493	6	0.8	137	4	US-09-270-767-59938	Sequence 59938, A
421	6	0.8	107	4	US-09-795-515-27	Sequence 27, Appl	494	6	0.8	138	4	US-09-472-087-79	Sequence 79, Appl
422	6	0.8	107	4	US-09-795-515-28	Sequence 28, Appl	495	6	0.8	138	4	US-09-270-767-57429	Sequence 57429, A
423	6	0.8	107	4	US-09-795-515-29	Sequence 29, Appl	496	6	0.8	139	4	US-09-252-991A-22593	Sequence 22593, A
424	6	0.8	107	4	US-09-348-224-8	Sequence 8, Appli	497	6	0.8	139	4	US-09-902-540-10025	Sequence 10025, A
425	6	0.8	107	4	US-09-348-224-26	Sequence 26, Appl	498	6	0.8	140	4	US-09-248-796A-27587	Sequence 27587, A
426	6	0.8	107	4	US-09-348-224-27	Sequence 27, Appl	499	6	0.8	141	4	US-09-286-981B-2	Sequence 2, Appli
427	6	0.8	107	4	US-09-348-224-28	Sequence 28, Appl	500	6	0.8	141	4	US-09-270-767-43497	Sequence 43497, A
428	6	0.8	107	4	US-09-348-224-29	Sequence 29, Appl	501	6	0.8	142	4	US-09-252-991A-21627	Sequence 21627, A
429	6	0.8	107	4	US-09-854-133-113	Sequence 113, App	502	6	0.8	143	3	US-09-039-859-7	Sequence 7, Appli
430	6	0.8	107	5	PCT-US91-01360-3	Sequence 3, Appli	503	6	0.8	143	4	US-09-252-991A-22066	Sequence 22066, A
431	6	0.8	108	2	US-08-710-749-24	Sequence 24, Appl	504	6	0.8	143	4	US-09-252-991A-229827	Sequence 229827, A
432	6	0.8	108	4	US-09-147-875A-25	Sequence 25, Appl	505	6	0.8	144	1	US-08-133-979A-21	Sequence 21, Appl
433	6	0.8	108	4	US-09-726-219A-241	Sequence 241, App	506	6	0.8	144	2	US-08-436-890-21	Sequence 21, Appl
434	6	0.8	108	4	US-09-726-219A-242	Sequence 242, App	507	6	0.8	144	2	US-08-451-213-21	Sequence 21, Appl
435	6	0.8	108	4	US-09-726-219A-243	Sequence 243, App	508	6	0.8	145	4	US-09-602-787A-330	Sequence 330, App
436	6	0.8	108	4	US-09-726-219A-251	Sequence 251, App	509	6	0.8	145	4	US-09-640-211A-698	Sequence 698, App
437	6	0.8	108	4	US-09-726-219A-252	Sequence 252, App	510	6	0.8	145	4	US-09-902-540-13747	Sequence 13747, A
438	6	0.8	108	4	US-09-726-219A-253	Sequence 253, App	511	6	0.8	146	4	US-09-252-991A-24703	Sequence 24703, A
439	6	0.8	110	3	US-08-836-561-33	Sequence 33, Appl	512	6	0.8	146	4	US-09-902-540-13495	Sequence 13495, A
440	6	0.8	110	4	US-09-434-122-33	Sequence 33, Appl	513	6	0.8	147	4	US-09-602-787A-332	Sequence 332, App
441	6	0.8	110	4	US-09-107-532A-6721	Sequence 6721, Ap	514	6	0.8	148	4	US-09-328-352-8000	Sequence 8000, Ap
442	6	0.8	110	4	US-09-489-039A-10081	Sequence 10081, A	515	6	0.8	150	3	US-08-857-076-17	Sequence 17, Appl
443	6	0.8	110	4	US-09-902-540-11433	Sequence 11433, A	516	6	0.8	150	4	US-09-663-600A-196	Sequence 196, App
444	6	0.8	112	4	US-09-543-681A-4827	Sequence 4827, Ap	517	6	0.8	150	4	US-09-902-540-12171	Sequence 12171, A
445	6	0.8	112	4	US-09-710-279-2114	Sequence 2114, Ap	518	6	0.8	151	4	US-09-252-991A-16814	Sequence 16814, A
446	6	0.8	113	2	US-08-256-568B-85	Sequence 85, Appl	519	6	0.8	151	4	US-09-328-352-5731	Sequence 5751, Ap
447	6	0.8	113	3	US-09-038-369B-85	Sequence 85, Appl	520	6	0.8	151	4	US-09-540-236-2801	Sequence 2801, Ap
448	6	0.8	113	3	US-08-836-075A-82	Sequence 82, Appl	521	6	0.8	151	4	US-09-248-796A-16825	Sequence 16825, A
449	6	0.8	113	3	US-08-836-075A-98	Sequence 98, Appl	522	6	0.8	152	4	US-09-270-767-48811	Sequence 48811, A
450	6	0.8	113	4	US-09-378-900A-85	Sequence 85, Appl	523	6	0.8	153	4	US-09-732-210-1748	Sequence 1748, Ap
451	6	0.8	113	4	US-09-899-044-85	Sequence 85, Appl	524	6	0.8	153	4	US-09-270-767-32681	Sequence 32681, A
452	6	0.8	113	4	US-09-489-039A-8111	Sequence 8131, Ap	525	6	0.8	153	4	US-09-270-767-47898	Sequence 47898, A
453	6	0.8	113	4	US-09-878-281A-218	Sequence 218, App	526	6	0.8	153	4	US-09-902-540-12086	Sequence 12086, A
454	6	0.8	114	4	US-09-710-279-2252	Sequence 2252, Ap	527	6	0.8	155	1	US-08-209-747-15	Sequence 15, Appl
455	6	0.8	114	4	US-09-513-999C-5777	Sequence 5777, Ap	528	6	0.8	155	1	US-08-458-298-15	Sequence 29828, Ap
456	6	0.8	117	1	US-08-274-661B-38	Sequence 38, Appl	529	6	0.8	155	4	US-09-489-039A-7828	Sequence 7828, Ap
457	6	0.8	117	4	US-09-513-999C-6175	Sequence 6175, Ap	530	6	0.8	156	4	US-09-134-000C-6299	Sequence 6299, Ap
458	6	0.8	119	4	US-09-732-210-678	Sequence 678, App	531	6	0.8	157	4	US-09-328-352-4155	Sequence 4165, Ap
459	6	0.8	119	4	US-09-270-767-47348	Sequence 47348, A	532	6	0.8	157	4	US-09-902-540-14881	Sequence 14881, A
460	6	0.8	120	4	US-09-308-345A-21	Sequence 21, Appl	533	6	0.8	158	4	US-09-252-991A-22352	Sequence 22352, A
461	6	0.8	122	4	US-09-198-452A-510	Sequence 510, App	534	6	0.8	158	4	US-09-134-000C-4025	Sequence 4025, App
462	6	0.8	122	4	US-09-270-767-33422	Sequence 33422, A	535	6	0.8	158	4	US-09-265-585C-130	Sequence 130, App
463	6	0.8	122	4	US-09-270-767-48639	Sequence 48639, A	536	6	0.8	159	4	US-09-252-991A-22914	Sequence 22914, A
464	6	0.8	122	4	US-09-902-540-13323	Sequence 13323, A	537	6	0.8	159	4	US-09-602-787A-102	Sequence 102, App
465	6	0.8	123	4	US-09-198-452A-625	Sequence 625, App	538	6	0.8	159	4	US-09-270-767-37981	Sequence 37981, A

539	6	0.8	159	4	US-09-270-767-46525	Sequence 46525, A	612	191	4	US-08-671-548C-2	Sequence 2, Appli
540	6	0.8	159	4	US-09-270-767-53198	Sequence 53198, A	613	191	4	US-09-252-991A-24515	Sequence 24515, A
541	6	0.8	160	3	US-09-117-257-38	Sequence 38, Appl	614	191	4	US-09-328-352-6761	Sequence 6761, Ap
542	6	0.8	160	3	US-08-489-352-38	Sequence 352, App	615	191	4	US-09-640-211A-1080	Sequence 1080, Ap
543	6	0.8	160	3	US-08-858-207A-322	Sequence 322, App	616	192	4	US-09-149-476-419	Sequence 419, App
544	6	0.8	160	4	US-09-252-991A-16641	Sequence 16641, A	617	192	4	US-09-543-681A-7846	Sequence 7846, Ap
545	6	0.8	160	4	US-09-621-976-6030	Sequence 6030, Ap	618	193	4	US-08-671-548C-16	Sequence 16, Appl
546	6	0.8	160	4	US-09-270-767-39354	Sequence 39354, A	619	194	4	US-09-248-796A-27860	Sequence 27860, A
547	6	0.8	160	4	US-09-270-767-45565	Sequence 45565, A	620	195	2	US-08-403-852D-24	Sequence 24, Appl
548	6	0.8	160	4	US-09-270-767-54571	Sequence 54571, A	621	195	3	US-08-510-646B-25	Sequence 25, Appl
549	6	0.8	161	4	US-09-902-540-10892	Sequence 10892, A	622	195	3	US-09-231-818-24	Sequence 24, Appl
550	6	0.8	161	4	US-09-902-540-16115	Sequence 16115, A	623	195	4	US-09-635-359B-24	Sequence 24, Appl
551	6	0.8	162	3	US-09-446-504-27	Sequence 27, Appl	624	195	4	US-09-583-110-4558	Sequence 4558, Ap
552	6	0.8	162	3	US-09-712-266-27	Sequence 27, Appl	625	196	4	US-09-711-164-379	Sequence 379, App
553	6	0.8	162	4	US-09-439-148-5	Sequence 5, Appl	626	196	4	US-09-543-681A-7659	Sequence 7659, Ap
554	6	0.8	162	4	US-09-270-767-43246	Sequence 43246, A	627	197	1	US-08-567-509-1	Sequence 1, Appli
555	6	0.8	164	4	US-09-270-767-33348	Sequence 33348, A	628	197	2	US-08-779-870-1	Sequence 1, Appli
556	6	0.8	164	4	US-09-270-767-48565	Sequence 48565, A	629	197	4	US-08-529-055-44	Sequence 44, Appl
557	6	0.8	165	4	US-09-513-999C-7900	Sequence 7900, Ap	630	198	4	US-08-529-055-36	Sequence 36, Appl
558	6	0.8	166	4	US-09-252-991A-19472	Sequence 19472, A	631	198	4	US-08-529-055-61	Sequence 61, Appl
559	6	0.8	166	4	US-09-889-463A-12	Sequence 12, Appl	632	198	4	US-09-270-767-36571	Sequence 36571, A
560	6	0.8	167	3	US-09-062-440-8	Sequence 8, Appl	633	198	4	US-09-270-767-44202	Sequence 44202, A
561	6	0.8	167	3	US-09-062-440-9	Sequence 9, Appl	634	198	4	US-09-270-767-51788	Sequence 51788, A
562	6	0.8	167	3	US-09-062-440-11	Sequence 11, Appl	635	198	4	US-09-538-092-1045	Sequence 1045, Ap
563	6	0.8	167	3	US-09-712-495-8	Sequence 8, Appl	636	198	4	US-09-949-016-11711	Sequence 11711, A
564	6	0.8	167	3	US-09-712-495-9	Sequence 9, Appl	637	200	4	US-09-270-767-32508	Sequence 32508, A
565	6	0.8	167	3	US-09-712-495-11	Sequence 11, Appl	638	200	4	US-09-270-767-47725	Sequence 47725, A
566	6	0.8	167	4	US-09-252-991A-31370	Sequence 31370, A	639	201	4	US-09-270-767-32368	Sequence 32368, A
567	6	0.8	167	4	US-09-902-540-14730	Sequence 14730, A	640	201	4	US-09-270-767-47585	Sequence 47585, A
568	6	0.8	168	3	US-08-679-006-30	Sequence 30, Appl	641	202	4	US-09-949-016-7318	Sequence 7318, Ap
569	6	0.8	168	4	US-09-107-532A-3745	Sequence 3745, Ap	642	203	3	US-09-134-001C-3696	Sequence 3696, Ap
570	6	0.8	168	4	US-09-134-000C-4552	Sequence 4552, Ap	643	203	4	US-09-248-796A-20648	Sequence 20648, A
571	6	0.8	168	4	US-09-358-405-30	Sequence 30, Appl	644	204	4	US-09-328-352-6644	Sequence 6644, Ap
572	6	0.8	168	4	US-09-252-991A-31389	Sequence 31389, A	645	204	4	US-08-529-055-51	Sequence 51, Appl
573	6	0.8	169	4	US-09-270-767-36359	Sequence 36359, A	646	204	4	US-08-529-055-58	Sequence 58, Appl
574	6	0.8	169	4	US-09-270-767-39082	Sequence 39082, A	647	204	4	US-09-710-279-2394	Sequence 2394, Ap
575	6	0.8	169	4	US-09-270-767-51576	Sequence 51576, A	648	205	4	US-09-710-279-3020	Sequence 3020, Ap
576	6	0.8	169	4	US-09-270-767-54299	Sequence 54299, A	649	206	3	US-09-134-001C-4621	Sequence 4621, Ap
577	6	0.8	169	4	US-09-248-796A-26743	Sequence 26743, A	650	206	4	US-08-529-055-54	Sequence 54, Appl
578	6	0.8	170	4	US-09-732-210-558	Sequence 558, App	651	207	3	US-09-046-894-33	Sequence 33, Appl
579	6	0.8	170	4	US-08-529-055-60	Sequence 60, Appl	652	208	3	US-09-134-001C-4132	Sequence 4132, Ap
580	6	0.8	171	4	US-09-248-796A-27723	Sequence 27723, A	653	209	4	US-09-583-110-2988	Sequence 2988, Ap
581	6	0.8	172	4	US-09-583-110-3305	Sequence 3305, Ap	654	209	4	US-09-107-433-3989	Sequence 3989, Ap
582	6	0.8	173	4	US-09-270-767-32051	Sequence 32051, A	655	210	4	US-09-543-681A-7093	Sequence 7093, Ap
583	6	0.8	173	4	US-09-270-767-47268	Sequence 47268, A	656	211	4	US-09-902-540-10681	Sequence 10681, A
584	6	0.8	174	4	US-09-149-476-413	Sequence 413, App	657	212	4	US-09-543-681A-6069	Sequence 6069, Ap
585	6	0.8	174	4	US-09-270-767-40521	Sequence 40521, A	658	212	4	US-09-248-796A-15317	Sequence 15317, A
586	6	0.8	174	4	US-09-270-767-55737	Sequence 55737, A	659	213	2	US-08-941-263-3	Sequence 3, Appli
587	6	0.8	175	4	US-09-252-991A-28806	Sequence 28806, A	660	213	3	US-09-227-178-3	Sequence 3, Appli
588	6	0.8	176	4	US-09-780-717-2	Sequence 32224, A	661	213	3	US-08-397-411-12	Sequence 12, Appl
589	6	0.8	176	4	US-09-248-796A-20163	Sequence 20163, A	662	213	3	US-09-470-449-3	Sequence 3, Appli
590	6	0.8	176	4	US-09-248-796A-25947	Sequence 25947, A	663	213	4	US-09-726-775-3	Sequence 3, Appli
591	6	0.8	176	4	US-09-248-796A-24917	Sequence 24917, A	664	213	4	US-09-252-991A-25866	Sequence 25866, A
592	6	0.8	177	4	US-08-671-548C-14	Sequence 14, Appl	665	213	4	US-08-529-055-47	Sequence 47, Appl
593	6	0.8	178	4	US-09-732-210-1077	Sequence 1077, Ap	666	213	4	US-09-996-288-209	Sequence 209, App
594	6	0.8	180	4	US-09-252-991A-17913	Sequence 17913, A	667	213	4	US-09-996-288-231	Sequence 231, App
595	6	0.8	180	4	US-08-529-055-42	Sequence 42, Appl	668	213	4	US-09-603-208A-124	Sequence 124, App
596	6	0.8	181	4	US-08-353-476-93	Sequence 93, Appl	669	213	4	US-09-902-540-13705	Sequence 13705, A
597	6	0.8	182	2	US-08-858-207A-434	Sequence 434, App	670	214	4	US-09-543-681A-6408	Sequence 6408, Ap
598	6	0.8	182	3	US-08-529-055-50	Sequence 50, Appl	671	214	4	US-09-270-767-42972	Sequence 42972, A
599	6	0.8	183	4	US-09-122-443-13	Sequence 13, Appl	672	214	4	US-09-893-737-306	Sequence 306, App
600	6	0.8	184	3	US-09-558-089-13	Sequence 13, Appl	673	215	4	US-09-252-991A-22038	Sequence 22038, A
601	6	0.8	184	4	US-09-558-087-13	Sequence 13, Appl	674	216	4	US-09-543-681A-6821	Sequence 6821, Ap
602	6	0.8	184	4	US-09-558-087-13	Sequence 13, Appl	675	216	4	US-09-071-035-312	Sequence 312, App
603	6	0.8	184	4	US-08-529-055-46	Sequence 46, Appl	676	217	4	US-09-484-577A-30	Sequence 30, Appl
604	6	0.8	185	4	US-09-902-540-14912	Sequence 14912, A	677	217	4	US-09-270-767-43455	Sequence 43455, A
605	6	0.8	186	4	US-09-270-767-45734	Sequence 45734, A	678	218	4	US-09-248-796A-16056	Sequence 16056, A
606	6	0.8	187	4	US-09-248-796A-19329	Sequence 19329, A	679	218	4	US-09-107-433-3578	Sequence 3578, Ap
607	6	0.8	187	4	US-08-529-055-59	Sequence 59, Appl	680	218	4	US-09-902-540-13913	Sequence 13913, A
608	6	0.8	188	4	US-09-902-540-12348	Sequence 12348, A	681	219	2	US-08-401-068-6	Sequence 6, Appli
609	6	0.8	188	4	US-09-252-991A-30049	Sequence 30049, A	682	219	2	US-08-846-338-6	Sequence 6, Appli
610	6	0.8	189	4			683	219	2		
611	6	0.8	189	4			684	219	2		

685	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App	758	6	0.8	246	4	US-09-134-000C-5137	Sequence 5137, Ap
686	6	0.8	219	4	US-09-438-185A-593	Sequence 593, App	759	6	0.8	246	4	US-09-244-805-32	Sequence 32, Appl
687	6	0.8	220	4	US-09-853-450-38	Sequence 38, Appl	760	6	0.8	248	4	US-09-248-796A-18654	Sequence 18654, A
688	6	0.8	221	4	US-09-198-452A-292	Sequence 292, App	761	6	0.8	248	4	US-09-248-796A-19980	Sequence 19980, A
689	6	0.8	222	2	US-08-190-199A-67	Sequence 67, Appl	762	6	0.8	248	4	US-10-144-198-33	Sequence 33, Appl
690	6	0.8	222	4	US-08-232-991A-21377	Sequence 21377, A	763	6	0.8	248	4	US-09-902-540-11644	Sequence 11644, A
691	6	0.8	223	2	US-08-190-199A-63	Sequence 63, Appl	764	6	0.8	249	2	US-08-685-992-8	Sequence 8, Appli
692	6	0.8	223	4	US-09-252-991A-17072	Sequence 17072, A	765	6	0.8	249	2	US-09-144-925-8	Sequence 8, Appli
693	6	0.8	224	4	US-09-489-039A-13921	Sequence 13921, A	766	6	0.8	249	4	US-09-949-016-8151	Sequence 8151, Ap
694	6	0.8	224	4	US-09-248-796A-18609	Sequence 18609, A	767	6	0.8	249	4	US-09-489-039A-9843	Sequence 9843, Ap
695	6	0.8	224	4	US-09-438-185A-281	Sequence 281, App	768	6	0.8	250	4	US-09-134-000C-4602	Sequence 4602, Ap
696	6	0.8	225	4	US-09-270-767-3278	Sequence 3278, A	769	6	0.8	251	1	US-08-209-747-8	Sequence 8, Appli
697	6	0.8	225	4	US-09-270-767-47945	Sequence 47945, A	770	6	0.8	251	1	US-08-458-298-8	Sequence 8, Appli
698	6	0.8	225	4	US-09-710-279-1594	Sequence 1594, Ap	771	6	0.8	251	4	US-09-902-540-15293	Sequence 15293, A
699	6	0.8	226	4	US-09-252-991A-17294	Sequence 17294, A	772	6	0.8	252	4	US-09-252-991A-16901	Sequence 16901, A
700	6	0.8	226	4	US-09-270-767-60023	Sequence 60023, A	773	6	0.8	252	4	US-09-583-110-3303	Sequence 3303, Ap
701	6	0.8	227	4	US-09-252-991A-30027	Sequence 30027, A	774	6	0.8	252	4	US-09-270-767-47090	Sequence 47090, A
702	6	0.8	229	4	US-09-107-532A-6064	Sequence 6064, Ap	775	6	0.8	253	4	US-09-336-910A-7	Sequence 7, Appli
703	6	0.8	229	4	US-10-112-802-1	Sequence 1, Appli	776	6	0.8	253	4	US-09-902-540-14305	Sequence 14305, A
704	6	0.8	231	4	US-09-270-767-43196	Sequence 43196, A	777	6	0.8	253	4	US-09-902-540-14305	Sequence 14305, A
705	6	0.8	232	4	US-08-529-055-70	Sequence 70, Appl	778	6	0.8	254	4	US-09-252-991A-22771	Sequence 22771, A
706	6	0.8	232	4	US-09-248-796A-14122	Sequence 14122, A	779	6	0.8	254	4	US-09-134-000C-4199	Sequence 4199, Ap
707	6	0.8	233	4	US-09-252-991A-20802	Sequence 20802, A	780	6	0.8	254	4	US-09-586-106D-159	Sequence 159, App
708	6	0.8	233	4	US-09-252-991A-21274	Sequence 21274, A	781	6	0.8	254	4	US-09-949-016-6948	Sequence 6948, Ap
709	6	0.8	233	4	US-09-252-991A-23516	Sequence 23516, A	782	6	0.8	255	4	US-09-553-498-8	Sequence 8, Appli
710	6	0.8	233	4	US-09-270-767-43719	Sequence 43719, A	783	6	0.8	255	4	US-09-618-869-8	Sequence 8, Appli
711	6	0.8	234	3	US-08-836-236-4	Sequence 4, Appli	784	6	0.8	255	4	US-09-902-540-16637	Sequence 16637, A
712	6	0.8	234	3	US-08-836-236-5	Sequence 5, Appli	785	6	0.8	256	4	US-09-292-412-2	Sequence 2, Appli
713	6	0.8	234	3	US-08-715-628B-3	Sequence 3, Appli	786	6	0.8	256	4	US-09-252-991A-32307	Sequence 32307, A
714	6	0.8	234	4	US-09-535-679-4	Sequence 4, Appli	787	6	0.8	256	4	US-09-107-532A-3657	Sequence 3657, Ap
715	6	0.8	234	4	US-09-535-679-5	Sequence 5, Appli	788	6	0.8	256	4	US-09-583-110-4113	Sequence 4113, Ap
716	6	0.8	235	2	US-08-130-199A-61	Sequence 61, Appl	789	6	0.8	256	4	US-10-138-701-6	Sequence 6, Appli
717	6	0.8	235	2	US-08-303-569B-5	Sequence 5, Appli	790	6	0.8	256	4	US-09-292-411A-2	Sequence 2, Appli
718	6	0.8	235	2	US-08-116-247-5	Sequence 5, Appli	791	6	0.8	256	4	US-09-902-540-12724	Sequence 12724, A
719	6	0.8	235	4	US-09-795-515-5	Sequence 5, Appli	792	6	0.8	257	4	US-09-328-352-4324	Sequence 4324, Ap
720	6	0.8	235	4	US-09-270-767-48485	Sequence 48485, A	793	6	0.8	258	4	US-09-724-623-105	Sequence 105, App
721	6	0.8	235	4	US-09-248-796A-18489	Sequence 18489, A	794	6	0.8	258	4	US-09-023-942A-8	Sequence 8, Appli
722	6	0.8	235	4	US-09-848-224-5	Sequence 5, Appli	795	6	0.8	258	4	US-09-081-385-150	Sequence 150, App
723	6	0.8	235	4	US-09-949-016-7903	Sequence 7903, Ap	796	6	0.8	258	4	US-09-270-767-32398	Sequence 32398, A
724	6	0.8	236	2	US-08-190-199A-65	Sequence 65, Appl	797	6	0.8	258	4	US-09-270-767-43894	Sequence 43894, A
725	6	0.8	236	3	US-08-411-768B-8	Sequence 8, Appli	798	6	0.8	258	4	US-09-270-767-59125	Sequence 59125, A
726	6	0.8	236	4	US-09-543-681A-6359	Sequence 6359, Ap	799	6	0.8	259	4	US-09-270-767-45089	Sequence 45089, A
727	6	0.8	236	4	US-09-827-688-2	Sequence 2, Appli	800	6	0.8	260	3	US-09-134-001C-4009	Sequence 4009, Ap
728	6	0.8	237	3	US-09-320-878-11	Sequence 11, Appl	801	6	0.8	260	4	US-09-489-039A-7421	Sequence 7421, Ap
729	6	0.8	237	3	US-09-105-537-18	Sequence 18, Appl	802	6	0.8	260	4	US-09-270-767-33511	Sequence 33511, A
730	6	0.8	237	3	US-09-216-295-19	Sequence 19, Appl	803	6	0.8	260	4	US-09-270-767-46440	Sequence 46440, A
731	6	0.8	237	4	US-09-657-440-11	Sequence 11, Appl	804	6	0.8	260	4	US-09-248-796A-17592	Sequence 17592, A
732	6	0.8	237	4	US-09-232-991A-19656	Sequence 19656, A	805	6	0.8	261	4	US-09-489-039A-10725	Sequence 10725, A
733	6	0.8	237	4	US-09-543-681A-5471	Sequence 5471, Ap	806	6	0.8	263	4	US-09-252-991A-23754	Sequence 23754, A
734	6	0.8	237	4	US-09-632-570-19	Sequence 19, Appl	807	6	0.8	264	3	US-09-035-382-4	Sequence 4, Appli
735	6	0.8	237	4	US-09-632-575-49	Sequence 49, Appl	808	6	0.8	264	4	US-09-252-991A-27675	Sequence 27675, A
736	6	0.8	238	4	US-09-328-352-6703	Sequence 6703, Ap	809	6	0.8	264	4	US-09-134-000C-4403	Sequence 4403, Ap
737	6	0.8	238	4	US-09-543-681A-4429	Sequence 4429, Ap	810	6	0.8	264	4	US-09-902-540-16652	Sequence 16652, A
738	6	0.8	239	4	US-09-540-236-3366	Sequence 3366, Ap	811	6	0.8	266	4	US-09-050-739-153	Sequence 153, App
739	6	0.8	239	4	US-09-248-796A-15852	Sequence 15852, A	812	6	0.8	266	4	US-09-655-908-20	Sequence 20, Appl
740	6	0.8	239	4	US-09-107-433-3281	Sequence 3281, Ap	813	6	0.8	266	4	US-09-248-796A-20084	Sequence 20084, A
741	6	0.8	240	2	US-08-956-047-25	Sequence 25, Appl	814	6	0.8	267	4	US-09-902-540-13043	Sequence 13043, A
742	6	0.8	240	4	US-09-540-236-2994	Sequence 2994, Ap	815	6	0.8	267	4	US-09-489-039A-13450	Sequence 13450, A
743	6	0.8	240	4	US-09-270-767-48132	Sequence 48132, Ap	816	6	0.8	267	4	US-09-976-594-212	Sequence 212, App
744	6	0.8	241	4	US-09-370-838-194	Sequence 194, App	817	6	0.8	267	4	US-09-248-796A-18561	Sequence 18561, A
745	6	0.8	241	4	US-09-387-372-4	Sequence 4, Appli	818	6	0.8	267	4	US-09-902-540-14651	Sequence 14651, A
746	6	0.8	241	4	US-09-270-767-38616	Sequence 38616, A	819	6	0.8	268	4	US-09-328-352-8118	Sequence 8118, Ap
747	6	0.8	241	4	US-09-270-767-40578	Sequence 40578, A	820	6	0.8	268	4	US-09-540-236-3336	Sequence 3336, Ap
748	6	0.8	241	4	US-09-270-767-53833	Sequence 53833, A	821	6	0.8	269	4	US-09-583-110-3865	Sequence 3865, Ap
749	6	0.8	241	4	US-09-270-767-55794	Sequence 55794, A	822	6	0.8	269	4	US-09-270-767-42664	Sequence 42664, A
750	6	0.8	241	4	US-09-894-133-194	Sequence 133, App	823	6	0.8	270	3	US-08-878-474-1	Sequence 1, Appli
751	6	0.8	241	4	US-09-581-345-5	Sequence 5, Appli	824	6	0.8	270	4	US-09-107-433-5194	Sequence 5194, Ap
752	6	0.8	241	4	US-09-902-540-9790	Sequence 9790, Ap	825	6	0.8	271	4	US-09-540-236-2326	Sequence 2326, Ap
753	6	0.8	242	4	US-09-583-110-3522	Sequence 3522, Ap	826	6	0.8	271	4	US-09-270-767-46455	Sequence 46455, A
754	6	0.8	242	4	US-09-959-392-34	Sequence 34, Appl	827	6	0.8	271	6	5175255-1	Patent No. 5175255
755	6	0.8	242	4	US-09-949-016-10911	Sequence 10911, A	828	6	0.8	271	6	5175255-1	Patent No. 5175255
756	6	0.8	245	4	US-09-071-035-310	Sequence 310, App	829	6	0.8	272	4	US-09-902-540-16810	Sequence 16810, A
757	6	0.8	246	4	US-09-336-536-31	Sequence 31, Appl	830	6	0.8	273	4	US-09-252-991A-25600	Sequence 25600, A

831	6	0.8	274	4	US-09-489-039A-14339	Sequence 14339, A	904	6	0.8	305	4	US-09-248-796A-24107	Sequence 24107, A
832	6	0.8	276	3	US-08-961-083-134	Sequence 134, App	905	6	0.8	305	4	US-09-949-016-7706	Sequence 7706, Ap
833	6	0.8	276	4	US-09-232-991A-17951	Sequence 17951, A	906	6	0.8	306	4	US-09-489-039A-10306	Sequence 10306, A
834	6	0.8	276	4	US-09-536-784-134	Sequence 134, App	907	6	0.8	306	4	US-09-107-433-2663	Sequence 2663, Ap
835	6	0.8	276	4	US-09-902-540-15737	Sequence 15737, A	908	6	0.8	307	3	US-09-134-001C-3792	Sequence 3792, Ap
836	6	0.8	279	4	US-09-314-701-60	Sequence 60, Appl	909	6	0.8	307	4	US-09-270-767-44911	Sequence 44911, A
837	6	0.8	279	4	US-09-543-681A-4433	Sequence 4433, Ap	910	6	0.8	308	4	US-09-352-991A-27249	Sequence 27249, A
838	6	0.8	279	4	US-09-270-767-33415	Sequence 33415, A	911	6	0.8	308	4	US-09-328-352-6762	Sequence 6762, Ap
839	6	0.8	279	4	US-09-270-767-48632	Sequence 48632, A	912	6	0.8	309	4	US-09-270-767-44995	Sequence 44995, A
840	6	0.8	279	4	US-10-144-198-10	Sequence 10, Appl	913	6	0.8	310	4	US-09-543-681A-68958	Sequence 68958, Ap
841	6	0.8	280	4	US-09-489-039A-7715	Sequence 7715, Ap	914	6	0.8	310	4	US-09-538-092-690	Sequence 690, App
842	6	0.8	280	4	US-09-583-110-4231	Sequence 4231, Ap	915	6	0.8	311	4	US-09-107-532A-4438	Sequence 4438, Ap
843	6	0.8	281	4	US-09-252-991A-29199	Sequence 29199, A	916	6	0.8	311	4	US-09-107-532A-4439	Sequence 4439, Ap
844	6	0.8	282	4	US-09-248-796A-14445	Sequence 14445, A	917	6	0.8	311	4	US-09-107-433-2823	Sequence 2823, Ap
845	6	0.8	283	4	US-09-270-767-45300	Sequence 45300, A	918	6	0.8	312	4	US-09-538-092-42	Sequence 42, Appl
846	6	0.8	284	3	US-08-592-214A-24	Sequence 24, Appl	919	6	0.8	313	3	US-09-387-574-4	Sequence 4, Appli
847	6	0.8	284	3	US-08-659-188-20	Sequence 20, Appl	920	6	0.8	313	3	US-09-396-651B-3	Sequence 3, Appli
848	6	0.8	284	3	US-08-655-227-20	Sequence 20, Appl	921	6	0.8	313	3	US-09-668-096-4	Sequence 4, Appli
849	6	0.8	284	3	US-08-655-241-20	Sequence 20, Appl	922	6	0.8	313	3	US-09-470-512A-2	Sequence 2, Appli
850	6	0.8	284	3	US-09-149-976-24	Sequence 24, Appl	923	6	0.8	313	3	US-09-470-512A-10	Sequence 10, Appl
851	6	0.8	284	3	US-09-338-326-20	Sequence 20, Appl	924	6	0.8	313	4	US-09-543-681A-8278	Sequence 8278, Ap
852	6	0.8	284	4	US-09-134-000C-5638	Sequence 5638, Ap	925	6	0.8	313	4	US-09-248-796A-17065	Sequence 17065, A
853	6	0.8	284	4	US-09-583-450-20	Sequence 20, Appl	926	6	0.8	313	4	US-09-949-016-8602	Sequence 8602, Ap
854	6	0.8	285	4	US-09-540-236-2157	Sequence 2157, Ap	927	6	0.8	314	4	US-09-252-991A-33054	Sequence 33054, A
855	6	0.8	288	3	US-08-312-949-4	Sequence 4, Appli	928	6	0.8	314	4	US-09-270-767-32458	Sequence 32458, A
856	6	0.8	288	3	US-08-446-201-4	Sequence 4, Appli	929	6	0.8	314	4	US-09-270-767-42020	Sequence 42020, A
857	6	0.8	288	4	US-09-232-991A-20608	Sequence 20608, A	930	6	0.8	314	4	US-09-270-767-47675	Sequence 47675, A
858	6	0.8	288	4	US-09-949-016-10862	Sequence 10862, A	931	6	0.8	315	1	US-08-118-270-28	Sequence 28, Appl
859	6	0.8	288	5	PCT-US95-04801-7	Sequence 7, Appli	932	6	0.8	315	4	US-09-248-796A-18699	Sequence 18699, A
860	6	0.8	289	1	US-08-072-070-4	Sequence 4, Appli	933	6	0.8	315	4	US-09-252-991A-19140	Sequence 19140, A
861	6	0.8	289	1	US-08-469-434-4	Sequence 4, Appli	934	6	0.8	315	4	US-09-538-092-41	Sequence 41, Appl
862	6	0.8	289	1	US-08-214-222-4	Sequence 4, Appli	935	6	0.8	315	4	US-09-902-540-15838	Sequence 15838, A
863	6	0.8	289	2	US-08-467-852A-5	Sequence 5, Appli	936	6	0.8	315	5	PCT-US93-08528-28	Sequence 28, Appl
864	6	0.8	289	2	US-08-468-718-4	Sequence 4, Appli	937	6	0.8	316	3	US-09-504-358-10	Sequence 10, Appl
865	6	0.8	289	2	US-08-247-491A-5	Sequence 5, Appli	938	6	0.8	316	4	US-09-954-314-10	Sequence 10, Appl
866	6	0.8	289	4	US-09-543-681A-8235	Sequence 8235, Ap	939	6	0.8	316	4	US-09-328-352-6555	Sequence 6555, Ap
867	6	0.8	289	4	US-09-583-110-3563	Sequence 3563, Ap	940	6	0.8	316	4	US-10-230-562-10	Sequence 10, Appl
868	6	0.8	290	3	US-09-134-001C-4938	Sequence 4938, Ap	941	6	0.8	316	4	US-09-902-540-12782	Sequence 12782, A
869	6	0.8	290	4	US-09-107-532A-3841	Sequence 3841, Ap	942	6	0.8	317	4	US-08-937-067-6	Sequence 6, Appli
870	6	0.8	290	4	US-09-743-847-2	Sequence 2, Appli	943	6	0.8	317	4	US-09-252-991A-29954	Sequence 29954, A
871	6	0.8	290	4	US-09-248-796A-18749	Sequence 18749, A	944	6	0.8	317	4	US-09-328-352-8169	Sequence 8169, Ap
872	6	0.8	291	4	US-09-134-000C-4458	Sequence 4458, Ap	945	6	0.8	317	4	US-09-583-110-3082	Sequence 3082, Ap
873	6	0.8	292	4	US-09-634-238-236	Sequence 236, App	946	6	0.8	317	4	US-09-949-016-6300	Sequence 6300, Ap
874	6	0.8	292	4	US-09-270-767-43846	Sequence 43846, A	947	6	0.8	318	4	US-09-252-991A-31545	Sequence 31545, A
875	6	0.8	292	4	US-09-107-433-4868	Sequence 4868, Ap	948	6	0.8	318	4	US-09-252-991A-32832	Sequence 32832, A
876	6	0.8	293	4	US-09-252-991A-27745	Sequence 27745, A	949	6	0.8	319	4	US-09-270-767-44572	Sequence 44572, A
877	6	0.8	293	4	US-09-949-016-8027	Sequence 8027, Ap	950	6	0.8	320	4	US-09-328-352-4526	Sequence 4526, Ap
878	6	0.8	294	4	US-09-252-991A-26450	Sequence 26450, A	951	6	0.8	320	4	US-09-328-352-4536	Sequence 4536, Ap
879	6	0.8	295	4	US-09-198-452A-268	Sequence 268, App	952	6	0.8	320	4	US-09-107-433-4531	Sequence 4531, Ap
880	6	0.8	295	4	US-09-270-767-45025	Sequence 45025, A	953	6	0.8	322	4	US-09-252-991A-32158	Sequence 32158, A
881	6	0.8	295	4	US-09-438-185A-258	Sequence 258, App	954	6	0.8	322	4	US-09-107-532A-4662	Sequence 4662, Ap
882	6	0.8	296	4	US-09-270-767-42478	Sequence 42478, A	955	6	0.8	322	4	US-09-949-016-8722	Sequence 8722, Ap
883	6	0.8	296	4	US-09-270-767-48808	Sequence 48808, A	956	6	0.8	322	4	US-09-949-016-8723	Sequence 8723, Ap
884	6	0.8	297	4	US-09-314-701-14	Sequence 14, Appl	957	6	0.8	323	4	US-09-134-000C-4836	Sequence 4836, Ap
885	6	0.8	297	4	US-09-252-991A-29778	Sequence 29778, A	958	6	0.8	323	4	US-09-248-796A-16307	Sequence 16307, A
886	6	0.8	297	4	US-09-489-039A-10089	Sequence 10089, A	959	6	0.8	323	4	US-09-248-796A-17766	Sequence 17766, A
887	6	0.8	298	4	US-09-543-681A-6110	Sequence 6110, Ap	960	6	0.8	323	4	US-09-902-540-14738	Sequence 14738, A
888	6	0.8	298	4	US-09-248-796A-27737	Sequence 27737, A	961	6	0.8	326	4	US-09-489-039A-11326	Sequence 11326, A
889	6	0.8	299	4	US-09-270-767-42307	Sequence 42307, A	962	6	0.8	326	6	5171684-7	Patent No. 5171684
890	6	0.8	299	4	US-09-710-279-1192	Sequence 1192, Ap	963	6	0.8	326	6	5171684-7	Patent No. 5171684
891	6	0.8	299	4	US-09-710-279-1768	Sequence 1768, Ap	964	6	0.8	327	4	US-09-270-767-42565	Sequence 42565, A
892	6	0.8	300	4	US-09-270-767-44496	Sequence 44496, A	965	6	0.8	328	4	US-09-187-999-31	Sequence 31, Appl
893	6	0.8	301	4	US-09-489-039A-10251	Sequence 10251, A	966	6	0.8	328	4	US-09-635-872A-8	Sequence 8, Appli
894	6	0.8	301	4	US-09-902-540-12303	Sequence 12303, A	967	6	0.8	328	4	US-09-636-077A-8	Sequence 8, Appli
895	6	0.8	302	3	US-08-303-861-20	Sequence 20, Appl	968	6	0.8	328	4	US-09-636-060C-8	Sequence 8, Appli
896	6	0.8	302	3	US-09-457-046B-24	Sequence 24, Appl	969	6	0.8	328	4	US-09-986-552-8	Sequence 8, Appli
897	6	0.8	302	4	US-09-232-991A-22159	Sequence 22159, A	970	6	0.8	328	4	US-09-636-596C-8	Sequence 8, Appli
898	6	0.8	302	4	US-09-107-532A-6924	Sequence 6924, Ap	971	6	0.8	328	4	US-10-023-894-10	Sequence 10, Appl
899	6	0.8	302	4	US-09-866-570B-24	Sequence 24, Appl	972	6	0.8	328	4	US-10-306-686-8	Sequence 8, Appli
900	6	0.8	303	4	US-09-248-796A-15374	Sequence 15374, A	973	6	0.8	331	4	US-09-328-352-6400	Sequence 6400, Ap
901	6	0.8	304	4	US-09-248-796A-15270	Sequence 15270, A	974	6	0.8	332	4	US-09-252-991A-21777	Sequence 21777, A
902	6	0.8	304	4	US-09-902-540-14051	Sequence 14051, A	975	6	0.8	332	4	US-09-252-991A-24064	Sequence 24064, A
903	6	0.8	305	4	US-09-248-796A-17837	Sequence 17837, A	976	6	0.8	332	4	US-09-252-991A-31956	Sequence 31956, A

```

977 6 0.8 333 4 US-09-543-681A-4411 Sequence 4411, Ap
978 6 0.8 333 4 US-09-270-767-59028 Sequence 59028, A
979 6 0.8 334 1 US-08-279-058B-10 Sequence 10, Appl
980 6 0.8 334 4 US-08-328-323-10 Sequence 10, Appl
981 6 0.8 334 4 US-08-818-780-91 Sequence 91, Appl
982 6 0.8 334 4 US-09-270-767-33176 Sequence 33176, A
983 6 0.8 334 4 US-09-270-767-45019 Sequence 45019, A
984 6 0.8 334 4 US-09-248-796A-17169 Sequence 17169, A
985 6 0.8 334 4 US-09-438-185A-11 Sequence 11, Appl
986 6 0.8 335 4 US-09-482-273-118 Sequence 118, App
987 6 0.8 335 4 US-09-583-110-3726 Sequence 3726, Ap
988 6 0.8 336 3 US-08-804-166-8 Sequence 8, Appl1
989 6 0.8 336 3 US-08-910-991-8 Sequence 8, Appl1
990 6 0.8 336 4 US-09-543-681A-5330 Sequence 5330, Ap
991 6 0.8 336 4 US-09-489-039A-9200 Sequence 9200, Ap
992 6 0.8 336 4 US-09-756-186-8 Sequence 8, Appl1
993 6 0.8 337 4 US-09-232-991A-17374 Sequence 17374, A
994 6 0.8 338 1 US-08-210-394-1 Sequence 1, Appl1
995 6 0.8 338 3 US-09-134-001C-4795 Sequence 4795, Ap
996 6 0.8 338 4 US-09-248-796A-18170 Sequence 18170, A
997 6 0.8 338 4 US-09-538-092-144 Sequence 144, App
998 6 0.8 339 4 US-09-252-991A-26600 Sequence 26600, A
999 6 0.8 339 4 US-09-134-000C-4665 Sequence 4665, Ap
1000 6 0.8 341 4 US-09-336-536-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4
Query Match 100.0%; Score 797; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 797; Conservative 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Qy 61 IIKSLYATGFFDVRVETADQGLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDVRVETADQGLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SOYFNQATLNOAVAGLKEEYLGKLNQITPKVTKLARNVDDITIDEGSKAKITDIE 180
Db 121 SOYFNQATLNOAVAGLKEEYLGKLNQITPKVTKLARNVDDITIDEGSKAKITDIE 180
Qy 181 FEGNQVYSDRKLQMQLSITGGIITWLTFRSNQFNEQKFAQDMEKVDTFYQNNGYFDFRIL 240
Db 181 FEGNQVYSDRKLQMQLSITGGIITWLTFRSNQFNEQKFAQDMEKVDTFYQNNGYFDFRIL 240
Qy 241 DTDIOTNEDKTKOTIKITVHEGGFRMGKVSIEGDTNEVPKAELEKLLTWKPKGWYERQQ 300
Db 241 DTDIOTNEDKTKOTIKITVHEGGFRMGKVSIEGDTNEVPKAELEKLLTWKPKGWYERQQ 300
```

```

Db 241 DTDIOTNEDKTKOTIKITVHEGGFRMGKVSIEGDTNEVPKAELEKLLTWKPKGWYERQQ 300
Qy 301 MTAVLGEIQNRMGSGAGYSEISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSGAGYSEISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDVVRRELRLQMESAPYDTSKLRQSKERVELLGYFNVQFQDAVPLAGTDPKVDLNNSLTE 420
Db 361 RDVVRRELRLQMESAPYDTSKLRQSKERVELLGYFNVQFQDAVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLNAGWDTDTGLVMSAGVSQDNLFGTCKSALRASRSKTTLNGSLSTDPVETA 480
Db 421 RSTGSLDLNAGWDTDTGLVMSAGVSQDNLFGTCKSALRASRSKTTLNGSLSTDPVETA 480
Qy 481 DGVSGLGVYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGVYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHADFTIKYKGTDTGDSFGKWLKYGTVGMRNKTTDSALWPTRGYLTGVAEIA 600
Db 541 YNKAPKHADFTIKYKGTDTGDSFGKWLKYGTVGMRNKTTDSALWPTRGYLTGVAEIA 600
Qy 601 LPQSKLQYVSATHNOTWFFPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
Db 601 LPQSKLQYVSATHNOTWFFPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAADARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAADARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYAGGAVTWLSPLGPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFOFQGLGTF 797
Db 781 KPEDEIQRFOFQGLGTF 797

RESULT 2
US-09-994-192-2
; Sequence 2, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2
Query Match 19.7%; Score 157; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.6e-152;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELRLQMESAPYDTSKLRQSKERVEL 391
Db 332 TKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELRLQMESAPYDTSKLRQSKERVEL 391
Qy 392 LGYFDNVQFQDAVPLAGTDPKVDLNNSLTERSTGSLDLNAGWDTDTGLVMSAGVSQDNLFG 451
Db 392 LGYFDNVQFQDAVPLAGTDPKVDLNNSLTERSTGSLDLNAGWDTDTGLVMSAGVSQDNLFG 451
```

us-10-606-618-4.oligo.rai

```

; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SEQ ID NO 1992
; SEQ ID NO 1992

```

```

US-09-489-039A-8163
; Sequence 8163, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8163
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8163

```

Qy 727 SSSATGGR 734
Db 76 SSSATGGR 83

US-09-205-258-1092
; Sequence 1992, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins

```

/ FILE NAME: C:\FBI\2007\FBI
/ CURRENT APPLICATION NUMBER: US/09/205,258
/ CURRENT FILING DATE: 1998-12-04
/ EARLIER APPLICATION NUMBER: PCT/US98/114322
/ EARLIER FILING DATE: 1998-06-04
/ EARLIER APPLICATION NUMBER: 60/048,885
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,375
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,881
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,880
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,896
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/049,020
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,876
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,895
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,884
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,894
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,971
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,964
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,882
/ EARLIER FILING DATE: 1997-06-06
/ EARLIER APPLICATION NUMBER: 60/048,899

```

Query Match 1.0%; Score 8; DB 4; Length 97;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 8; Conservative 0; Mismatches 0; Indels

Qy 756 SAGGAVTW 763
|||||
Db 14 SAGGAVTW 21

RESULT 5

US-09-270-767-45805
; Sequence 45805, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45805
; LENGTH: 230
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-45805

Query Match 1.0%; Score 8; DB 4; Length 230;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 RGYLTGN 596
Db 188 RGYLTGN 195

RESULT 6
US-09-902-540-15552
; Sequence 15552, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15552
; LENGTH: 274
; TYPE: PRT
; ORGANISM: *Myxococcus xanthus*
US-09-902-540-15552

Query Match 1.0%; Score 8; DB 4; Length 274;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 KAELEKLL 288
Db 177 KAELEKLL 184

RESULT 7
US-09-252-991A-24628
; Sequence 24628, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS AERUGINOSA* FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 24628
; LENGTH: 648
; TYPE: PRT
; ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-24628

Query Match 1.0%; Score 8; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 VRVETADG 81
Db 94 VRVETADG 101

RESULT 8
US-09-543-681A-4998
; Sequence 4998, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PROTEUS MIRABILIS*
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4998
; LENGTH: 1589
; TYPE: PRT
; ORGANISM: *Proteus mirabilis*
US-09-543-681A-4998

Query Match 1.0%; Score 8; DB 4; Length 1589;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TADGQLLL 85
Db 563 TADGQLLL 570

RESULT 9
US-09-674-973A-147
; Sequence 147, Application US/09674973A
; Patent No. 6759046
; GENERAL INFORMATION:
; APPLICANT: No. 6759046sk Hydro ASA
; TITLE OF INVENTION: Peptides
; FILE REFERENCE: 26625-296
; CURRENT APPLICATION NUMBER: US/09/674,973A
; CURRENT FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 459
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 147
; LENGTH: 23
; TYPE: PRT
; ORGANISM: *Homo sapiens*
US-09-674-973A-147

Query Match 0.9%; Score 7; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 ELEKLLT 289
Db 5 ELEKLLT 11

RESULT 10
US-08-971-089-10

```

; NAME/KEY: UNSURE
; LOCATION: 51
; OTHER INFORMATION: Xaa=Ile or Leu or Val
US-09-513-999C-7231

Query Match          0.9%; Score 7; DB 4; Length 60;
Best Local Similarity 100.0%; Pred.No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      458 LRASRSK 464
      |||||
Db      38 LRASRSK 44

RESULT 12
US-09-328-352-6252
; Sequence 6252, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6252
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6252

Query Match          0.9%; Score 7; DB 4; Length 86;
Best Local Similarity 100.0%; Pred.No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      654 GGLGSVR 660
      |||||
Db      18 GGLGSVR 24

```

```

US-09-489-039A-10485
; Sequence 10485, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10485
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10485

Query Match 0.9%; Score 7; DB 4; Length 86;
Best local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY - 483 VSLGYDV 489
      |||||
Db 71 VSLGYDV 77

RESULT 14
US-09-461-325-325
Sequence 325, Application US/09461325A

```

```
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-325

Query Match      0.9%  Score 7;  DB 4;  Length 88;
Best Local Similarity 100.0%;  Pred. No. 61;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      423 TGSIDL 429
Db      36 TGSIDL 42

Search completed: July 6, 2005, 15:43:23
Job time : 62 secs

; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-012-542-325

Query Match      0.9%  Score 7;  DB 4;  Length 88;
Best Local Similarity 100.0%;  Pred. No. 61;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      423 TGSIDL 429
Db      36 TGSIDL 42

Search completed: July 6, 2005, 15:43:23
Job time : 62 secs

; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-325

Query Match      0.9%  Score 7;  DB 4;  Length 88;
Best Local Similarity 100.0%;  Pred. No. 61;
Matches 7;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      423 TGSIDL 429
Db      36 TGSIDL 42

RESULT 15
US-10-012-542-325
; Sequence 325, Application US/10012542
; Patent No. 662741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:20:52 ; Search time 44 Seconds
(without alignments)
1742.835 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLGISPLAF.....LKKKPEDEIQRFQGLGTF 797

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	94.4	797	D82000	outer membrane pro
2	752	94.4	797	G81228	outer membrane pro
3	9	1.1	328	T46206	hypothetical prote
4	9	1.1	435	T49132	hypothetical prote
5	8	1.0	129	A96984	hypothetical prote
6	8	1.0	225	E84423	hypothetical prote
7	8	1.0	335	B75057	glycerate dehydrog
8	8	1.0	337	C82190	formate dehydroge
9	8	1.0	376	A71175	probable dehydroge
10	8	1.0	426	T04985	probable transamin
11	8	1.0	429	G42365	flagellar hook-len
12	8	1.0	474	IMBP4	site-specific reco
13	8	1.0	583	G83375	probable glycosyl
14	8	1.0	903	JE0337	dynammin-related pr
15	8	1.0	903	T50334	dynammin-related pr
16	8	1.0	1363	T43220	insulin-like growt
17	8	1.0	1577	A35140	hemolysin A precur
18	8	1.0	4919	T31105	hypothetical prote
19	7	0.9	75	E85707	hypothetical prote
20	7	0.9	75	F90849	probable regulator
21	7	0.9	76	1CEECDC	cell division cont
22	7	0.9	95	T26611	hypothetical prote
23	7	0.9	101	T23316	hypothetical prote
24	7	0.9	101	T35232	hypothetical prote
25	7	0.9	109	E72537	hypothetical prote
26	7	0.9	118	S14079	pim1 protein - mou
27	7	0.9	131	A87461	hypothetical prote
28	7	0.9	148	T52550	probable transcrip
29	7	0.9	150	D81314	small protein B ho

30	7	0.9	171	2	C95143	hypothetical prote
31	7	0.9	175	2	T05669	hypothetical prote
32	7	0.9	184	2	C69142	hypothetical prote
33	7	0.9	184	2	S4652	f42hi0.6 protein -
34	7	0.9	210	2	S36297	T-cell receptor ga
35	7	0.9	214	2	H86931	probable acyltrans
36	7	0.9	218	2	T45455	probable acyltrans
37	7	0.9	234	2	G71918	probable efflux tr
38	7	0.9	234	2	F64595	membrane fusion pr
39	7	0.9	238	2	A83224	probable ATP-bindi
40	7	0.9	255	2	F95228	hypothetical prote
41	7	0.9	255	2	B98093	hypothetical prote
42	7	0.9	264	2	A81668	conserved hypothet
43	7	0.9	264	2	E71509	hypothetical prote
44	7	0.9	268	2	T35568	probable lipoprote
45	7	0.9	269	2	T36001	probable integral
46	7	0.9	280	2	E87429	conserved hypothet
47	7	0.9	288	1	SNBYC1	proteasome endopep
48	7	0.9	305	2	A75334	lacyl-carrier-prot
49	7	0.9	305	2	T22009	hypothetical prote
50	7	0.9	306	2	T48715	hypothetical prote
51	7	0.9	306	2	AB2885	transcription regu
52	7	0.9	311	2	B97661	probable transcrip
53	7	0.9	311	2	H98278	hypothetical prote
54	7	0.9	311	2	AI3004	hypothetical prote
55	7	0.9	314	2	F96574	hypothetical prote
56	7	0.9	315	2	C96802	hypothetical prote
57	7	0.9	316	2	S61237	hypothetical prote
58	7	0.9	320	1	A43824	capsid protein - b
59	7	0.9	324	2	AC0548	periplasmic flagel
60	7	0.9	336	2	G84562	delta-aminolevulin
61	7	0.9	347	2	T06671	hypothetical prote
62	7	0.9	349	2	G97121	hypothetical prote
63	7	0.9	354	2	B89768	gcpE protein limpo
64	7	0.9	355	2	S29274	conserved hypothet
65	7	0.9	355	2	AC1925	cytochrome c oxida
66	7	0.9	359	2	T14742	poly (3-hydroxybut
67	7	0.9	363	2	S72209	hypothetical prote
68	7	0.9	366	2	C69391	3-isopropylmalate
69	7	0.9	373	2	S47911	enolase (eno) homo
70	7	0.9	373	2	A47380	PDS1 protein - yea
71	7	0.9	380	2	AC3494	RING finger-contai
72	7	0.9	384	2	T02968	oligopeptide trans
73	7	0.9	387	2	JC4578	cyclin A-type (clo
74	7	0.9	397	1	Z6BPT9	recombination prot
75	7	0.9	401	2	B83369	ribonucleoside-tri
76	7	0.9	416	2	F89779	conserved hypothet
77	7	0.9	417	2	JT0950	hypothetical prote
78	7	0.9	420	2	T43932	phosphoglycerate k
79	7	0.9	420	2	D64492	cell division cont
80	7	0.9	422	1	JGAGLR	N-ethylammelane ch
81	7	0.9	428	2	S76184	lactose-binding pr
82	7	0.9	429	2	AB3574	hypothetical prote
83	7	0.9	432	2	G75199	multidrug resistan
84	7	0.9	437	1	B71233	probable cell divi
85	7	0.9	444	2	T27866	hypothetical prote
86	7	0.9	456	2	C71226	hypothetical prote
87	7	0.9	460	2	D90084	RNA-polymerase sig
88	7	0.9	464	2	A64974	hypothetical prote
89	7	0.9	464	2	B90989	hypothetical prote
90	7	0.9	464	2	E85834	probable membrane
91	7	0.9	469	2	T08310	probable membrane
92	7	0.9	471	2	AF1586	helicase homolog H
93	7	0.9	476	2	E97631	site-specific reco
94	7	0.9	489	1	H70729	probable membrane
95	7	0.9	497	2	D95102	cytochrome P450 Rv
96	7	0.9	497	2	F97970	hypothetical prote
97	7	0.9	498	2	B90456	site-specific DNA-
98	7	0.9	499	2	T34328	hypothetical prote
99	7	0.9	508	2	T20355	hypothetical prote
100	7	0.9	515	2	B90302	ATP-dependent RNA
101	7	0.9	518	2	JC4024	poliovirus recepto
102	7	0.9	518	2	F84391	orc / cell divisio

103	7	0.9	521	2	A86909	hypothetical prote	176	6	0.8	70	2	G91236	50S ribosomal subu
104	7	0.9	526	1	KRBOVI	keratin, 54K type	177	6	0.8	70	2	G86083	50S ribosomal subu
105	7	0.9	537	2	T38015	hypothetical prote	178	6	0.8	71	2	E69345	SSU ribosomal prot
106	7	0.9	545	2	AB0290	probable membrane	179	6	0.8	72	1	B24033	small acid-soluble
107	7	0.9	562	2	S61295	heat shock protein	180	6	0.8	74	2	AI0349	conserved hypothet
108	7	0.9	564	2	H82919	conserved hypothet	181	6	0.8	74	2	AB2071	hypothetical prote
109	7	0.9	587	2	JC5300	Ran GTPase activat	182	6	0.8	76	2	A48784	Ig kappa V regions
110	7	0.9	589	2	T52070	RNA1 protein homol	183	6	0.8	76	2	B88318	protein age-1 (imp
111	7	0.9	589	2	A36983	RNA1 homolog fugu	184	6	0.8	77	2	F70241	hypothetical prote
112	7	0.9	619	2	S40938	hypothetical prote	185	6	0.8	77	2	AC2101	lipoprotein (impor
113	7	0.9	620	2	S38994	origin recognition	186	6	0.8	78	2	A64450	ribosomal protein
114	7	0.9	623	2	AD2295	hypothetical prote	187	6	0.8	78	2	AF2345	hypothetical prote
115	7	0.9	625	2	A72592	glutamine-fructose	188	6	0.8	79	2	S68245	phosphatidylcholin
116	7	0.9	649	1	H64476	lipote protein li	189	6	0.8	79	2	F70013	hypothetical prote
117	7	0.9	656	2	H84649	probable DnaJ prot	190	6	0.8	80	2	G81108	hypothetical prote
118	7	0.9	666	2	D82386	methyl-accepting c	191	6	0.8	80	2	A32364	photosystem I iron
119	7	0.9	728	2	S71467	diacylglycerol kin	192	6	0.8	80	2	G97805	hypothetical prote
120	7	0.9	745	2	D96829	homeobox protein (193	6	0.8	81	1	FEPM1S	photosystem I iron
121	7	0.9	747	2	S71478	homeotic protein A	194	6	0.8	81	1	FEWTA	photosystem I iron
122	7	0.9	771	2	T01315	hypothetical prote	195	6	0.8	81	1	FEWT1	photosystem I iron
123	7	0.9	784	2	E82731	outer membrane ant	196	6	0.8	81	1	FEZM1C	photosystem I iron
124	7	0.9	797	2	H83190	probable outer mem	197	6	0.8	81	2	S07170	photosystem I iron
125	7	0.9	812	2	AH1049	ribonuclease R (RN	198	6	0.8	81	2	S73295	photosystem I iron
126	7	0.9	823	2	T52425	kinesin-like prote	199	6	0.8	81	2	T07571	photosystem I iron
127	7	0.9	827	1	S56404	virulence-associat	200	6	0.8	81	2	S12198	photosystem I iron
128	7	0.9	827	2	C86114	probable enzyme va	201	6	0.8	81	2	AI3461	hypothetical prote
129	7	0.9	827	2	C91273	probable enzyme [i	202	6	0.8	81	2	A98247	hypothetical prote
130	7	0.9	856	2	F96998	phosphoenolpyruvat	203	6	0.8	81	2	H97567	hypothetical prote
131	7	0.9	881	2	L84737	kinesin heavy chai	204	6	0.8	83	2	F81267	30S ribosomal prot
132	7	0.9	888	2	D96619	protein T30E16.9 [205	6	0.8	83	2	S77417	prochlorophyllid
133	7	0.9	942	1	T91553	hypothetical prote	206	6	0.8	83	2	AI0032	probable type III
134	7	0.9	953	1	B30169	leukotoxin A - Pas	207	6	0.8	84	2	E97807	hypothetical prote
135	7	0.9	963	1	A41919	kinesin heavy chai	208	6	0.8	85	2	T08595	cysteine proteinas
136	7	0.9	983	2	AG2381	glycine cleavage s	209	6	0.8	85	2	AI0316	sec-independent pr
137	7	0.9	1054	2	D70425	conserved hypothet	210	6	0.8	86	2	H85939	type III secretion
138	7	0.9	1088	2	A69493	cysteine proteinas	211	6	0.8	86	2	D91094	type III secretion
139	7	0.9	1121	2	JC7329	WD-repeat protein	212	6	0.8	86	2	JQ0730	9K protein - Prote
140	7	0.9	1221	2	T25005	hypothetical prote	213	6	0.8	86	2	E82985	hypothetical prote
141	7	0.9	1222	2	B90593	hypothetical prote	214	6	0.8	86	2	AG3442	helix-turn-helix p
142	7	0.9	1234	2	T31623	hypothetical prote	215	6	0.8	87	2	T05709	auxin-induced prot
143	7	0.9	1259	2	T32901	hypothetical prote	216	6	0.8	88	2	C82468	hypothetical prote
144	7	0.9	1366	2	C85077	probable polyprot	217	6	0.8	88	2	E70880	hypothetical prote
145	7	0.9	1434	2	T30172	transmembrane prot	218	6	0.8	90	2	S15149	hypothetical prote
146	7	0.9	1442	2	T18538	patched protein -	219	6	0.8	90	2	B82799	Ig kappa chain V r
147	7	0.9	1449	2	B81963	IgA-specific serin	220	6	0.8	91	2	S17627	Ig kappa chain V r
148	7	0.9	1457	2	D81019	adhesion and penet	221	6	0.8	91	2	S17629	Ig kappa chain V r
149	7	0.9	1513	2	T44045	hypothetical prote	222	6	0.8	91	2	S17638	Ig kappa chain V r
150	7	0.9	1520	2	T44231	hypothetical prote	223	6	0.8	91	2	S17639	Ig kappa chain V r
151	7	0.9	1658	2	D75489	hypothetical prote	224	6	0.8	91	2	S17628	Ig kappa chain V r
152	7	0.9	1943	2	B64596	toxin-like outer m	225	6	0.8	91	2	S17637	Ig kappa chain V r
153	7	0.9	2174	2	E95965	hypothetical glyci	226	6	0.8	91	2	B69190	hypothetical prote
154	7	0.9	2274	2	T30258	adenomatous polyo	227	6	0.8	93	2	G71370	probable ribosomal
155	7	0.9	2431	1	MNVVSP	nonstructural poly	228	6	0.8	93	2	D70192	chaperonin (groES)
156	7	0.9	2478	2	AH2140	polyketide synthas	229	6	0.8	94	2	A60097	cortical cytoskele
157	7	0.9	3194	2	D71917	toxin-like outer m	230	6	0.8	94	2	S32105	chaperonin groES -
158	7	0.9	4385	2	T29042	hypothetical prote	231	6	0.8	94	2	JN0660	heat shock protein
159	7	0.9	4485	2	T08044	dynein gamma heavy	232	6	0.8	94	2	B40506	pRf2 protein - hum
160	7	0.9	5369	2	T44807	mycosubtilin synth	233	6	0.8	94	2	S75365	hypothetical prote
161	6	0.8	17	2	T55612	thyroid hormone re	234	6	0.8	95	2	D33730	Ig kappa chain V r
162	6	0.8	23	2	S45030	homeotic protein S	235	6	0.8	95	2	T03068	hypothetical prote
163	6	0.8	23	2	S60569	homeodomain protei	236	6	0.8	96	2	B26074	cysteine proteinas
164	6	0.8	25	2	D41606	homeotic protein M	237	6	0.8	96	2	S34937	heat shock protein
165	6	0.8	52	2	AI2399	hypothetical prote	238	6	0.8	96	2	C82048	chaperonin, 10 Kd
166	6	0.8	57	2	AB0373	hypothetical prote	239	6	0.8	96	2	JC4518	heat-shock protein
167	6	0.8	60	2	F75338	hypothetical prote	240	6	0.8	96	2	H97048	hypothetical prote
168	6	0.8	62	2	G70988	hypothetical prote	241	6	0.8	97	2	S26341	Ig light chain V r
169	6	0.8	65	2	AF2773	hypothetical prote	242	6	0.8	97	2	PH1084	Ig light chain V r
170	6	0.8	66	2	HF3083	hypothetical prote	243	6	0.8	97	2	C64029	hypothetical prote
171	6	0.8	67	2	F85904	hypothetical prote	244	6	0.8	97	2	F82416	hypothetical prote
172	6	0.8	68	2	H90086	hypothetical prote	245	6	0.8	98	2	H82577	hypothetical prote
173	6	0.8	68	2	F84002	hypothetical prote	246	6	0.8	99	2	S51210	Ig kappa chain V r
174	6	0.8	69	2	S33899	hypothetical prote	247	6	0.8	99	2	S53124	probable ribosomal
175	6	0.8	70	1	R5EC31	ribosomal protein	248	6	0.8	100	2	S29590	Ig kappa chain V r

249	6	0.8	100	2	S03636	homeotic protein H	322	6	0.8	126	2	D95410	hypothetical prote
250	6	0.8	101	2	F82421	conserved hypothet	323	6	0.8	127	2	F75092	ssu ribosomal prot
251	6	0.8	101	2	C89076	hypothetical prote	324	6	0.8	127	2	D97381	methylglyoxal synt
252	6	0.8	102	2	S11115	Ig kappa chain v r	325	6	0.8	127	2	AC2599	methylglyoxal synt
253	6	0.8	102	2	F87346	SSU ribosomal prot	326	6	0.8	127	2	A75086	translation initia
254	6	0.8	102	2	H87403	ribosomal protein	327	6	0.8	128	2	S39678	ywbH protein - Bac
255	6	0.8	102	2	A23931	anti-lipopolsacch	328	6	0.8	128	2	F84216	hypothetical prote
256	6	0.8	103	2	S29591	Ig kappa chain v r	329	6	0.8	128	2	S53584	probable membrane
257	6	0.8	103	2	G75257	hypothetical prote	330	6	0.8	129	2	B72853	AcMPV orf26 - Bom
258	6	0.8	104	2	B49049	Ig kappa chain v r	331	6	0.8	129	2	T41771	hypothetical prote
259	6	0.8	105	2	D95108	conserved hypothet	332	6	0.8	129	2	T46300	probable membrane
260	6	0.8	106	2	P80071	Ig kappa chain v r	333	6	0.8	129	2	S45868	hypothetical prote
261	6	0.8	106	2	S11114	Ig kappa chain v r	334	6	0.8	129	2	T36916	hypothetical prote
262	6	0.8	106	2	S11120	Ig kappa chain v r	335	6	0.8	130	1	JB0079	Ig kappa chain pre
263	6	0.8	106	2	G27887	Ig kappa chain v r	336	6	0.8	130	1	JB0010	chorion class B pr
264	6	0.8	106	2	G27887	Ig kappa chain v r	337	6	0.8	130	2	S01439	lens fiber membran
265	6	0.8	106	2	D86563	conserved hypothet	338	6	0.8	130	2	H83150	hypothetical prote
266	6	0.8	106	2	T24774	Ct466 hypothetical	339	6	0.8	131	1	S12972	hypothetical prote
267	6	0.8	107	1	PXPSP	hypothetical prote	340	6	0.8	131	1	C87416	amicyanin - Paraco
268	6	0.8	107	1	B36950	putidaredoxin [val	341	6	0.8	131	2	B71055	MutT/nudix family
269	6	0.8	107	2	S11112	urease (EC 3.5.1.5	342	6	0.8	132	2	C70161	hypothetical prote
270	6	0.8	107	2	S11118	Ig kappa chain v r	343	6	0.8	132	2	D72583	ribosomal protein
271	6	0.8	107	2	S11116	Ig kappa chain v r	344	6	0.8	133	2	S39540	homeotic protein G
272	6	0.8	107	2	PD0011	Ig kappa chain v r	345	6	0.8	133	2	C69849	hypothetical prote
273	6	0.8	107	2	S11113	Ig kappa chain v r	346	6	0.8	134	2	T01042	hypothetical prote
274	6	0.8	107	2	PT0395	Ig kappa chain v r	347	6	0.8	135	2	AF2055	hypothetical prote
275	6	0.8	107	2	PT0402	Ig light chain v r	348	6	0.8	135	2	B72768	hypothetical prote
276	6	0.8	107	2	S11119	Ig kappa chain v r	349	6	0.8	136	2	AB1544	hypothetical prote
277	6	0.8	107	2	PT0397	Ig kappa chain v r	350	6	0.8	136	2	T49582	positive regulatio
278	6	0.8	107	2	S11123	Ig kappa chain v r	351	6	0.8	136	2	S04043	hypothetical prote
279	6	0.8	107	2	PT0398	Ig kappa chain v r	352	6	0.8	137	2	T45079	embryonic abundant
280	6	0.8	107	2	S11121	Ig kappa chain v r	353	6	0.8	138	1	A69219	hypothetical prote
281	6	0.8	107	2	S11117	Ig kappa chain v r	354	6	0.8	138	2	B83135	conserved hypothet
282	6	0.8	107	2	A30562	Ig kappa chain v r	355	6	0.8	138	2	G85806	hypothetical prote
283	6	0.8	107	2	PT0406	Ig kappa chain v r	356	6	0.8	139	2	A82140	hypothetical prote
284	6	0.8	107	2	B30562	Ig kappa chain v r	357	6	0.8	139	2	H97449	probable isomerase
285	6	0.8	107	2	PC4405	Ig kappa chain v r	358	6	0.8	139	2	S32510	homeobox-containin
286	6	0.8	107	2	C48078	biliary glycoprote	359	6	0.8	140	2	B97462	organic hydroperox
287	6	0.8	107	2	T17701	hypothetical prote	360	6	0.8	140	2	AG2680	hemoglobin alpha-I
288	6	0.8	108	2	G30560	Ig kappa chain v r	361	6	0.8	141	1	HAL2C	kinesin heavy chai
289	6	0.8	109	2	C30515	Ig heavy chain v r	362	6	0.8	143	2	C44259	hypothetical prote
290	6	0.8	109	2	D91085	hypothetical prote	363	6	0.8	143	2	A69115	hypothetical prote
291	6	0.8	109	2	F85930	hypothetical prote	364	6	0.8	143	2	E30338	DNA transport mach
292	6	0.8	109	2	D65061	hypothetical prote	365	6	0.8	143	2	B69267	transposase IS240-
293	6	0.8	109	2	AH3240	conserved hypothet	366	6	0.8	143	2	S58429	conserved hypothet
294	6	0.8	110	2	S51383	probable membrane	367	6	0.8	143	2	AG2682	conserved hypothet
295	6	0.8	111	2	G85974	probable proteinas	368	6	0.8	143	2	E97464	probable SdhD subu
296	6	0.8	111	2	G91129	suppressor protein	369	6	0.8	144	2	D70843	hypothetical prote
297	6	0.8	112	2	S51121	genome polyprotein	370	6	0.8	145	2	C72668	hypothetical prote
298	6	0.8	113	2	PQ0274	polyprotein - hepa	371	6	0.8	145	2	T36527	hypothetical prote
299	6	0.8	113	2	PQ0273	polyprotein - hepa	372	6	0.8	145	2	AD1447	major tail shaft p
300	6	0.8	113	2	A55205	xis 5'-region hypo	373	6	0.8	145	2	F69214	heat shock protein
301	6	0.8	113	2	I51025	transcription fact	374	6	0.8	145	2	F90185	conserved hypothet
302	6	0.8	114	2	E97976	conserved hypothet	375	6	0.8	145	2	S26443	hypothetical prote
303	6	0.8	115	2	T29883	hypothetical prote	376	6	0.8	146	2	T51473	calmodulin-like pr
304	6	0.8	117	2	H71431	hypothetical prote	377	6	0.8	146	2	T22474	hypothetical prote
305	6	0.8	117	2	T13096	probable minor cap	378	6	0.8	146	2	H64126	hypothetical prote
306	6	0.8	117	2	S75884	hypothetical prote	379	6	0.8	146	2	B82167	conserved hypothet
307	6	0.8	119	2	A64249	ribosomal protein	380	6	0.8	146	2	AE2935	conserved hypothet
308	6	0.8	119	2	B84407	hypothetical prote	381	6	0.8	146	2	B98347	hypothetical prote
309	6	0.8	120	2	S22049	reverse transcript	382	6	0.8	147	2	PH0127	Ig heavy chain pre
310	6	0.8	120	2	AB2668	conserved hypothet	383	6	0.8	147	2	PH0131	Ig heavy chain pre
311	6	0.8	120	2	AH1813	hypothetical prote	384	6	0.8	147	2	PH0123	Ig heavy chain pre
312	6	0.8	121	2	H70471	conserved hypothet	385	6	0.8	147	2	PH0125	Ig heavy chain pre
313	6	0.8	122	2	F97779	hypothetical prote	386	6	0.8	147	2	PH0124	Ig heavy chain pre
314	6	0.8	123	2	G71189	hypothetical prote	387	6	0.8	147	2	PH0130	Ig heavy chain pre
315	6	0.8	124	2	F82205	chemotaxis protein	388	6	0.8	147	2	A29910	myosin calcium-bin
316	6	0.8	124	2	G75172	hypothetical prote	389	6	0.8	147	2	T28131	hypothetical prote
317	6	0.8	124	2	AD3428	transposase BME14	390	6	0.8	150	2	A97536	hypothetical prote
318	6	0.8	124	2	S05005	homeotic protein H	391	6	0.8	151	2	T15428	hypothetical prote
319	6	0.8	125	2	C82831	ribosomal-binding	392	6	0.8	151	2	A75297	ubiquitin-activati
320	6	0.8	125	2	T16848	hypothetical prote	393	6	0.8	152	2	S29752	profilin - Tetrahy
321	6	0.8	125	2	AC3195	hypothetical prote	394	6	0.8	153	1	JT0572	

395	153	0.8	1	WRBP15	early protein gp17	468	178	2	E98050	hypothetical prote
396	153	0.8	1	G69847	conserved hypotet	469	179	2	A53522	peptidylprolyl iso
397	153	0.8	1	S63367	ribosomal protein	470	179	2	B69695	ribosomal protein
398	153	0.8	2	AH2203	bacterioferritin c	471	179	2	T48416	hypothetical prote
399	153	0.8	2	G70077	hypothetical prote	472	179	2	AD2427	hypothetical prote
400	153	0.8	2	S34255	hypothetical prote	473	181	2	E83436	probable oxidase p
401	153	0.8	2	C86324	protein Fl4D16.23	474	182	2	A02947	probable fimbrial-
402	154	0.8	2	H70681	hypothetical prote	475	182	2	A91031	keratin, 60K type
403	154	0.8	2	T34825	hypothetical prote	476	182	2	AH1579	hypothetical prote
404	155	0.8	2	T15379	hypothetical prote	477	182	2	G90235	hypothetical prote
405	156	0.8	2	F84356	hypothetical prote	478	183	2	S26961	H+-transporting tw
406	156	0.8	2	AG0243	probable exported	479	183	2	T37965	probable 40S ribos
407	157	0.8	2	F82390	methylated-DNA-lpr	480	183	2	A40360	hypothetical prote
408	159	0.8	2	D72686	hypothetical prote	481	183	2	C85786	hypothetical prote
409	160	0.8	2	T11949	hypothetical prote	482	183	2	G90937	hypothetical prote
410	161	0.8	2	JC7151	vacuolar H+-ATPase	483	183	2	B90092	hypothetical prote
411	161	0.8	2	F71860	biotin carboxyl ca	484	184	2	A05045	hypothetical prote
412	161	0.8	2	G71407	transcription fact	485	184	2	T33006	hypothetical prote
413	161	0.8	2	S50931	hypothetical prote	486	184	2	B71897	hypothetical prote
414	162	0.8	1	RFMWA	phycocyanin	487	185	2	G75379	conserved hypotet
415	162	0.8	2	H70314	hypothetical prote	488	185	2	AI3454	hypothetical prote
416	164	0.8	1	D69783	transcription regu	489	185	2	G71113	probable pyruvate
417	164	0.8	2	AE1900	NADH dehydrogenase	490	186	2	T19073	hypothetical prote
418	165	0.8	2	D97283	ribosomal protein	491	186	2	AF3094	conserved hypotet
419	165	0.8	2	B72618	hypothetical prote	492	186	2	F90646	probable fimbrial
420	165	0.8	2	AG2428	hypothetical prote	493	186	2	F85497	probable drpp-4-de
421	166	0.8	2	S78003	cuticle structural	494	187	2	H95598	hypothetical prote
422	166	0.8	2	G90661	probable peptide c	495	187	2	D99192	hypothetical prote
423	166	0.8	2	E85512	translation releas	496	188	2	JU0451	hypothetical 21K p
424	166	0.8	2	E64748	ubiquinol-cytochro	497	188	2	I59116	myc protein - huma
425	167	0.8	2	C71803	fast skeletal trop	498	188	2	I79500	myc protein - huma
426	167	0.8	2	JW0065	early light-induce	499	188	2	C97438	hypothetical prote
427	167	0.8	2	S07473	probable gluconoki	500	188	2	AF2656	conserved hypotet
428	167	0.8	2	AC0481	hypothetical prote	501	189	2	E96569	probable IAA6 prot
429	167	0.8	2	D55224	NADH dehydrogenase	502	189	2	S58493	auxin-induced prot
430	167	0.8	2	G90175	serine proteinase	503	189	2	S70104	hypothetical prote
431	168	0.8	2	S41973	phosphotransferase	504	190	2	AD3329	acetylactate synth
432	169	0.8	1	WQECP3	hypothetical prote	505	191	1	JH0585	ribosomal protein
433	169	0.8	1	H69136	pTS system, glucos	506	191	2	B64597	adenylate kinase -
434	169	0.8	2	D85894	pTS system, glucos	507	191	2	C90518	recombination prot
435	169	0.8	2	A98040	molybdopterin co-f	508	191	2	H64887	probable phage-rel
436	169	0.8	2	T44852	type I interleukin	509	191	2	E64909	probable phage-rel
437	169	0.8	2	I51903	outer membrane pro	510	191	2	E74555	hypothetical prote
438	169	0.8	2	C70207	VPS29-like phospho	511	191	2	S74679	hypothetical prote
439	170	0.8	2	C75184	ribosomal protein	512	191	2	I40153	outer surface prot
440	170	0.8	2	S53648	hypothetical prote	513	191	2	E84375	hypothetical prote
441	170	0.8	2	F87482	chorion class B pr	514	191	2	A64704	hypothetical prote
442	171	0.8	1	JBA041	probable lppu prot	515	191	2	A71814	hypothetical prote
443	171	0.8	2	G70883	cytochrome c famil	516	192	2	S70267	outer surface prot
444	171	0.8	2	E87459	probable host-nucl	517	192	2	T05159	hypothetical prote
445	172	0.8	2	E81897	early light-induce	518	193	2	B85693	probable tail fibe
446	172	0.8	2	S07474	hypothetical prote	519	193	2	C90835	tail fiber assembl
447	172	0.8	2	B83696	probable minor fim	520	193	2	D81009	conserved hypotet
448	173	0.8	2	B85875	hypothetical prote	521	193	2	E82031	probable integral
449	173	0.8	2	A70914	hypothetical prote	522	193	2	S70276	outer surface prot
450	173	0.8	2	D90177	LSU ribosomal prot	523	193	2	S70287	outer surface prot
451	174	0.8	2	B75176	hypothetical prote	524	194	1	R5PM24	ribosomal protein
452	174	0.8	2	T03056	hypothetical prote	525	194	2	T16556	hypothetical prote
453	174	0.8	2	T27552	hypothetical prote	526	194	2	S70277	dof zinc finger pr
454	174	0.8	2	D86239	protein T10024.23	527	194	2	T52044	hypothetical prote
455	175	0.8	2	C39141	transcription repr	528	194	2	T20322	hypothetical prote
456	175	0.8	2	A82297	conserved hypotet	529	195	2	AE1823	hypothetical prote
457	175	0.8	2	JC7274	DNA binding protei	530	195	2	G83170	hypothetical prote
458	176	0.8	2	AD1174	conserved hypotet	531	196	2	B86653	hypothetical prote
459	176	0.8	2	AE1531	conserved hypotet	532	196	2	C64891	ferritochelin-bin
460	177	0.8	2	F83114	SOS ribosomal prot	533	196	2	AH2441	hypothetical prote
461	178	0.8	2	G91182	probable fimbrial	534	196	2	G97964	conserved hypotet
462	178	0.8	2	C86029	probable major fim	535	196	2	AB3601	ctdip-glucose 4-6-d
463	178	0.8	2	T01890	hypothetical prote	536	197	2	JC2339	neutrophil gelatin
464	178	0.8	2	I40104	outer surface prot	537	197	2	S72709	Lept1170 C3 229 pr
465	178	0.8	2	I40125	non-heme iron-cont	538	198	2	A25706	sorcin - Chinese h
466	178	0.8	2	B95183	hypothetical prote	539	198	2	S52094	hypothetical prote
467	178	0.8	2	A47071		540	199	2	C96570	

541	6	0.8	200	2	B96912	adenvylsulfate ki	614	6	0.8	221	2	A72097	probable ABC trans
542	6	0.8	200	2	S07397	lipocalin - mouse	615	6	0.8	221	2	G85225	probable ABC trans
543	6	0.8	200	2	S10946	transcription init	616	6	0.8	221	2	T15999	hypothetical prote
544	6	0.8	200	2	S10945	transcription init	617	6	0.8	222	2	F72572	probable TATA-box
545	6	0.8	200	2	AB1085	hypothetical prote	618	6	0.8	222	2	H82794	hypothetical prote
546	6	0.8	201	2	T38262	hypothetical prote	619	6	0.8	222	2	G87380	hypothetical prote
547	6	0.8	201	2	T49121	receptor like prot	620	6	0.8	222	2	S62001	MA15 protein - yea
548	6	0.8	201	2	G85253	receptor like prot	621	6	0.8	223	2	A84436	probable glutathio
549	6	0.8	202	2	T35545	probable two-compo	622	6	0.8	223	2	T36952	conserved hypotet
550	6	0.8	202	2	T46515	probable two-compo	623	6	0.8	223	2	S73367	hypothetical prote
551	6	0.8	202	2	C90034	hypothetical prote	624	6	0.8	223	2	B89567	protein T08A9.9 [i
552	6	0.8	202	2	T47319	hypothetical prote	625	6	0.8	224	2	S31845	chlorophyll a/b-bi
553	6	0.8	203	2	G86785	acetyltransferase	626	6	0.8	224	2	AG1196	ribose 5-phosphate
554	6	0.8	203	2	C97766	holliday junction	627	6	0.8	225	1	SYECDB	dethiobiotin synth
555	6	0.8	203	2	B72566	hypothetical prote	628	6	0.8	225	2	A99206	hypothetical prote
556	6	0.8	203	2	AD0223	probable glycosida	629	6	0.8	225	2	AH3080	RhtB family transp
557	6	0.8	203	2	S35563	sex-determining pr	630	6	0.8	226	2	G87518	lipote-protein li
558	6	0.8	204	2	S27526	5-bromo-4-chloroi	631	6	0.8	226	2	S23280	homeotic protein m
559	6	0.8	204	2	AI0542	probable peptide c	632	6	0.8	227	1	ADMSC	fructose-bisphosph
560	6	0.8	205	2	D90455	hypothetical prote	633	6	0.8	227	2	A38452	2-haloacid dehalog
561	6	0.8	206	2	AI0700	probable two-compo	634	6	0.8	227	2	T49711	hypothetical prote
562	6	0.8	206	2	AC2443	orotate phosphorib	635	6	0.8	227	2	B82408	ABC transporter, A
563	6	0.8	206	2	C82139	conserved hypotet	636	6	0.8	228	2	T37026	probable lipoprote
564	6	0.8	207	2	G71053	hypothetical prote	637	6	0.8	228	2	C90276	conserved hypotet
565	6	0.8	208	1	T1053	glutathione transf	638	6	0.8	230	2	T34822	ABC-transporter At
566	6	0.8	208	1	S29549	interleukin-6 - sh	639	6	0.8	230	2	C64396	precorrin-2 methyl
567	6	0.8	208	2	C64657	2-dehydro-3-deoxy-	640	6	0.8	230	2	E71224	probable HESA prot
568	6	0.8	208	2	T1859	2-dehydro-3-deoxy-	641	6	0.8	231	2	AG2277	hypothetical prote
569	6	0.8	209	1	XUFF11	glutathione transf	642	6	0.8	231	2	AE2297	hypothetical prote
570	6	0.8	209	2	I40142	outer surface prot	643	6	0.8	232	2	S75699	cAMP receptor prot
571	6	0.8	209	2	D86882	hypothetical prote	644	6	0.8	232	2	H72807	gp65 protein - Myc
572	6	0.8	210	1	JN0277	DNA-directed DNA p	645	6	0.8	233	2	S15960	hypothetical prote
573	6	0.8	210	2	F71308	probable 2-dehydro	646	6	0.8	233	2	T28914	hypothetical prote
574	6	0.8	210	2	JC4381	imidazoleglycerol-	647	6	0.8	234	2	T06995	probable MADS box
575	6	0.8	210	2	T06864	transcription regu	648	6	0.8	234	2	H81669	conserved hypotet
576	6	0.8	210	2	H75599	probable acetyltra	649	6	0.8	234	2	T20933	hypothetical prote
577	6	0.8	210	2	T26154	hypothetical prote	650	6	0.8	235	2	E69814	conserved hypotet
578	6	0.8	210	2	I58391	sarcoma amplified	651	6	0.8	235	2	S25058	lg kappa chain - m
579	6	0.8	211	1	E71262	VPS29-like phospho	652	6	0.8	235	2	T36923	hypothetical prote
580	6	0.8	211	2	H64216	ribosomal protein	653	6	0.8	236	2	S16164	coat protein - pot
581	6	0.8	211	2	B89830	hypothetical prote	654	6	0.8	236	2	S35766	coat protein - pot
582	6	0.8	211	2	T49930	hypothetical prote	655	6	0.8	236	2	S41326	coat protein - pot
583	6	0.8	212	2	T44591	hypothetical prote	656	6	0.8	236	2	JQ2298	coat protein - pot
584	6	0.8	213	2	E71511	hypothetical prote	657	6	0.8	237	2	C84065	transcription regu
585	6	0.8	213	2	B72548	hypothetical prote	658	6	0.8	237	2	S47351	p30 B9.10 protein
586	6	0.8	213	2	A95863	hypothetical prote	659	6	0.8	238	2	A97336	Na+ ABC transporte
587	6	0.8	214	2	AB2195	serine esterase [i	660	6	0.8	238	2	AI0077	conserved hypotet
588	6	0.8	214	2	T51657	myb-related transc	661	6	0.8	239	2	A75293	amino acid ABC tra
589	6	0.8	214	2	A97540	hypothetical prote	662	6	0.8	239	2	T51534	hypothetical prote
590	6	0.8	214	2	AC2759	cytochrome b561 At	663	6	0.8	240	2	S75021	3-ketoacyl-acyl ca
591	6	0.8	215	2	A71541	hypothetical prote	664	6	0.8	240	2	H90778	DNA-binding protei
592	6	0.8	216	2	D75567	GTP cyclohydrolase	665	6	0.8	241	2	T00751	probable protein k
593	6	0.8	216	2	A12635	two component resp	666	6	0.8	242	2	H69885	3-oxoacyl-acyl-ca
594	6	0.8	216	2	D86564	Yage family [impor	667	6	0.8	242	2	C85640	hypothetical prote
595	6	0.8	216	2	G72060	Yage family - Chla	668	6	0.8	242	2	G87696	hypothetical prote
596	6	0.8	216	2	C84900	hypothetical prote	669	6	0.8	242	2	A43904	homeotic protein G
597	6	0.8	216	2	S58100	ribosomal protein	670	6	0.8	243	1	B86746	probable phosphoes
598	6	0.8	216	2	F71378	hypothetical prote	671	6	0.8	243	2	B71512	hypothetical prote
599	6	0.8	217	1	K1BSAF	adenylate kinase (672	6	0.8	243	2	A43596	hypothetical prote
600	6	0.8	217	2	T01076	transcription fact	673	6	0.8	243	2	A69225	mip protein - Legi
601	6	0.8	218	2	T01076	transcription fact	674	6	0.8	243	2	JC7596	hypothetical prote
602	6	0.8	218	2	F84170	hypothetical prote	675	6	0.8	244	1	RDECPA	phosphadenylyl-su
603	6	0.8	219	2	B82727	2-keto-3-deoxy-6-p	676	6	0.8	244	2	B64003	hypothetical prote
604	6	0.8	219	2	S52646	GTP-binding protei	677	6	0.8	244	2	B69381	conserved hypotet
605	6	0.8	219	2	T09720	conserved hypotet	678	6	0.8	245	2	AB2286	NADH dehydrogenase
606	6	0.8	219	2	T33190	hypothetical prote	679	6	0.8	245	2	B86738	hypothetical prote
607	6	0.8	220	2	T51827	MADS-box protein l	680	6	0.8	246	2	AC3024	transcription regu
608	6	0.8	220	2	T05580	probable transcript	681	6	0.8	246	2	T00704	hypothetical prote
609	6	0.8	220	2	D85991	potential acrif/en	682	6	0.8	246	2	S74961	hypothetical prote
610	6	0.8	220	2	B65119	probable transcript	683	6	0.8	247	2	G83382	conserved hypotet
611	6	0.8	220	2	H91145	probable transcript	684	6	0.8	247	2	D69453	hypothetical prote
612	6	0.8	220	2	T15275	hypothetical prote	685	6	0.8	247	2	G64788	ybcx protein, phag
613	6	0.8	220	2	T12474	hypothetical prote	686	6	0.8	248	2	F69449	tryptophan synthas

687	6	0.8	248	2	I64230	sensory rhodopsin	760	0.8	266	2	T25230	hypothetical prote
688	6	0.8	249	1	A30113	NADH2 dehydrogenas	761	0.8	267	2	T22185	hypothetical prote
689	6	0.8	249	1	B30113	NADH2 dehydrogenas	762	0.8	267	2	H86320	probable MYB47 tra
690	6	0.8	249	2	AF1405	creatinine amidohy	763	0.8	267	2	E64175	hypothetical prote
691	6	0.8	249	2	AF1781	creatinine amidohy	764	0.8	267	2	E83232	probable ATP-bindi
692	6	0.8	250	2	H95161	conserved hypotet	765	0.8	267	2	S74998	hypothetical prote
693	6	0.8	250	2	G98037	conserved hypotet	766	0.8	267	2	E75471	transcription regu
694	6	0.8	250	2	G72650	hypothetical prote	767	0.8	267	2	A46122	homeotic protein H
695	6	0.8	250	2	D75119	hypothetical prote	768	0.8	267	2	A49068	cranosynotosis-as
696	6	0.8	251	2	I57668	luteinizing hormon	769	0.8	268	1	A49473	glutamate racemase
697	6	0.8	251	2	H65007	VacJ lipoprotein p	770	0.8	268	2	S31010	gene 65 protein -
698	6	0.8	251	2	E91032	lipoprotein precu	771	0.8	268	2	T46980	hypothetical prote
699	6	0.8	251	2	F85876	lipoprotein precu	772	0.8	268	2	AE0241	conserved hypotet
700	6	0.8	251	2	F70412	dihydroorotate deh	773	0.8	268	2	S18814	homeotic protein H
701	6	0.8	252	2	C95183	triosephosphate is	774	0.8	269	2	T16115	hypothetical prote
702	6	0.8	252	2	A28449	tropomyosin, cytos	775	0.8	269	2	B84013	hypothetical prote
703	6	0.8	252	2	T10697	immature seed prot	776	0.8	269	2	T26504	hypothetical prote
704	6	0.8	253	2	H69219	pyrroline-5-carbox	777	0.8	270	1	CCECID	cell division inhi
705	6	0.8	253	2	JQ2255	triose-phosphate i	778	0.8	270	2	B84968	septum site-determ
706	6	0.8	253	2	S44053	structural protein	779	0.8	270	2	AH0724	septum site-determ
707	6	0.8	253	2	F69134	hypothetical prote	780	0.8	270	2	F85695	cell division inhi
708	6	0.8	253	2	G81311	probable ATP/Gnp-b	781	0.8	270	2	E90837	cell division inhi
709	6	0.8	253	2	AI3588	transposase BME110	782	0.8	270	2	AE0253	septum site-determ
710	6	0.8	254	2	B87396	DNA-binding respon	783	0.8	270	2	S71793	head-inducing fact
711	6	0.8	254	2	T08476	inclusion membrane	784	0.8	271	2	C81230	septum site-determ
712	6	0.8	254	2	E84382	hypothetical prote	785	0.8	271	2	JQ0950	ICP 18.5 protein -
713	6	0.8	254	2	C81208	ABC transporter, A	786	0.8	271	2	B60176	hypothetical prote
714	6	0.8	254	2	H81784	probable ABC trans	787	0.8	272	2	C75548	hypothetical prote
715	6	0.8	255	1	ISECT	triose-phosphate i	788	0.8	273	2	S12637	transcription regu
716	6	0.8	255	2	A35255	chlorocatechol 1,2	789	0.8	273	2	F69199	transposase - Esch
717	6	0.8	255	2	AD0940	triosephosphate is	790	0.8	273	2	S23281	homeotic hypotet
718	6	0.8	255	2	D91234	triosephosphate is	791	0.8	273	2	S23281	homeotic hypotet m
719	6	0.8	255	2	D86081	triosephosphate is	792	0.8	274	2	A61030	nitrogenase (EC 1.
720	6	0.8	255	2	AE0011	triose-phosphate i	793	0.8	274	2	A43719	urep protein - pro
721	6	0.8	255	2	AI1374	conserved hypotet	794	0.8	275	1	S78606	probable transport
722	6	0.8	255	2	AG1744	conserved hypotet	795	0.8	275	2	S27805	porin - slime mold
723	6	0.8	255	2	C90431	conserved hypotet	796	0.8	275	2	S66062	signal peptidase I
724	6	0.8	255	2	B87595	transcription regu	797	0.8	275	2	E83655	signal peptidase-1
725	6	0.8	256	2	C89869	trans-2-enoyl-ACP	798	0.8	275	2	S05299	hypothetical prote
726	6	0.8	256	2	A54322	corticotropin / li	799	0.8	276	1	S47640	adenyl-1-sulfate k
727	6	0.8	256	2	H69348	hypothetical prote	800	0.8	276	2	T29125	ketoacyl reductase
728	6	0.8	256	2	E95936	hypothetical prote	801	0.8	276	2	T48842	halorhodopsin (s
729	6	0.8	257	1	S22363	gufa protein homol	802	0.8	276	2	C82136	septum site-determ
730	6	0.8	257	2	H91119	gufa protein homol	803	0.8	276	2	T38825	hypothetical prote
731	6	0.8	257	2	G85964	gufa protein homol	804	0.8	276	2	E83922	hypothetical prote
732	6	0.8	258	1	C69175	heat shock protein	805	0.8	277	1	H71320	hypothetical prote
733	6	0.8	258	2	C84758	hypothetical prote	806	0.8	277	2	S32571	mald protein - Str
734	6	0.8	258	2	T27393	hypothetical prote	807	0.8	277	2	H87213	conserved hypotet
735	6	0.8	259	2	H86809	oxidoreductase ypa	808	0.8	277	2	S03240	hypothetical prote
736	6	0.8	259	2	G98050	triose-phosphate i	809	0.8	277	2	E72564	hypothetical prote
737	6	0.8	259	2	JS0660	homeotic protein H	810	0.8	277	2	G97783	hypothetical prote
738	6	0.8	259	2	A38284	homeotic protein Q	811	0.8	277	2	AD3386	phytoene synthase
739	6	0.8	260	2	S70589	cytochrome-c oxida	812	0.8	278	2	A84131	plant-metabolite d
740	6	0.8	260	2	AB2536	hypothetical prote	813	0.8	278	2	D64489	hypothetical prote
741	6	0.8	260	2	C95380	conserved hypotet	814	0.8	278	2	D75585	urease accessory p
742	6	0.8	261	2	S53423	major intrinsic pr	815	0.8	278	2	B70513	hypothetical prote
743	6	0.8	262	2	S72890	hypothetical prote	816	0.8	279	2	T09620	probable lectin 2
744	6	0.8	262	2	A70577	hypothetical prote	817	0.8	279	2	F84112	transcription regu
745	6	0.8	263	2	T12407	NADH2 dehydrogenas	818	0.8	279	2	AH1882	nitrate transport
746	6	0.8	263	2	G64085	triose-phosphate i	819	0.8	279	2	G70807	hypothetical prote
747	6	0.8	263	2	A55279	major intrinsic pr	820	0.8	279	2	C75538	hypothetical prote
748	6	0.8	263	2	S73314	hypothetical prote	821	0.8	279	2	AI1012	hypothetical prote
749	6	0.8	263	2	I54780	APK1 antigen - hum	822	0.8	279	2	A83148	conserved hypotet
750	6	0.8	264	2	B71362	probable exodeoxyr	823	0.8	280	2	T07741	nitrate reductase
751	6	0.8	264	2	T10155	hypothetical prote	824	0.8	280	2	H95246	maltodextrin ABC t
752	6	0.8	264	2	AI2667	conserved hypotet	825	0.8	280	2	A82185	glycerol-3-phospha
753	6	0.8	265	2	D83287	hypothetical prote	826	0.8	280	2	T24454	hypothetical prote
754	6	0.8	265	2	A75448	rRNA methylase - D	827	0.8	281	1	MMECUE	sn-Glycerol-3-phos
755	6	0.8	265	2	S62363	D-2-chloropropioni	828	0.8	281	1	B64227	hypothetical prote
756	6	0.8	266	2	H70858	probable electron	829	0.8	281	1	S73813	MG246 homolog H91
757	6	0.8	266	2	S51833	arcelin-4 precursor	830	0.8	281	2	AI1912	lysophospholipase-
758	6	0.8	266	2	C96913	sulfate adenylate	831	0.8	281	2	A86012	hypothetical prote
759	6	0.8	266	2	P00393	genome polyprotein	832	0.8	281	2	A91166	hypothetical prote

833	6	0.8	281	2	C64241	hypothetical prote	906	0.8	296	2	F75209	hypothetical prote
834	6	0.8	281	2	T50208	yeast kt112 protei	907	0.8	297	2	G87187	phosphoribosylamin
835	6	0.8	281	2	T01445	hypothetical prote	908	0.8	297	2	G70708	probable purC prot
836	6	0.8	281	2	F89045	protein B0238.3 [l	909	0.8	297	2	A72130	hypothetical prote
837	6	0.8	281	2	AF3407	transporter, dme f	910	0.8	297	2	H87613	pilus assembly pro
838	6	0.8	282	2	T06637	hypothetical prote	911	0.8	297	2	G95384	probable Lyag-fami
839	6	0.8	282	2	A75473	probable sigma fac	912	0.8	297	2	AF2980	conserved hypothet
840	6	0.8	282	2	F82851	conserved hypothet	913	0.8	297	2	H98302	hypothetical prote
841	6	0.8	282	2	D97442	hypothetical prote	914	0.8	297	2	A40560	homeobox protein H
842	6	0.8	283	1	I41318	fimbrial adhesin K	915	0.8	297	2	I54320	homeobox protein H
843	6	0.8	283	2	T12062	xpsK protein - xan	916	0.8	298	2	G69862	heat-shock protein
844	6	0.8	283	2	D83846	hypothetical prote	917	0.8	298	2	S12635	apolipoprotein E p
845	6	0.8	284	2	B46494	conserved hypothet	918	0.8	298	2	D87450	transcription regu
846	6	0.8	284	2	H83119	probable transcript	919	0.8	298	2	I40434	flagellar biosynth
847	6	0.8	284	2	A96604	hypothetical prote	920	0.8	298	2	T33220	hypothetical prote
848	6	0.8	284	2	T29001	hypothetical prote	921	0.8	298	2	T38937	rna binding protei
849	6	0.8	284	2	G71152	probable cobalt tr	922	0.8	298	2	T43542	rna-binding protei
850	6	0.8	285	2	A97492	probable transcript	923	0.8	298	2	F84324	hypothetical prote
851	6	0.8	285	2	H71938	flagellar motor sw	924	0.8	299	2	FN0638	vgh protein - Stap
852	6	0.8	286	2	AF2829	hydrolase [importe	925	0.8	299	2	A99422	hypothetical prote
853	6	0.8	286	2	G59182	thiosulfate sulfur	926	0.8	299	2	E70737	hypothetical prote
854	6	0.8	286	2	H97341	dihydrodipicolinat	927	0.8	299	2	AG2340	hypothetical prote
855	6	0.8	286	2	A81969	probable chromosom	928	0.8	299	2	S18813	homeotic protein H
856	6	0.8	287	1	S72569	probable aldehyde	929	0.8	300	2	AI3101	transcription regu
857	6	0.8	287	2	E98111	hypothetical prote	930	0.8	300	2	I40215	hypothetical prote
858	6	0.8	287	2	B82978	conserved hypothet	931	0.8	300	2	F75065	hypothetical prote
859	6	0.8	287	2	T24640	hypothetical prote	932	0.8	300	2	H75200	hypothetical prote
860	6	0.8	287	2	F64648	hypothetical prote	933	0.8	300	2	D71234	hypothetical prote
861	6	0.8	287	2	AE3578	glycine betaine/l-	934	0.8	300	2	AF2846	permease [imported
862	6	0.8	288	2	B83946	pyruvate synthase	935	0.8	300	2	F97623	hypothetical prote
863	6	0.8	288	2	C56281	7alpha-cephem-meth	936	0.8	301	2	C69837	5-oxo-1,2,5-tricar
864	6	0.8	288	2	S18438	sporulation protei	937	0.8	301	2	S50737	probable membrane
865	6	0.8	288	2	AB0231	probable exported	938	0.8	301	2	C96961	cell division prot
866	6	0.8	288	2	JS0659	homeotic protein H	939	0.8	302	1	WZBB9	gene 9 protein - h
867	6	0.8	289	1	S32294	probable glucosyl-1	940	0.8	302	2	T40490	probable 26s prote
868	6	0.8	289	1	S55649	deoxyuridine triph	941	0.8	302	2	F81016	conserved hypothet
869	6	0.8	289	2	A95158	homoserine kinase	942	0.8	302	2	F90158	DNA repair endo/ex
870	6	0.8	289	2	A98024	homoserine kinase	943	0.8	302	2	H87476	conserved hypothet
871	6	0.8	289	2	AB0282	conserved hypothet	944	0.8	302	2	B82968	probable transcript
872	6	0.8	289	2	H86532	Cr144 hypothetical	945	0.8	302	2	S75481	polysialic acid tr
873	6	0.8	289	2	B72099	conserved hypothet	946	0.8	303	2	AC0092	probable chemotaxi
874	6	0.8	289	2	C71501	probable outer mem	947	0.8	303	2	JC2410	ADP-ribosyl cyclas
875	6	0.8	289	2	B86794	hypothetical prote	948	0.8	303	2	F71680	hypothetical prote
876	6	0.8	289	2	S75157	ABC-type transport	949	0.8	303	2	H81818	conserved hypothet
877	6	0.8	290	1	KIRFAS	phosphoribulokinas	950	0.8	303	2	S75557	hypothetical prote
878	6	0.8	290	2	AB6038	involved in lipopo	951	0.8	303	2	B47089	probable Arac-type
879	6	0.8	290	2	H91190	involved in lipopo	952	0.8	303	2	B96909	probable permease
880	6	0.8	290	2	S47839	hypothetical prote	953	0.8	303	2	G71166	hypothetical prote
881	6	0.8	291	2	AH3074	short-chain dehydr	954	0.8	304	1	B69449	conserved hypothet
882	6	0.8	291	2	A96212	probable short-cha	955	0.8	304	2	T46647	pyridoxine biosynt
883	6	0.8	291	2	AB1659	conserved hypothet	956	0.8	305	2	T03155	ribonucleoside-dip
884	6	0.8	292	1	B35819	phosphoribulokinas	957	0.8	305	2	JN0518	acyltransferase (E
885	6	0.8	292	2	D97199	probable membrane	958	0.8	305	2	AD2494	mrp restriction sy
886	6	0.8	292	2	S23239	hypothetical prote	959	0.8	305	2	H75091	hypothetical prote
887	6	0.8	293	1	D69300	4-hydroxybenzoate	960	0.8	306	2	E64138	phosphoribosylamin
888	6	0.8	293	2	A89818	hypothetical prote	961	0.8	306	2	A89952	primosomal protein
889	6	0.8	293	2	AH01095	conserved hypothet	962	0.8	306	2	AE3100	inosine-uridine pr
890	6	0.8	293	2	JN0651	rRNA methyltransfe	963	0.8	306	2	E98186	inosine-uridine pr
891	6	0.8	293	2	T75441	conserved hypothet	964	0.8	306	2	AF3230	transcriptional re
892	6	0.8	293	2	T32229	hypothetical prote	965	0.8	306	2	T36764	probable ABC-type
893	6	0.8	293	2	A97313	transcription regu	966	0.8	307	2	H83660	cysteine synthase
894	6	0.8	293	2	AH01143	probable membrane	967	0.8	307	2	AH1269	primosome componen
895	6	0.8	294	1	KRMS3	tissue factor prec	968	0.8	307	2	AB1632	primosome componen
896	6	0.8	294	2	T11379	NADH2 dehydrogenas	969	0.8	307	2	S30432	hypothetical prote
897	6	0.8	294	2	T35492	probable endonucle	970	0.8	307	2	G90270	Na+/Ca2+ exchangin
898	6	0.8	294	2	B81427	H ₂ -transporting tw	971	0.8	307	2	G69211	conserved hypothet
899	6	0.8	294	2	G97449	hypothetical prote	972	0.8	307	2	T24423	hypothetical prote
900	6	0.8	295	2	F69976	conserved hypothet	973	0.8	308	2	S70735	ferrochelatase (EC
901	6	0.8	295	2	H97713	30S ribosomal prot	974	0.8	308	2	D69348	conserved hypothet
902	6	0.8	295	2	A60131	homeotic protein X	975	0.8	308	2	A99993	hypothetical prote
903	6	0.8	296	2	D75597	glucose-1-phosphat	976	0.8	309	2	D97607	tropinesterase (at
904	6	0.8	296	2	E71717	ribosomal protein	977	0.8	309	2	D64752	dihydrodipicolinat
905	6	0.8	296	2	S39746	hypothetical prote	978	0.8	309	2	C83136	probable epimerase

Db 201 GGIWTLTRSGNQFQAEKMEKVDFYQNNGYDFPRILDTDIQTNEKTKQTIKTVH 260
Qy 261 EGGFRKGVKISIGDITNEVPKAELEKLLTWKPGKWERQOQMTAVLGBIQRNMGSAGYAYS 320
Db 261 EGGFRKGVKISIGDITNEVPKAELEKLLTWKPGKWERQOQMTAVLGBIQRNMGSAGYAYS 320
Qy 321 EISVQPLPNAETKTVDPLVHIEFGKIKYVNEIHTGNKTRDEVRELRQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDPLVHIEFGKIKYVNEIHTGNKTRDEVRELRQMESAPYDTS 380
Qy 381 KLQSKERVLLGYFDNVQFVDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQSKERVLLGYFDNVQFVDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFGTGSAAALRASRSKTTILNGSLSTPDPYFTADGCVSLGYDVYVKGAFDPRKAS 500
Db 441 SAGVSQDNLFGTGSAAALRASRSKTTILNGSLSTPDPYFTADGCVSLGYDVYVKGAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNAKPHYADFIKKYKTDG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNAKPHYADFIKKYKTDG 560
Qy 561 TDGSFSGWLYKGTGWRGNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHTQWTFPP 620
Db 561 TDGSFSGWLYKGTGWRGNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHTQWTFPP 620
Qy 621 LSKTFTMLGGEVGIAGGYRTKEIPFENFYGGGLGVRGYSGLTGPVKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYRTKEIPFENFYGGGLGVRGYSGLTGPVKVYDEYGEKIS 680
Qy 681 YGNGKANVAEALLFPMGAKDARTVRLSLFADAGSVWMDKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNGKANVAEALLFPMGAKDARTVRLSLFADAGSVWMDKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772

RESULT 3
T46206
hypothetical protein T8P19.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
R;Choine, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23008
A;Accession: T46206
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <CHO>
A;Cross-references: UNIPROT:Q9SMN7; EMBL:AL13315
A;Experimental source: cultivar Columbia; BAC clone T8P19
C;Genetics:
A;Map position: 3
A;Introns: 39/2; 62/3; 94/3; 133/2; 179/3; 277/1
A;Note: T8P19.130

Query Match 1.1%; Score 9; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSVRGY 662
Db 152 GGLGSVRGY 160

RESULT 4
T49132
hypothetical protein F26G5.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C;Accession: T49132
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25017
A;Accession: T49132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-435 <DAN>
A;Cross-references: UNIPROT:Q9LXP7; EMBL:AL1353814; GSPDB:GN00061; ATSP:F26G5.110
A;Experimental source: cultivar Columbia; BAC clone F26G5
C;Genetics:
A;Gene: ATSP:F26G5.110
A;Map position: 3
A;Introns: 12/1; 34/2; 135/3; 188/3; 212/2; 238/3; 277/2; 326/3; 350/1; 395/1

Query Match 1.1%; Score 9; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSVRGY 662
Db 296 GGLGSVRGY 304

RESULT 5
A96984
hypothetical protein CAC0683 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: A96984
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A96984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <KUR>
A;Cross-references: UNIPROT:Q97L79; GB:AE001437; PIDN:AAK78660.1; PID:gl5023560; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0683

Query Match 1.0%; Score 8; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 670 KVVDEYGE 677
Db 17 KVVDEYGE 24

RESULT 6
E84423
hypothetical protein At2g01340 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84423
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84423
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <STO>
A;Cross-references: UNIPROT:Q9ZU33; GB:AE002093; NID:g4262241; PIDN:AAAD14534.1; GSPDB:GN
C;Genetics:
A;Gene: At2g01340
A;Map position: 2

```

Query Match      1.0%; Score 8; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 PKAELEKL 287
    |||||
Db 144 PKAELEKL 151

RESULT 7
glycerate dehydrogenase PAB2374 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B75057
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: B75057
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <RAW>
A:Cross-references: UNIPROT:Q9UYR1; GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB5035
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: gdh-like; PAB2374
C:Superfamily: phosphoglycerate dehydrogenase

Query Match      1.0%; Score 8; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 LGYDVYVK 492
    |||||
Db 145 LGYDVYVK 152

RESULT 8
formate dehydrogenase accessory protein VC1519 [imported] - Vibrio cholerae (strain N169
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: C82190
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82190
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <HEI>
A:Cross-references: UNIPROT:O9KRW5; GB:A5004230; GB:AB003852; NID:G9656018; PIDN:AAP9467
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1519
A:Map position: 1
C:Superfamily: formate dehydrogenase accessory protein FdhD

Query Match      1.0%; Score 8; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 VYDEYGEK 678
    |||||
Db 81 VYDEYGEK 88

RESULT 9
A71175

```

```

probable dehydrogenase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: A71175
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: A71175
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <RAW>
A:Cross-references: UNIPROT:O58320; GB:AP000002; NID:G3236129; PIDN:BAA29686.1; PID:G3257
A:Experimental source: strain OT3
A>Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0597

Query Match      1.0%; Score 8; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 LGYDVYVK 492
    |||||
Db 186 LGYDVYVK 193

RESULT 10
T04985
probable transaminase (EC 2.6.1.-) T16L1.170 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04985
R:Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15393
A:Accession: T04985
A:Molecule type: DNA
A:Residues: 1-426 <BEV>
A:Cross-references: UNIPROT:O81895; EMBL:AL031394
A:Experimental source: cultivar Columbia; BAC clone T16L1
C:Genetics:
A:Map position: 4
A:Introns: 19/1; 41/3; 80/3; 101/3; 136/3; 153/3; 260/3; 329/3
A>Note: T16L1.170
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match      1.0%; Score 8; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 SLGYDVYK 491
    |||||
Db 351 SLGYDVYK 358

RESULT 11
G42365
flagellar hook-length control protein fliK - Bacillus subtilis
N:Alternate names: hypothetical protein 7 (flaA operon)
C:Species: Bacillus subtilis
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C:Accession: G42365; G59624; S14500
R:Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A>Title: The flaA locus of Bacillus subtilis is part of a large operon coding for flagell
A:Reference number: A42365; MUID:91258343; PMID:1828465
A:Accession: G42365
A:Molecule type: DNA
A:Residues: 1-429 <ALB>
A:Cross-references: UNIPROT:P23451; EMBL:X56049; NID:G39904; PIDN:CAA39526.1; PID:G39910

```

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maues
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69624
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-429 <KUN>
A;Cross-references: GB:AL009126; NID:G2633902; PIDN:CAB13500.1; PID:ell185218;
A;Experimental source: strain 168
C;Genetics:
A;Gene: fliK

Query Match 1.0%; Score 8; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 PNAETKTIV 335
|||||
DB 286 PNAETKTIV 293
|||||

RESULT 12

IMBP4
site-specific recombinase for integration and excision - *Bacillus* phage phi-105
N;Alternate names: immunity region protein 3, 4, 5, 6
C;Species: *Bacillus* phage phi-105

C;Date: 31-Dec-1988 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T13541; C24521; D24521; E24521; F24521

R; Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.

submitted to the EMBL Data Library, July 1998

A;Description: Complete nucleotide sequence of *Bacillus subtilis* phage phi-105.

A;Reference number: Z17688

A;Accession: T13541

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-474 <KOB>

A;Cross-references: UNIPROT:Q9T200; EMBL:AB016282; PIDN:BA336659.1

R;Cully, D.F.; Garro, A.J.

A;Title: Nucleotide sequence of the immunity region of *Bacillus subtilis* bacteriophage P

Gene 38, 153-164, 1985

A;Reference number: A91535; MUID:96056972; PMID:3934047

A;Accession: C24521

A;Molecule type: DNA

A;Residues: 1-78, 'MTHC' <CUL>

A;Cross-references: GB:M11920; NID:G215477; PIDN:AAA88399.1; PID:g1196717

A;Accession: D24521

A;Molecule type: DNA

A;Residues: 149-160, 'AR', 163, 'H', 'HSDSQRRVR', 381-383, 'RIQRRARS', 392 <CU2>

A;Cross-references: GB:M11920; NID:G215477; PIDN:AAA88401.1; PID:g1196719

A;Accession: E24521

A;Molecule type: DNA

A;Residues: 189-318, 'HAP', <CU3>

A;Cross-references: GB:M11920

A;Accession: F24521

A;Molecule type: DNA

A;Residues: 'MP', 319-376, 'RNTK', 381, 'PGPWS', <CU4>

A;Cross-references: GB:M11920

C;Superfamily: phage phi-105 site-specific recombinase

C;Keywords: early protein

Query Match 1.0%; Score 8; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 IDEGKSAK 175
|||||
DB 53 IDEGKSAK 60
|||||

RESULT 13

G83375

probable glycosyl hydrolase PA2164 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: G83375

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: G83375

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-583 <STO>

A;Cross-references: UNIPROT:Q911V1; GB:AE004643; GB:AE004091; NID:G9948178; PIDN:AAG0555;

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA2164

C;Superfamily: glycosyltrehalose trehalohydrolase

Query Match 1.0%; Score 8; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 VRVETADG 81
|||||
DB 29 VRVETADG 36
|||||

RESULT 14

JE0327

dynamin-related protein MSP1 - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: JE0327

R;Pellegrini, L.; Belenguer, P.; Menon, Y.; Ducommun, B.

Biochem Biophys Res Commun 251, 720-726, 1998

A;Title: Identification of a fission yeast dynamin-related protein involved in mitochondr

A;Reference number: JE0327; MUID:99008891; PMID:9790976

A;Accession: JE0327

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-903 <PEL>

A;Cross-references: UNIPROT:P87320; GB:Y07891; NID:G2231081; PIDN:CAA69196.1; PID:G223108

C;Genetics:

A;Gene: MSP1

Query Match 1.0%; Score 8; DB 2; Length 903;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 SAALRASR 462
|||||
DB 417 SAALRASR 424
|||||

RESULT 15

T50334

dynamin-related protein [imported] - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C;Accession: T50334

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25062
A;Accession: T50334
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-903 <LYN>
A;Cross-references: UNIPROT:P87320; EMBL:AL157874; PIDN:CAB75996.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h(-); cosmid c1718
C;Genetics:
A;Gene: SPDB:SPBC1718.06
A;Map position: 2

Query Match 1.0%; Score 8; DB 2; Length 903;
Best Local Similarity 100.0%; Pred.No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 SAALRASR 462
Db 417 SAALRASR 424
|||||

Search completed: July 6, 2005, 15:44:23
Job time : 66 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:56:39 ; Search time 49.7902 Seconds
(without alignments)
1830.683 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178
Perfect score: 885
Sequence: 1 MKLKQIASALMMLGSLAPLAF.....RNRVDITIDECKSAKITD 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	797	2 O30912	O30912 neisseria m
2	879	99.3	797	2 O9KIH0	O9KIH0 neisseria m
3	875	98.9	797	2 O9JX31	O9JX31 neisseria m
4	863	97.5	792	2 P95359	P95359 neisseria g
5	469	53.0	771	2 O7NVY6	O7NVY6 chromobacte
6	390	44.1	758	2 O82U03	O82U03 nitrosomona
7	375	42.4	769	2 O63T20	O63T20 burkholderi
8	374	42.3	769	2 O62D22	O62D22 burkholderi
9	371.5	42.0	778	2 O7VYC2	O7VYC2 bordetella
10	371.5	42.0	778	2 O7WA52	O7WA52 bordetella
11	371.5	42.0	778	2 O7WJ86	O7WJ86 bordetella
12	356	40.2	818	2 O8PAW1	O8PAW1 xanthomonas
13	355.5	40.2	788	2 O8PWL3	O8PWL3 xanthomonas
14	354	40.0	785	2 O8XZ13	O8XZ13 ralstonia s
15	346	39.1	784	2 O9PB12	O9PB12 xylella fas
16	345	39.0	784	2 O87B11	O87B11 xylella fas
17	313.5	35.4	804	2 O7MTG8	O7MTG8 vibrio vuln
18	313.5	35.4	804	2 O8DBF3	O8DBF3 vibrio vuln
19	305.5	34.5	803	2 O8ZPA3	O8ZPA3 salmonella
20	305.5	34.5	804	2 O8ZRP0	O8ZRP0 salmonella
21	304.5	34.4	795	2 O667J7	O667J7 yersinia ps
22	304.5	34.4	795	2 O8ZH58	O8ZH58 yersinia pe
23	299.5	33.8	808	2 O6Q8T1	O6Q8T1 uncultured
24	298.5	33.7	804	2 O87ME5	O87ME5 vibrio para
25	297.5	33.6	797	2 O9S341	O9S341 photorhabdu
26	297.5	33.6	797	2 O7N8N9	O7N8N9 photorhabdu
27	295.5	33.4	797	2 O9HXY4	O9HXY4 pseudomonas
28	295.5	33.4	810	1 UP05 ECOLI	P39170 escherichia
29	292.5	33.1	786	2 O8BMH2	O8BMH2 pseudomonas
30	292.5	33.1	803	2 O9KPW0	O9KPW0 vibrio chol
31	292.5	33.1	810	2 O8KR94	O8KR94 escherichia

32	292.5	33.1	814	2 O6D8D5	O6D8D5 erwinia car
33	291.5	32.9	805	2 O6LN32	O6LN32 photobacter
34	289	32.7	795	2 O886N5	O886N5 pseudomonas
35	281	31.8	785	2 O9R2E3	O9R2E3 escherichia
36	281	31.8	787	2 O88H14	O88H14 pseudomonas
37	262	29.6	826	2 O8EGG7	O8EGG7 shewanella
38	255	28.8	825	2 O6FCG7	O6FCG7 acinetobact
39	244	27.6	789	2 O51930	O51930 pasteurella
40	244	27.6	803	2 O83DT2	O83DT2 coxiella bu
41	243	27.5	791	2 O9CJL1	O9CJL1 pasteurella
42	242	27.3	790	2 O8GBX8	O8GBX8 pasteurella
43	239	27.0	768	2 O9ZE03	O9ZE03 rickettsia
44	236.5	26.7	792	2 O32625	O32625 haemophilus
45	236.5	26.7	793	1 D153_HAEIN	O32629 haemophilus

ALIGNMENTS

RESULT 1					
O30912	O30912	PRELIMINARY;	PRT;	797 AA.	
AC	O30912;				
DT	01-JAN-1998	(TrEMBLrel. 05, Created)			
DT	01-JAN-1998	(TrEMBLrel. 05, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	Outer membrane protein Omp85.				
GN	Name=Omp85;				
OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;				
OC	Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=HH;				
RX	MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;				
RA	Manning D.S., Reschke D.K., Judd R.C.;				
RT	"Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp87.";				
RL	Microb. Pathog. 25:11-21(1998).				
DR	EMBL; AF021245; AAC17599.1; -.				
DR	InterPro; IPR000184; Bac_surfAg D15.				
DR	InterPro; IPR010827; Surf_Ag VNR.				
DR	PFam; PF01103; Bac surface Ag; 1.				
DR	PFam; PF07244; Surf_Ag VNR; 5.				
SQ	SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;				
Query Match 100.0%; Score 885; DB 2; Length 797;					
Best Local Similarity 100.0%; Pred. No. 3.7e-64;					
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Oy	1	MKLKQIASALMMLGISPLAFADTTQDIRVEGLQRTPESTVFNLPVKVGDVTYNDTHGSA 60			
Db	1	MKLKQIASALMMLGISPLAFADTTQDIRVEGLQRTPESTVFNLPVKVGDVTYNDTHGSA 60			
Oy	61	IIKSLVATGFFDDVRVETADGQLLTIVERTIGSLNITGAKMLQNDAIKKONLESFGLAQ 120			
Db	61	IIKSLVATGFFDDVRVETADGQLLTIVERTIGSLNITGAKMLQNDAIKKONLESFGLAQ 120			
Oy	121	SOYFNQATLNQAVAGLKEEYLRGKLNITPKVKLARNVDITIDEGKSAKITD 178			
Db	121	SOYFNQATLNQAVAGLKEEYLRGKLNITPKVKLARNVDITIDEGKSAKITD 178			
RESULT 2					
O9KIH0	O9KIH0	PRELIMINARY;	PRT;	797 AA.	
AC	O9KIH0;				
DT	01-OCT-2000	(TrEMBLrel. 15, Created)			
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	Outer membrane protein Omp85.				

```

GN OrderedLocusNames=NMB0182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tetzelin H., Saunders N.J., Heideberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwin M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Hatt D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RT Science 287:1809-1815(2000).
RL EMBL; AE002375; AAP40639.1; -.
DR PUR; G81228; G81228.
DR TIGR; NMB0182; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88436 MW; B68BFC5A43D22EE8 CRC64;

Query Match 99.3%; Score 879; DB 2; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.1e-63;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 3
Q9JX31 PRELIMINARY; PRT; 797 AA.
AC Q9JX31;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein OMP85.
GN Name=omp85;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."

```

```

RL Nature 404:502-506(2000).
DR EMBL; AL162752; CAB83401.1; -.
DR PIR; D82000; D82000.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88404 MW; 65DB47E0C9E1D1F CRC64;

Query Match 98.9%; Score 875; DB 2; Length 797;
Best Local Similarity 98.9%; Pred. No. 2.4e-63;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 4
P9S359 PRELIMINARY; PRT; 792 AA.
AC P9S359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN Name=omp85;
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FA19;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
RT are similar to Haemophilus influenzae D-15-Ag and Pasteurella
RT multocida Oms87."
RL Microb. Pathog. 25:11-21(1998).
DR EMBL; U81959; AAC17600.1; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 792 AA; 87868 MW; 90E32D24AA0513D8 CRC64;

Query Match 97.5%; Score 863; DB 2; Length 792;
Best Local Similarity 98.3%; Pred. No. 2.3e-62;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

```

```

RESULT 5
Q7NVY6 PRELIMINARY; PRT; 771 AA.
AC Q7NVY6;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Probable outer membrane protein.
GN OrderedLocusNames=CV2204;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A.A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.P.A., Loureiro M.P., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanz H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
DR EMBL; AB016917; AAQ59877.1; -
DR InterPro; IPR00184; Bac surfag D15.
DR Pfam; PF01103; Surf Ag VNR.
DR Pfam; PF07244; Surf Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 771 AA; 85250 MW; 272FA6D8B5F03BE8 CRC64;

Query Match 53.0%; Score 469; DB 2; Length 771;
Best Local Similarity 54.4%; Pred. No. 5.3e-30;
Matches 98; Conservative 28; Mismatches 52; Indels 2; Gaps 1;

QY 1 MKLKIATASALMMLGIGSLAFA--DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHG 58
Db 1 MKLRLVAAMGLTVAATVMAADPFVVKDIRVEGLQRTPESTVFNYLPVKVGDYNDTHG 60
QY 59 SALKIATYATGPDVVRVETADGQLLTIVERTPTIGSLNITGAKMLQNDIAKNLESFGL 118
Db 61 KEAKALFGTGFNDVRVESRGDTLTVTAERPVITQLNINGAKEPSKQDLKALNDNGF 120
QY 119 AQSOYENQATLNOAVAGLKEEYLGKLNITQTPKVTKLARNVDITIDEGSKAKITD 178
Db 121 AESLIPDQALLDGAQVQLKRYYSRGSISVEITPTVTKLNRNVAVTLDINEGVTAIRKE 180

RESULT 6
Q82U03 PRELIMINARY; PRT; 758 AA.
ID Q82U03

```

```

AC Q82U03;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Bacterial surface antigen (D15).
GN OrderedLocusNames=NE1710;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IPO 14298;
RX MEDLINE=22586410; PubMed=12700255;
DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773 (2003).
DR EMBL; BX321862; CAD85621.1; -
DR InterPro; IPR00184; Bac surfag D15.
DR Pfam; PF01103; Surf Ag VNR.
DR Pfam; PF07244; Surf Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 758 AA; 85016 MW; 6B9630B7124B06C9 CRC64;

Query Match 44.1%; Score 390; DB 2; Length 758;
Best Local Similarity 44.3%; Pred. No. 1.6e-23;
Matches 78; Conservative 37; Mismatches 61; Indels 0; Gaps 0;

QY 1 MKLKIATASALMMLGIGSLAFA--DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLRLVLLPFSLYSLGCMANDSLVVRDIRVEGLQRTPESTVFNYLPVKVGDVLDKSKASA 60
QY 61 IKSLEYATGPDVVRVETADGQLLTIVERTPTIGSLNITGAKMLQNDIAKNLESFGLAQ 120
Db 61 AIKALYATGTFDVKLKGSEGLLVQVQRPATQISNGAKEFDKDLKEGLKQAGLSE 120
QY 121 SOYFNQATLNOAVAGLKEEYLGKLNITQTPKVTKLARNVDITIDEGSKAKI 176
Db 121 SRIFSRSLLEKAEQELKQYISRGKYAVKITTTPLERRNIGINPDIEKGKTARI 176

RESULT 7
Q63T20 PRELIMINARY; PRT; 769 AA.
ID Q63T20
AC Q63T20;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Putative outer membrane protein.
GN ORFNames=BFSL2151;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchave M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;

```

RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR EMBL: BX571965; CAH36153.1; --
SQ SEQUENCE 769 AA; 84906 MW; 9E0E33B0197B11B1 CRC64;

Query Match 42.4%; Score 375; DB 2; Length 769;
Best Local Similarity 44.7%; Pred. No. 2.8e-22;
Matches 76; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

QY 7 ASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGTNDYTHGSAIKSLY 66
DB 15 AALAAHGLAAATAPFVQDDIKIEGLQVAGSVFAYLPKQGTFTDYGKASRAIRLY 74

QY 67 ATGFFDDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFNQ 126
DB 75 ATGFFDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFNQ 126

QY 127 ATLNQAVAGKEEYLRGKLNQITPKVTKLARNVDITIDEGKSAKI 176
DB 135 ALVDKAEQELKRGYLRGKLNQITPKVTKLARNVDITIDEGKSAKI 184

RESULT 8
Q62JD2 PRELIMINARY; PRT; 769 AA.

ID Q62JD2
AC Q62JD2
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Outer membrane protein, OMP85 family.
GN ORFNames=BMA1547;
OS Burkholderia mallei ATCC 23344.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=243160;
RN [1]
RP SEQUENCE FROM N.A.

QY 6 IASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGTNDYTHGSAIKSL 65
DB 18 LAALAPALAH-AFPEFVVRDIRVEGIQRTDAGTVFGLYVVKVGEKPTDEATEAVRRL 76

QY 66 YATGFDDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFN 125
DB 77 YGTGFDDVQIQTDNNVVVVVQVQERTIASIFNGMREFDSKATKSLAQVGFGEGRIFD 136

QY 126 QATLNQAVAGKEEYLRGKLNQITPKVTKLARNVDITIDEGKSAKITD 178
DB 137 QSMLEAEQELKRGYLRGKLNQITPKVTKLARNVDITIDEGKSAKITD 189

Query Match 42.3%; Score 374; DB 2; Length 769;
Best Local Similarity 44.7%; Pred. No. 3.4e-22;
Matches 76; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

QY 7 ASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGTNDYTHGSAIKSLY 66
DB 15 AALAAHGLAAATAPFVQDDIKIEGLQVAGSVFAYLPKQGTFTDYGKASRAIRLY 74

QY 67 ATGFFDDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFNQ 126
DB 75 ATGFFDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFNQ 126

QY 127 ATLNQAVAGKEEYLRGKLNQITPKVTKLARNVDITIDEGKSAKI 176
DB 135 ALVDKAEQELKRGYLRGKLNQITPKVTKLARNVDITIDEGKSAKI 184

RESULT 9
Q7VC2 PRELIMINARY; PRT; 778 AA.

ID Q7VC2
AC Q7VC2
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Probable surface antigen.
GN OrderedLocusNames=BP1535;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.

QY 6 IASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGTNDYTHGSAIKSL 65
DB 18 LAALAPALAH-AFPEFVVRDIRVEGIQRTDAGTVFGLYVVKVGEKPTDEATEAVRRL 76

QY 66 YATGFDDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFN 125
DB 77 YGTGFDDVQIQTDNNVVVVVQVQERTIASIFNGMREFDSKATKSLAQVGFGEGRIFD 136

QY 126 QATLNQAVAGKEEYLRGKLNQITPKVTKLARNVDITIDEGKSAKITD 178
DB 137 QSMLEAEQELKRGYLRGKLNQITPKVTKLARNVDITIDEGKSAKITD 189

Query Match 42.3%; Score 374; DB 2; Length 769;
Best Local Similarity 44.7%; Pred. No. 3.4e-22;
Matches 76; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

QY 7 ASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGTNDYTHGSAIKSLY 66
DB 15 AALAAHGLAAATAPFVQDDIKIEGLQVAGSVFAYLPKQGTFTDYGKASRAIRLY 74

QY 67 ATGFFDDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFNQ 126
DB 75 ATGFFDVRVETADGQLLTIVERTPTIGSLNTGARMQLQNDIAKKNLSFGLAQSYFNQ 126

QY 127 ATLNQAVAGKEEYLRGKLNQITPKVTKLARNVDITIDEGKSAKI 176
DB 135 ALVDKAEQELKRGYLRGKLNQITPKVTKLARNVDITIDEGKSAKI 184

RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.",
RL Nat. Genet. 35:32-40(2003).
DR ENBL; BX640427; CAE36837.1; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR005479; CphP synth_L_D2.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 778 AA; 86342 MW; 15C8F0F43B865298 CRC64;

Query Match 42.0%; Score 371.5; DB 2; Length 778;
Best Local Similarity 41.8%; Pred. No. 5.5e-22;
Matches 72; Conservative 40; Mismatches 60; Indels 1; Gaps 1;

QY 6 IASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGTVDYNDTHGSAIKSL 65
DB 18 LAALLAPALAH-AFEPFVVRDIRVEGIQTDTAGTVFGLPVKVGKFTDEEATEAVRRL 76

QY 66 YATGFDDVRVETADGQLLTIVERTIGSLNTGAKMLQNDIAKKNLSEFGLAQSOYFN 125
DB 77 YGTGFSDVQIQTDNNVVVVQVQERTIASISFNGRPFDSKAITKSLAQVGEGRIFD 136

QY 126 QATLNOAVAGLKEEYLGKGLNIQTPKVKLARNRVDITIDEGSKAKITD 178
DB 137 QSMLEAEYELKEQYLAQKGYEVTVATVTPLPNRVGVSGFDFEGEVAKIRE 189

RESULT 11
Q7WJ86 PRELIMINARY; PRT; 778 AA.
AC Q7WJ86;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Probable surface antigen.
GN OrderedLocusNames=BB2613;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.",
RL Nat. Genet. 35:32-40(2003).
DR ENBL; BX640444; CAE33106.1; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR005479; CphP synth_L_D2.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.

KW Complete proteome.
SQ SEQUENCE 778 AA; 86352 MW; BF0CA34EFPF501CCP CRC64;

Query Match 42.0%; Score 371.5; DB 2; Length 778;
Best Local Similarity 41.6%; Pred. No. 5.5e-22;
Matches 72; Conservative 40; Mismatches 60; Indels 1; Gaps 1;

QY 6 IASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGTVDYNDTHGSAIKSL 65
DB 18 LAALLAPALAH-AFEPFVVRDIRVEGIQTDTAGTVFGLPVKVGKFTDEEATEAVRRL 76

QY 66 YATGFDDVRVETADGQLLTIVERTIGSLNTGAKMLQNDIAKKNLSEFGLAQSOYFN 125
DB 77 YGTGFSDVQIQTDNNVVVVQVQERTIASISFNGRPFDSKAITKSLAQVGEGRIFD 136

QY 126 QATLNOAVAGLKEEYLGKGLNIQTPKVKLARNRVDITIDEGSKAKITD 178
DB 137 QSMLEAEYELKEQYLAQKGYEVTVATVTPLPNRVGVSGFDFEGEVAKIRE 189

RESULT 12
Q8PAW1 PRELIMINARY; PRT; 818 AA.
AC Q8PAW1;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Outer membrane antigen.
GN Name=oma; OrderedLocusNames=XCC1365;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach C.B., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.C., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takica M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.",
RL Nature 417:459-463(2002).
DR ENBL; AE012236; AAM40663.1; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 818 AA; 90685 MW; B4770C972C08FA26 CRC64;

Query Match 40.2%; Score 356; DB 2; Length 818;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 74; Conservative 33; Mismatches 64; Indels 0; Gaps 0;

QY 6 IASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGTVDYNDTHGSAIKSL 65
DB 43 LAAGLSLPAALAAAEPPFVSDIRVDGLQRIASGTVFTYLPVNRGTVDGKVAOSIRAL 102

QY 66 YATGFDDVRVETADGQLLTIVERTIGSLNTGAKMLQNDIAKKNLSEFGLAQSOYFN 125

Db 103 YRTGFFEDVQDRQGNILVTVKERPAINKLVTGKNKDKSEBLLKGLGDIUTGEGTFD 162

QY 126 QATLNOAVAGLKEYLGRGKLNQITPKVTKLARNRVDIDITDEGKSAKI 176

Db 163 RLSDLRVQELTQYNNRGKYNVEITPTVSPLDNRVDVAIAIKEGKAABI 213

RESULT 13

Q8PML3 ID Q8PML3 PRELIMINARY; PRT; 788 AA.

AC Q8PML3; MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Outer membrane antigen.

DE Names=Oma; OrderedLocusNames=XAC1413;

OS Xanthomonas axonopodis (pv. citri).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=92829;

RN [1]

RP STRAIN=306 / ATCC 13902 / XV 101;

RC MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madalira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamara R.B., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RL Nature 417:459-463(2002).

DR EMBL; AE011773; AM36284.1; -.

DR InterPro; IPR000184; Bac surfAg D15.

DR InterPro; IPR010827; Surf Ag VNR.

DR Pfam; PF01103; Bac surface Ag; 1.

DR Pfam; PF07244; Surf_Ag_VNR; 5.

KW Complete proteome.

SQ SEQUENCE 788 AA; 87704 MW; C76CB1E017A4B224 CRC64;

Query Match 40.2%; Score 355.5; DB 2; Length 788;

Best Local Similarity 43.3%; Pred. No. 1.1e-20;

Matches 74; Conservative 35; Mismatches 61; Indels 1; Gaps 1;

QY 6 IASALMMLGISPLAFADFTIQDIRVEGLQRTPTSPFNPLPVKVGDTYNDTHGSIAIKSL 65

Db 14 LAAGLSLPAVA-LAVEPFVASDIRVDGLQRIASGTVFTYLPVNRGDTVDKADAIRAL 72

QY 66 YATGFFDDVVEFADGQLLTIVERTIGSLNTGAKMLONDAIKNLSFGLAQSOYFN 125

Db 73 YRTGFFEDVQDRQGNILVTVKERPAINKLVTGKNKDKSEBLLKGLGDIUTGEGTFD 132

QY 126 QATLNOAVAGLKEYLGRGKLNQITPKVTKLARNRVDIDITDEGKSAKI 176

Db 133 RLSDLRVQELTQYNNRGKYNVEITPTVSPLDNRVDVAIAIKEGKAABI 183

RESULT 14

Q8XZ13 ID Q8XZ13 PRELIMINARY; PRT; 765 AA.

AC Q8XZ13; MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

QY 103 YRTGFFEDVQDRQGNILVTVKERPAINKLVTGKNKDKSEBLLKGLGDIUTGEGTFD 162

QY 126 QATLNOAVAGLKEYLGRGKLNQITPKVTKLARNRVDIDITDEGKSAKI 176

Db 133 RLSDLRVQELTQYNNRGKYNVEITPTVSPLDNRVDVAIAIKEGKAABI 183

RESULT 15

Q9PEI2 ID Q9PEI2 PRELIMINARY; PRT; 784 AA.

AC Q9PEI2; MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Outer membrane antigen.

DE OrderedLocusNames=Xfi1046;

OS Xylella fastidiosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xylella.

OX NCBI_TaxID=2371;

RN [1]

RP STRAIN=9a5c;

RC MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;

RX Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,

RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.

GN Names=RS05280; OrderedLocusNames=RS01412;

OS Ralstonia solanacearum (Pseudomonas solanacearum).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Ralstonia.

OX NCBI_TaxID=305;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GM11000;

RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;

RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,

RA Chandler M., Choigne N., Claudel-Renard C., Cunnac S., Denange N.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,

RA Weissenbach J., Boucher C.A.;

RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";

RL Nature 415:497-502(2002).

DR EMBL; AL646064; CAD15114.1; -.

DR Pfam; PF01103; Bac surface Ag; 1.

DR Pfam; PF07244; Surf Ag VNR; 5.

DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.

KW Complete proteome.

SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 40.0%; Score 354; DB 2; Length 765;

Best Local Similarity 40.1%; Pred. No. 1.5e-20;

Matches 73; Conservative 34; Mismatches 67; Indels 8; Gaps 1;

QY 3 LKQIASALMMLGISPL-----APADFTIQDIRVEGLQRTPTSPFNPLPVKVGDTYN 54

Db 2 IRQHRPPLSMLAASVLTVTCAGQAHAVEPPIKDIRVEGVQVPGTVFGYLPVKVGTEFT 61

QY 55 DTHGSNLIKSHYATGFFDDVVEFADGQLLTIVERTIGSLNTGAKMLONDAIKNLE 114

Db 62 DKGAESIRALYNTGFFKDVQIRAEAGNVLVVRVEERPAISQLEFIGEKFDKDLRRSLR 121

QY 115 SFLGAQSOYFNQATLNOAVAGLKEYLGRGKLNQITPKVTKLARNRVDIDITDEGKSA 174

Db 122 GVGVAERYDKSLDRAEQELKRVSVRGYAADVQITVTPDANRVSVTFIVDSGPVA 181

QY 175 KI 176

Db 182 KI 183

RESULT 15

Q9PEI2 ID Q9PEI2 PRELIMINARY; PRT; 784 AA.

AC Q9PEI2; MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)

DE Outer membrane antigen.

DE OrderedLocusNames=Xfi1046;

OS Xylella fastidiosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xylella.

OX NCBI_TaxID=2371;

RN [1]

RP STRAIN=9a5c;

RC MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;

RX Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,

RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,

RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,

RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,

RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,

RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,

Search completed: July 6, 2005, 15:18:05
Job time : 52.7902 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:18:21 ; Search time 223.733 Seconds

(without alignments)
1374.310 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 4152

Sequence: 1 MKLKQATASALMMLGISPLAF.....LKKPEDEIQRFQGLGTF 797

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4152	100.0	797	9	US-09-994-192-4
2	4152	100.0	797	17	US-10-606-618-4
3	4140	99.7	797	14	US-10-181-660-3
4	4140	99.7	797	15	US-10-320-800-6
5	4140	99.7	797	16	US-10-181-600-3
6	4136	99.6	797	14	US-10-181-660-11
7	4136	99.6	797	16	US-10-181-660-11
8	4049	97.5	776	14	US-10-181-660-5
9	4049	97.5	776	14	US-10-181-660-13
10	4049	97.5	776	16	US-10-181-600-5
11	4049	97.5	776	16	US-10-181-600-13

12	3956.5	95.3	792	14	US-10-181-660-7	Sequence 7, Appli
13	3956.5	95.3	792	16	US-10-181-600-7	Sequence 7, Appli
14	3937.5	94.8	792	9	US-09-994-192-2	Sequence 2, Appli
15	3937.5	94.8	792	16	US-10-467-534-92	Sequence 92, Appli
16	3937.5	94.8	792	17	US-10-606-618-2	Sequence 2, Appli
17	3859.5	93.0	771	14	US-10-181-660-9	Sequence 9, Appli
18	3859.5	93.0	771	16	US-10-181-600-9	Sequence 9, Appli
19	1109	26.7	813	16	US-10-896-725-2	Sequence 2, Appli
20	1109	26.7	813	16	US-10-896-725-4	Sequence 4, Appli
21	703	16.9	896	14	US-10-210-296-5	Sequence 5, Appli
22	703	16.9	896	15	US-10-449-462-5	Sequence 5, Appli
23	532	12.8	847	10	US-09-988-067B-8	Sequence 8, Appli
24	526	12.7	925	15	US-10-335-977-4919	Sequence 4919, Ap
25	454.5	10.9	795	15	US-10-289-762-314	Sequence 314, App
26	452.5	10.9	790	15	US-10-312-273-147	Sequence 147, App
27	433	10.4	792	16	US-10-467-534-25	Sequence 25, Appli
28	431	10.4	792	17	US-10-498-327-55	Sequence 55, Appli
29	400.5	9.6	614	15	US-10-335-977-4918	Sequence 4918, Ap
30	286	6.9	252	16	US-10-437-963-114029	Sequence 114029,
31	253	6.1	889	16	US-10-878-939-4	Sequence 4, Appli
32	253	6.1	919	16	US-10-878-933-2	Sequence 2, Appli
33	251	6.0	609	16	US-10-833-884-2	Sequence 2, Appli
34	251	6.0	609	16	US-10-833-884-4	Sequence 4, Appli
35	246	5.9	665	16	US-10-437-963-126949	Sequence 126949,
36	241.5	5.8	512	16	US-10-425-115-317331	Sequence 317331,
37	237	5.7	587	16	US-10-833-884-6	Sequence 6, Appli
38	209	5.0	602	14	US-10-010-160-16	Sequence 16, Appli
39	200	4.6	469	15	US-10-166-349-7	Sequence 7, Appli
40	190	4.6	469	15	US-10-678-986-1	Sequence 1, Appli
41	190	4.6	469	16	US-10-408-765A-2300	Sequence 2300, Ap
42	189	4.6	469	16	US-10-408-765A-1346	Sequence 1346, Ap
43	188.5	4.5	463	15	US-10-166-349-9	Sequence 9, Appli
44	186	4.5	469	15	US-10-166-349-8	Sequence 8, Appli
45	184.5	4.4	468	16	US-10-408-765A-1807	Sequence 1807, Ap

ALIGNMENTS

RESULT 1

US-09-994-192-4
; Sequence 4, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Om85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UMSBCL47AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match 100.0%; Score 4152; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 2,1e-295;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKLKQATASALMMLGISPLAFDETIQDIRVEGLQRTPESTVENYLPVKVGDTYNDTHGSA	60
DB	1	MKLKQATASALMMLGISPLAFDETIQDIRVEGLQRTPESTVENYLPVKVGDTYNDTHGSA	60
QY	61	IIKSLYATGFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120
DB	61	IIKSLYATGFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120

Qy	121	SOYFNOATLNQAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDTIDGKSAKITDIE	180
Db	121	SOYFNOATLNQAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDTIDGKSAKITDIE	180
Qy	181	PEGNOVYSDRKLQMSLTGGIWTWLTNRNQNEQKFAODMEKVTDFYQNGYFDFRIL	240
Db	181	PEGNOVYSDRKLQMSLTGGIWTWLTNRNQNEQKFAODMEKVTDFYQNGYFDFRIL	240
Qy	241	DTDIQTNEDEKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ	300
Db	241	DTDIQTNEDEKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ	300
Qy	301	MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHIITGNKKT	360
Db	301	MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHIITGNKKT	360
Qy	361	RDEVVRELQMESAPYDTSKLQRSKERVLLGVFDNVQFQDAVPLAGTDPKVDLNNSLTE	420
Db	361	RDEVVRELQMESAPYDTSKLQRSKERVLLGVFDNVQFQDAVPLAGTDPKVDLNNSLTE	420
Qy	421	RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDDPYFTA	480
Db	421	RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDDPYFTA	480
Qy	481	DGVSGLGYDVYVKAPDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
Db	481	DGVSGLGYDVYVKAPDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
Qy	541	YNKAPHYADFIKYGKTDGTSFGKWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIA	600
Db	541	YNKAPHYADFIKYGKTDGTSFGKWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIA	600
Qy	601	LPGSKLQYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR	660
Db	601	LPGSKLQYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR	660
Qy	661	GYESGTLGPKVYDEYGEKISYGNKKANVSAEILLFPMPGAADARTVRLSLFADAGSVWDG	720
Db	661	GYESGTLGPKVYDEYGEKISYGNKKANVSAEILLFPMPGAADARTVRLSLFADAGSVWDG	720
Qy	721	KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK	780
Db	721	KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK	780
Qy	781	KPEDEIQRFQFQLGTTTF 797	
Db	781	KPEDEIQRFQFQLGTTTF 797	

RESULT 2
US-10-606-618-4
; Sequence 4, Application US/10606618
; Publication No. US20050074458A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBCL47AUSA
; CURRENT APPLICATION NUMBER: US/10/606,618
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-606-618-4

Query Match	100.0.0%;	Score 4152;	DB 17;	Length 797;
Best Local Similarity	100.0.0%;	Pred. No. 2.1e-295;		
Matches 797;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKLKQJASALMLGIGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60	
Db	1	MKLKQJASALMLGIGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60	
Qy	61	IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120	
Db	61	IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120	
Qy	121	SOYFNOATLNQAVAGLKEEYLGKLNQIQTPKVTKLARNRVDIITIDEGKSAKITDIE	180	
Db	121	SOYFNOATLNQAVAGLKEEYLGKLNQIQTPKVTKLARNRVDIITIDEGKSAKITDIE	180	
Qy	181	PEGNOVYSDRKLQMSLTGEGGIWTWLTNRNQNEQKFAODMEKVTDFYQNGYFDFRIL	240	
Db	181	PEGNOVYSDRKLQMSLTGEGGIWTWLTNRNQNEQKFAODMEKVTDFYQNGYFDFRIL	240	
Qy	241	DTDIQTNEDEKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ	300	
Db	241	DTDIQTNEDEKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ	300	
Qy	301	MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHIITGNKKT	360	
Db	301	MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHIITGNKKT	360	
Qy	361	RDEVVRELQMESAPYDTSKLQRSKERVVELLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE	420	
Db	361	RDEVVRELQMESAPYDTSKLQRSKERVVELLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE	420	
Qy	421	RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFTDPYFTA	480	
Db	421	RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFTDPYFTA	480	
Qy	481	DGVSGLGYDVYVKAPDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540	
Db	481	DGVSGLGYDVYVKAPDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540	
Qy	541	YNKAPHYADFIKYGKTDGTSFGKWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIA	600	
Db	541	YNKAPHYADFIKYGKTDGTSFGKWLKGTGVMGRNKTDLSALWPTRGYLTGVNAEIA	600	
Qy	601	LPGSKLQYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR	660	
Db	601	LPGSKLQYYSATHNQWTFPPLSKTFTLLMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR	660	
Qy	661	GYESGTLGPKVYDEYGEKISYGNKKANVSAEILLFPMPGAADARTVRLSLFADAGSVWDG	720	
Db	661	GYESGTLGPKVYDEYGEKISYGNKKANVSAEILLFPMPGAADARTVRLSLFADAGSVWDG	720	
Qy	721	KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK	780	
Db	721	KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK	780	
Qy	781	KPEDEIQRFQFQLGTTTF 797		
Db	781	KPEDEIQRFQFQLGTTTF 797		

RESULT 3

US-10-181-660-3

;

Sequence 3, Application US/10181660

;

Publication No. US20030027097A1

;

GENERAL INFORMATION:

;

APPLICANT: CHIRON SPA

;

TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS

;

FILE REFERENCE: P023785W0

;

CURRENT APPLICATION NUMBER: US/10/181,660

;

CURRENT FILING DATE: 2003-03-31

;

PRIOR APPLICATION NUMBER: GB-0001067.8

;

PRIOR FILING DATE: 2000-01-17

RESULT 3
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17

;; PRIOR APPLICATION NUMBER: GB-0005699.4
;; PRIOR FILING DATE: 2000-03-09
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: Seqwin99, version 1.02
;; SEQ ID NO 3
;; LENGTH: 797
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-10-181-660-3

Query Match 99.7%; Score 4140; DB 14; Length 797;
Best Local Similarity 99.7%; Pred. No. 1.6e-294;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLQIASALMMLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQVFNQATLNOAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
DB 121 SQVFNQATLNOAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 FEGNOVYSDRKLWOMSLTEGGIWTWLTNRNOEQKFAQDMKVDFYQNGYDFPRIL 240
DB 181 FEGNOVYSDRKLWOMSLTEGGIWTWLTNRNOEQKFAQDMKVDFYQNGYDFPRIL 240
QY 241 DTDIQTNEDEKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
DB 241 DTDIQTNEDEKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
QY 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELROMESAPYDTSKLQSKRVERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTE 420
DB 361 RDEVVRRELROMESAPYDTSKLQSKRVERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTE 420
QY 421 RSTGSLDLGAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLNGSLSTFDPYFTA 480
DB 421 RSTGSLDLGAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLNGSLSTFDPYFTA 480
QY 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKGTGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKGTGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
QY 601 LPGSKLOQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660
DB 601 LPGSKLOQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAEALLFPMGAKADARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAEALLFPMGAKADARTVRLSLFADAGSVWDG 720
QY 721 KTVDDNSSATGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
DB 721 KTVDDNSSATGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
QY 781 KPDEIQRFQFOLGTTT 797
DB 781 KPDEIQRFQFOLGTTT 797

RESULT 4

US-10-320-800-6

;; Sequence 6, Application US/10320800
;; Publication No. US20030215469A1
;; GENERAL INFORMATION:
;; APPLICANT: ROBINSON, ANDREW
;; APPLICANT: GORRINGE, ANDREW
;; APPLICANT: HUDSON, MICHAEL
;; APPLICANT: REDDIN, KAREN
;; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
;; FILE REFERENCE: 1581.0790001
;; CURRENT APPLICATION NUMBER: US/10/320,800
;; CURRENT FILING DATE: 2002-12-17
;; PRIOR APPLICATION NUMBER: PCT/GB99/03626
;; PRIOR FILING DATE: 1999-11-02
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6
;; LENGTH: 797
;; TYPE: PRT
;; ORGANISM: Neisseria meningitidis
US-10-320-800-6

Query Match 99.7%; Score 4140; DB 15; Length 797;
Best Local Similarity 99.7%; Pred. No. 1.6e-294;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLQIASALMMLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQVFNQATLNOAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
DB 121 SQVFNQATLNOAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 FEGNOVYSDRKLWOMSLTEGGIWTWLTNRNOEQKFAQDMKVDFYQNGYDFPRIL 240
DB 181 FEGNOVYSDRKLWOMSLTEGGIWTWLTNRNOEQKFAQDMKVDFYQNGYDFPRIL 240
QY 241 DTDIQTNEDEKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
DB 241 DTDIQTNEDEKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
QY 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELROMESAPYDTSKLQSKRVERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTE 420
DB 361 RDEVVRRELROMESAPYDTSKLQSKRVERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTE 420
QY 421 RSTGSLDLGAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLNGSLSTFDPYFTA 480
DB 421 RSTGSLDLGAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLNGSLSTFDPYFTA 480
QY 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKGTGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKGTGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
QY 601 LPGSKLOQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660
DB 601 LPGSKLOQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAEALLFPMGAKADARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAEALLFPMGAKADARTVRLSLFADAGSVWDG 720

QY 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFOFQLGTTTF 797
Db 781 KPEDEIQRFOFQLGTTTF 797
RESULT 5
US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-3
Query Match 99.7%; Score 4140; DB 16; Length 797;
Best Local Similarity 99.7%; Pred. No. 1.6e-294;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLKQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLSEFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLSEFGLAQ 120
QY 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDIDITIDEGSAKITDIE 180
Db 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDIDITIDEGSAKITDIE 180
QY 181 FEGNQVYSDRKLQMSLTGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
Db 181 FEGNQVYSDRKLQMSLTGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
QY 241 DTDIQTNEDEKTKQITIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEDEKTKQITIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELQMSAPYDTSKLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQMSAPYDTSKLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420
QY 421 RSTGSLDLSAGVQDITGLVMSAGVSQDNLFQTKGSAALRASRSKTTLNGSLSTFTDIFYFTA 480
Db 421 RSTGSLDLSAGVQDITGLVMSAGVSQDNLFQTKGSAALRASRSKTTLNGSLSTFTDIFYFTA 480
QY 481 DGVSLGVDYVKGKAPDRPKASTSIKQYKTTTAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSLGVDYVKGKAPDRPKASTSIKQYKTTTAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKTKDGTGDSFGKWLKGTGVGGRNKTDTSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHYADFIKKYKTKDGTGDSFGKWLKGTGVGGRNKTDTSALWPTRGYLTGVNAEIA 600

Db 541 YNKAPKHYADFIKKYKTKDGTGDSFGKWLKGTGVGGRNKTDTSALWPTRGYLTGVNAEIA 600
QY 601 LPSGKLQYYSATHNQWFFPLSKTFTMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR 660
Db 601 LPSGKLQYYSATHNQWFFPLSKTFTMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAAELLPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAAELLPMPGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFOFQLGTTTF 797
Db 781 KPEDEIQRFOFQLGTTTF 797
RESULT 6
US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11
Query Match 99.6%; Score 4136; DB 14; Length 797;
Best Local Similarity 99.6%; Pred. No. 3.1e-294;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLKQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLSEFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLSEFGLAQ 120
QY 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDIDITIDEGSAKITDIE 180
Db 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDIDITIDEGSAKITDIE 180
QY 181 FEGNQVYSDRKLQMSLTGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
Db 181 FEGNQVYSDRKLQMSLTGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
QY 241 DTDIQTNEDEKTKQITIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEDEKTKQITIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELQMSAPYDTSKLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQMSAPYDTSKLQSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420


```
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
QY 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKGTGNGRKNKTDLSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKGTGNGRKNKTDLSALWPTRGYLTGVNAEIA 600
QY 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
DB 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDYGEKISYGNKKNKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDYGEKISYGNKKNKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQLTGTF 797
DB 781 KPEDEIQRFQFQLTGTF 797

RESULT 7
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-11

Query Match 99.6%; Score 4136; DB 16; Length 797;
Best Local Similarity 99.6%; Pred. No. 3.1e-294;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLKQIASALMVLGISPLAFADFTIQDIRVEGLQRTPESTVFNFVLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMVLGISPLAFADFTIQDIRVEGLQRTPESTVFNFVLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLQNAVAGLKEEYLGKLNQITPKVTKLARNRVDIDITIDEGSKAKITDIE 180
DB 121 SQYFNQATLQNAVAGLKEEYLGKLNQITPKVTKLARNRVDIDITIDEGSKAKITDIE 180
QY 181 FEGNOVYSDRKLKRMQSLTEGGIWTWLTNRQNFNEQKFAQDMKRVDTFYQNGYFFDFRIL 240
DB 181 FEGNOVYSDRKLKRMQSLTEGGIWTWLTNRQNFNEQKFAQDMKRVDTFYQNGYFFDFRIL 240
QY 241 DTDIOTNEDKTKOTIKITVHEGGRFRWKVYSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
DB 241 DTDIOTNEDKTKOTIKITVHEGGRFRWKVYSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
```

```
DB 241 DTDIOTNEDKTKOTIKITVHEGGRFRWKVYSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
QY 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
DB 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
QY 361 RDEVVRRELQMSAPYDTSKLORSKERVELLGVDNVQFDVAVPLAGTDPKVDLNMSLTE 420
DB 361 RDEVVRRELQMSAPYDTSKLORSKERVELLGVDNVQFDVAVPLAGTDPKVDLNMSLTE 420
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
QY 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKGTGNGRKNKTDLSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKGTGNGRKNKTDLSALWPTRGYLTGVNAEIA 600
QY 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
DB 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDYGEKISYGNKKNKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDYGEKISYGNKKNKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQLTGTF 797
DB 781 KPEDEIQRFQFQLTGTF 797

RESULT 8
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match 97.5%; Score 4049; DB 14; Length 776;
Best Local Similarity 99.9%; Pred. No. 7.2e-288;
Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNFVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
DB 1 DFTIQDIRVEGLQRTPESTVFNFVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
QY 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLQNAVAGLKEEYL 141
DB 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLQNAVAGLKEEYL 120
```


Query Match 97.5%; Score 4049; DB 16; Length 776;
Best Local Similarity 99.9%; Pred. No. 7.2e-288;
Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
DB 1 DFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60

QY 82 QLLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 141
DB 61 QLLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 120

QY 142 GRGKLNIIQITPKVTKLARNVDIITIDEGKSAKITDIEFEGNOVYSDRKLQMOMSLTEG 201
DB 121 GRGKLNIIQITPKVTKLARNVDIITIDEGKSAKITDIEFEGNOVYSDRKLQMOMSLTEG 180

QY 202 GIWTLTRSNQFNEQKFAQDMKVDFYQNGGYDFRILDTDIQTNEDEKTKQIKITVHE 261
DB 181 GIWTLTRSNQFNEQKFAQDMKVDFYQNGGYDFRILDTDIQTNEDEKTKQIKITVHE 240

QY 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSGAGYAYSE 321
DB 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSGAGYAYSE 300

QY 322 ISVQPLPNAETKTVDVFLHI EPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 381
DB 301 ISVQPLPNAETKTVDVFLHI EPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 360

QY 382 LQSSKERVLLGYFDNVQFPAVPLAGTDPKVDLNMSLTERSTGSLDL SAGVQDTGLVMS 441
DB 361 LQSSKERVLLGYFDNVQFPAVPLAGTDPKVDLNMSLTERSTGSLDL SAGVQDTGLVMS 420

QY 442 AGVSQNLFGTGSAAALRASRKTTLNGSLSFDPYFTADGSLGVYGVYKAFDPKRAST 501
DB 421 AGVSQNLFGTGSAAALRASRKTTLNGSLSFDPYFTADGSLGVYGVYKAFDPKRAST 480

QY 502 SIQOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHVADFIKYGKTDGT 561
DB 481 SIQOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHVADFIKYGKTDGT 540

QY 562 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFFPL 621
DB 541 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFFPL 600

QY 622 SKTFTLMLGGEVGIAGGYGRTKEIPIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKISY 681
DB 601 SKTFTLMLGGEVGIAGGYGRTKEIPIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKISY 660

QY 682 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGA 741
DB 661 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGA 720

QY 742 GNTHKSTFTNRLYSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIORFQFQLTGTF 797
DB 721 GNTHKSTFTNRLYSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIORFQFQLTGTF 776

RESULT 11

US-10-181-600-13
; Sequence 13, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02

RESULT 12

US-10-181-660-7
; Sequence 7, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31

```
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-7

Query Match          95.3%; Score 3956.5; DB 14; Length 792;
Best Local Similarity 95.4%; Pred. No. 4.5e-281;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;

Qy 1 M K L Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Db 1 M K L Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Qy 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Db 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Qy 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Db 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Qy 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S N O F N E Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Db 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S D R F D R Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Qy 241 D T D I Q T N E D K T Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Db 241 D T D I Q T N E D K T R Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Qy 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Db 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A G T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Qy 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Db 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Qy 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Db 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Qy 481 D G V S L G Y D V Y G K A F D P R K A S T S I K O Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
Db 481 D G V S L G Y D I Y G K A F D P R K A S T S V K Q Y K T T T A G G V R M G I P V T E Y D R V N F G L A A E H L T V N T 540
Qy 541 Y N K A P H Y A D F I K Y K G T D G T G S F K G M L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600
Db 541 Y N K A P K Y A D F I R K Y K T D G A D G S F K G L L Y K G T V G W G R N K T D S A S W P T R G Y L T G V N A E I A 600
Qy 601 L P G S K L Q Y Y S A T H N Q T W F P P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G G L G S V R 660
Db 601 L P G S K L Q Y Y S A T H N Q T W F P P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G G L G S V R 660
Qy 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
Db 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
Qy 721 K T Y D N D S S S A T G R V N I Y A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K F Y A Y P L K K 780
Db 721 R T Y - - - - T A E N G N N K S V Y - S E N A H K S T F T N E L R Y S A G G A V T W L S P L G P M K F S I A Y P L K K 775
Qy 781 K P E D E I Q R F Q L G T T F 797
Db 776 K P E D E I Q R F Q L G T T F 792
```

```
RESULT 13
US-10-181-600-7
; Sequence 7, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-7

Query Match          95.3%; Score 3956.5; DB 16; Length 792;
Best Local Similarity 95.4%; Pred. No. 4.5e-281;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;

Qy 1 M K L Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Db 1 M K L Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Qy 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Db 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Qy 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Db 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Qy 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S N O F N E Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Db 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S D R F D R Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Qy 241 D T D I Q T N E D K T Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Db 241 D T D I Q T N E D K T R Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Qy 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Db 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A G T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Qy 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Db 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Qy 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Db 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Qy 481 D G V S L G Y D V Y G K A F D P R K A S T S I K O Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
Db 481 D G V S L G Y D I Y G K A F D P R K A S T S V K Q Y K T T T A G G V R M G I P V T E Y D R V N F G L A A E H L T V N T 540
Qy 541 Y N K A P H Y A D F I K Y K G T D G T G S F K G M L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600
Db 541 Y N K A P K Y A D F I R K Y K T D G A D G S F K G L L Y K G T V G W G R N K T D S A S W P T R G Y L T G V N A E I A 600
Qy 601 L P G S K L Q Y Y S A T H N Q T W F P P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G G L G S V R 660
Db 601 L P G S K L Q Y Y S A T H N Q T W F P P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G G L G S V R 660
Qy 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
Db 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
```

```
QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 721 RTY-----TAAENGNNKSVY-SENAHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 775
QY 781 KPEDEIQRFQFQGLGTTTF 797
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 776 KPEDEIQRFQFQGLGTTTF 792
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 14
US-09-994-192-2
; Sequence 2, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2

Query Match 94.8%; Score 3937.5; DB 9; Length 792;
Best Local Similarity 95.1%; Pred. No. 1.1e-279;
Matches 758; Conservative 16; Mismatches 18; Indels 5; Gaps 2;

QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQVFNQATLQNAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SQVFNQATLQNAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 FEGNQVYSRDKLRQMSLTGEGGIWTLTRSNQFNEOKFAQDMKVTDFYQNGYDFDPRIL 240
Db 181 FEGNQVYSRDKLRQMSLTGEGGIWTLTRSDRFRQKFAQDMKVTDFYQNGYDFDPRIL 240
QY 241 DTDIQTNEDEKTKQTIKTVHEGGRFRGWKVSIEGDTNEVPKAEKLLTMKPGKWERQ 300
Db 241 DTDIQTNEDEKTKQTIKTVHEGGRFRGWKVSIEGDTNEVPKAEKLLTMKPGKWERQ 300
QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLNABTKTVDFVLHIEPGRKIYVNEIHTGNKT 360
Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLNABTKTVDFVLHIEPGRKIYVNEIHTGNKT 360
QY 361 RDEVRELRQMSAPYDTSKLQRKERVLLGYFDNVQFQDAVPLAGTDPKVDLNLMSLTE 420
Db 361 RDEVRELRQMSAPYDTSKLQRKERVLLGYFDNVQFQDAVPLAGTDPKVDLNLMSLTE 420
QY 421 RSTGSLDLQAGVQDQTLGIVMSAGVSQDNLFGTGSAAALRASRSKTLTLNGSLSFPTDYPFTA 480
Db 421 RSTGSLDLQAGVQDQTLGIVMSAGVSQDNLFGTGSAAALRASRSKTLTLNGSLSFPTDYPFTA 480
QY 481 DGVSLGYDVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSLGYDVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGDSFGKGLWYKGTVGWGRNKTDTSALWPTRGYLTGVNAEIA 600
```

```
Db 541 YNKAPKRYADFIKQYKGTGADGSPKGLLYKGTVGWGRNKTDTSALWPTRGYLTGVNAEIA 600
QY 601 LPSGKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
Db 601 LPSGKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABLLFPMPGAADKARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSABLLFPMPGAADKARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 721 RTY-----TAAENGNNKSVY-SENAHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 775
QY 781 KPEDEIQRFQFQGLGTTTF 797
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 776 KPEDEIQRFQFQGLGTTTF 792
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 15
US-10-467-534-92
; Sequence 92, Application US/10467534
; Publication No. US20040131625A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/10/467,534
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-534-92

Query Match 94.8%; Score 3937.5; DB 16; Length 792;
Best Local Similarity 95.1%; Pred. No. 1.1e-279;
Matches 758; Conservative 16; Mismatches 18; Indels 5; Gaps 2;

QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQVFNQATLQNAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SQVFNQATLQNAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 FEGNQVYSRDKLRQMSLTGEGGIWTLTRSNQFNEOKFAQDMKVTDFYQNGYDFDPRIL 240
Db 181 FEGNQVYSRDKLRQMSLTGEGGIWTLTRSDRFRQKFAQDMKVTDFYQNGYDFDPRIL 240
QY 241 DTDIQTNEDEKTKQTIKTVHEGGRFRGWKVSIEGDTNEVPKAEKLLTMKPGKWERQ 300
Db 241 DTDIQTNEDEKTKQTIKTVHEGGRFRGWKVSIEGDTNEVPKAEKLLTMKPGKWERQ 300
QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLNABTKTVDFVLHIEPGRKIYVNEIHTGNKT 360
Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLNABTKTVDFVLHIEPGRKIYVNEIHTGNKT 360
```

Qy	361	RDEVVRELQMESAPYDTSKLQSKERVELLGYFDNVQFDVPLAGTDPKVDLNMSLTE	420
Db	361	RDEVVRELQMESAPYDTSKLQSKERVELLGYFDNVQFDVPLAGTDPKVDLNMSLTE	420
Qy	421	RSTGSLDLSAGWQDTCGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSTDPYFTA	480
Db	421	RSTGSLDLSAGWQDTCGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSTDPYFTA	480
Qy	481	DGVSGLGYDVYTKAFDPRKASTSIKQYKTTTATAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
Db	481	DGVSGLGYDIIYGKAFDPRKASTSVKQYKTTTAGGGVRMGIPTVEYDRVNFGLAAEHLTVNT	540
Qy	541	YNKAPRYADFIKKYKTDGDSFKGWLKGTVGWGRNKTDLSALWPTRGYLTGVNAEIA	600
Db	541	YNKAPRYADFIKQYKTDGADGSFKGLLYKGTVGWGRNKTDLSALWPTRGYLTGVNAEIA	600
Qy	601	LPGSKLOYYSATHNOTWFFPLSKTFTLMLGGEVGIAGGYGRKTEIPPFENFYGGGLGSVR	660
Db	601	LPGSKLOYYSATHNOTWFFPLSKTFTLMLGGEVGIAGGYGRKTEIPPFENFYGGGLGSVR	660
Qy	661	GYESGTLGPKVYDEYGEKISYGGNKKANVSARELLFPMPGAKDARTVRLSLFADAGSVWDG	720
Db	661	GYESGTLGPKVYDEYGEKISYGGNKKANVSARELLFPMPGAKDARTVRLSLFADAGSVWDG	720
Qy	721	KTYDDNSSSNTGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKPRIAYPLKK	780
Db	721	RTY----TAAENGNNKSVY-SENAHKSTFTNELRYSAGGAVTWLSPLGPMKFIYAYPLKK	775
Qy	781	KPEDEIQRFOFOLGTTTF	797
Db	776	KPEDEIQRFOFOLGTTTF	792

Search completed: July 6, 2005, 15:42:19
Job time : 227.733 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:57:40 ; Search time 51.7532 seconds
(without alignments)
1481.738 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 4152

Sequence: 1 MKLKQIASALMMLGISPLAF.....LKKKPEDEIQRFQGLGTTTF 797

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4140	99.7	797	2 G81228	outer membrane pro
2	4136	99.6	797	2 D82000	outer membrane pro
3	1279.5	30.8	797	2 H83190	probable outer mem
4	1241	29.9	784	2 H82731	outer membrane ant
5	1212	29.2	803	2 AB0530	outer membrane pro
6	1197	28.8	795	2 AC0129	probable surface a
7	1178.5	28.4	810	2 A64742	hypothetical prote
8	1178.5	28.4	810	2 C90651	hypothetical prote
9	1178.5	28.4	810	2 C85502	hypothetical prote
10	1168	28.1	803	2 B82099	surface antigen VC
11	1136	27.4	797	2 JC4078	protective surface
12	1135	27.3	808	2 F64102	protective surface
13	906	21.8	774	2 D97527	empl protein precu
14	906	21.8	774	2 AE2746	group 1 outer memb
15	877.5	21.1	769	2 F87486	outer membrane pro
16	850.5	20.5	781	2 AH3355	outer membrane pro
17	785	18.9	768	2 D71266	outer membrane pro
18	766	18.4	768	2 B97725	outer membrane pro
19	649	15.6	778	2 C70412	outer membrane pro
20	639.5	15.4	739	2 A81430	outer membrane pro
21	582.5	14.0	617	2 H84957	hypothetical prote
22	533	12.8	916	2 G64601	protective surface
23	526	12.7	906	2 F71910	probable outer mem
24	452.5	10.9	790	2 D86528	omp85 analog (limp
25	452.5	10.9	790	2 D72094	omp85 analog - Chi
26	446	10.7	792	2 H81693	outer membrane pro
27	433	10.4	792	2 B71539	probable omp85 ana
28	393.5	9.5	853	2 A71339	probable outer mem
29	364.5	8.8	821	2 B70199	outer membrane pro

30	348	8.4	846	2 F75525	outer membrane pro
31	307	7.4	833	2 AF2089	hypothetical prote
32	306.5	7.4	579	2 F83327	conserved hypotet
33	299.5	7.2	861	2 S77409	hypothetical prote
34	283.5	6.8	617	2 AF2897	conserved hypotet
35	283.5	6.8	641	2 H97672	hypothetical prote
36	272.5	6.6	853	2 D70304	hypothetical prote
37	254.5	6.1	578	2 B64012	hypothetical prote
38	239	5.8	615	2 A82025	probable outer mem
39	237	5.7	635	2 G81003	conserved hypotet
40	232	5.6	676	2 AE2417	hypothetical prote
41	220	5.3	623	2 A13488	outer membrane pro
42	218	5.3	628	2 B87448	conserved hypotet
43	212.5	5.1	577	2 F86119	hypothetical prote
44	211.5	5.1	577	2 F91278	hypothetical prote
45	211.5	5.1	577	2 S56445	hypothetical 64.8K

ALIGNMENTS

RESULT 1

G81228
outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58 ser C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81228
R;Tetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickley, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: AB1000; MUID:20175755; PMID:10710307
A;Accession: G81228
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <TET>
A;Cross-references: UNIPROT:Q9K1H0; GB:AE002375; GB:AE002098; MID:g725394; PIDN:AAF4063; C;Genetics:
A;Experimental source: serogroup B, strain MC58
A;Gene: NMB0182
C;Superfamily: protective surface antigen D-15

Query Match	99.7%	Score	4140;	DB	2;	Length	797;
Best Local Similarity	99.7%	Pred. No.	1.6e-240;				
Matches	795;	Conservative	0;	Mismatches	2;	Indels	0;
						Gaps	0;
QY	1	1	1	1	1	1	1
Db	1	1	1	1	1	1	1
QY	61	1	1	1	1	1	1
Db	61	1	1	1	1	1	1
QY	121	1	1	1	1	1	1
Db	121	1	1	1	1	1	1
QY	181	1	1	1	1	1	1
Db	181	1	1	1	1	1	1
QY	241	1	1	1	1	1	1
Db	241	1	1	1	1	1	1
QY	301	1	1	1	1	1	1
Db	301	1	1	1	1	1	1
QY	361	1	1	1	1	1	1

```
Db 361 RDEVVRRELQMESAPYDTSKLQSKRERVVLLGYFDNVQFDVPLAGTPDKVDLNMSLTE 420
QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFPTDPYFTA 480
Db 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFPTDPYFTA 480
QY 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTDTGDSFGKWLKYGTVGWRNKTDTSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHYADFIKKYKGTDTGDSFGKWLKYGTVGWRNKTDTSALWPTRGYLTGVNAEIA 600
QY 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIORFQFQGLGTTTF 797
Db 781 KPEDEIORFQFQGLGTTTF 797

RESULT 2
D82000
outer membrane protein OMP85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: D82000
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D82000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <PAR>
A;Cross-references: UNIPROT:Q9JX31; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB8340
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
C;Gene: omp85; NMA0085
C;Superfamily: protective surface antigen D-15

Query Match 99.6%; Score 4136; DB 2; Length 797;
Best Local Similarity 99.6%; Pred. No. 2.8e-240;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLQJASALMVLGISPLAFADFTIQDIRVEGQRTEPSTVENYLPVKVGDYNDTHGSA 60
Db 1 MKLQJASALMVLGISPLAFADFTIQDIRVEGQRTEPSTVENYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNQAVAGLKEEYVLRGKLNQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYVLRGKLNQITPKVTKLARNRVIDITIDEGKSAKITDIE 180

QY 181 FEGNOVYSRDKLRQMSLTGGIWTWLTNRNQNEQKFAQDMKVDTFYQNNGYDFDFRIL 240
Db 181 FEGNOVYSRDKLRQMSLTGGIWTWLTNRNQNEQKFAQDMKVDTFYQNNGYDFDFRIL 240
```

```
QY 241 DTDIQTNEDKTKQTIKIVHEGGRFRWGKVISIEGDTNEVPKAELEKLLTMKPGKWYERQQ 300
Db 241 DTDIQTNEDKTKQTIKIVHEGGRFRWGKVISIEGDTNEVPKAELEKLLTMKPGKWYERQQ 300

QY 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360

QY 361 RDEVVRRELQMESAPYDTSKLQSKRERVVLLGYFDNVQFDVPLAGTPDKVDLNMSLTE 420
Db 361 RDEVVRRELQMESAPYDTSKLQSKRERVVLLGYFDNVQFDVPLAGTPDKVDLNMSLTE 420

QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFPTDPYFTA 480
Db 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFPTDPYFTA 480

QY 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

QY 541 YNKAPKHYADFIKKYKGTDTGDSFGKWLKYGTVGWRNKTDTSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHYADFIKKYKGTDTGDSFGKWLKYGTVGWRNKTDTSALWPTRGYLTGVNAEIA 600

QY 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPPLSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660

QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720

QY 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780

QY 781 KPEDEIORFQFQGLGTTTF 797
Db 781 KPEDEIORFQFQGLGTTTF 797

RESULT 3
H83190
probable outer membrane protein PA3648 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83190
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <STO>
A;Cross-references: UNIPROT:Q9HYV4; GB:AE004784; GB:AE004091; NID:g9949799; PIDN:AAG0703
A;Experimental source: strain PA01
C;Genetics:
C;Gene: PA3648
C;Superfamily: protective surface antigen D-15

Query Match 30.8%; Score 1279.5; DB 2; Length 797;
Best Local Similarity 33.3%; Pred. No. 7e-69;
Matches 273; Conservative 157; Mismatches 338; Indels 51; Gaps 7;

QY 3 LKQIASALMVLGISPLAFADFTIQDIRVEGQRTEPSTVENYLPVKVGDYNDTHGSAII 62
Db 6 LPAALLSALM--IAEVHAESFTVSDIRVNGLQVRVSAQSFAALPLNVGETIDIDQALVQAT 62

QY 63 KSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 122
Db 63 KSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 122
```


Db 63 RSLFKTGFQDIOIGRDCGNVLVTVVERPSSISIEBGNKAISKEDLLKGLKQSLAEGE 122
Qy 123 YFNQATLNOAVAGLKEBYLGRGKLNIOITPKVTKLARNRVDDITIDEGSKAKITDIEFE 182
Db 123 IFORATLGEVGRNELQRYVAGRYSAEVAEVIQPPNRVALKININEGTVAASHINNV 182
Qy 183 GNOVYSRDKLMRQMSLTGEGITWTLTNSQFNEQKPAQDKVKTDFYQNNGYDFPRLDT 242
Db 183 GNVVSEEDITDLPFLKTTWLSFFKNDKXAREKLSGDLRLRSYYLDGRYINMDIAT 242
Qy 243 DIQNEKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMPKGRKYERQOMT 302
Db 243 QVSTTPDKHVIYTVNINEGKVTIRDVKLTGDL-KVPEEVEKRLLLVQKGQVFSRKVMT 301
Qy 303 AVLGEIQNRWMSAGYAYSEISVQPLPNAETKTVDFVLHIEPGRKIYNEHIITGNKTRD 362
Db 302 TTSDLITRRLNGEGYTFANVNGPEAHDDDKTTSVTFVDPGKRAYVNRINFRGNTKTD 361
Qy 363 EVVRELROMESAPYDTSKLORSKERVLLGYFDNVQFADVPLAGTDPKVDLNMSTERS 422
Db 362 EVLRENRQEGGWASTYILDQSKARLERLGYPKEVNVETPAVPGTDDQVDVNVSEEQP 421
Qy 423 TGSLDLSAGVQDPTGLVMSAGVQDNLFQGTGSAALRASRSTKTLNGLSFTDPYFTADG 482
Db 422 SSGITASVGFPAQAGLILGGSISQNNFLGTGNKVSIGLTSREYQTRYNFGFVDPYWTVDG 481
Qy 483 VSLGYDVYKAFPRKASTSIGKYKTTAGATIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542
Db 482 VSLGYNAFYKRTDYDELVDVVASVSNLSGAGMSIGYPISETSRLTGYLSVQRDQDTGR 541
Qy 543 KAPHYADFTKYKGTGDTGSGPKGWLKGTGWRNKTDLSALWPTFGYLTGVNAEIALP 602
Db 542 YTVDIEYDFLDKGG-----DNFTN--FKASIGSESTLNKGLVATRGHQSGLTLETLTP 593
Qy 603 GSKLQYYSATHNQWTFPPLSKTFTMLGGBGVAGYGRKTEIPFFNFYGGGLGVSRGY 662
Db 594 GSDLSFYKIDYRGVQFAPLTDNTMRPHTELGYDGDYGVSTERLPFFENYTAGFNSVRGF 653
Qy 663 ESGTLGP-----KVDYEYGEKISYGGNKKANVSAAELLPMP 698
Db 654 KDSTLGRSPSPVARNPDPGTPMKNQGPDSKGRVTDPDQDPEAFGNGNILLITGGAELLPPL 713
Qy 699 GAKDARTVRLSLFADAGSVNDGTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSG 758
Db 714 FVKDQRLVTLFWDVGS-----TFDTPCTKTTCNDGIX-----TDNLASSVG 758
Qy 759 GAVTWLSPGLGPMKFRVAYPLKKKPEDBIQRFQFOLGTF 797
Db 759 VGLTWITALGFLSFLATPIKKPDNAETQVQFSLGQTF 797
RESULT 4
E82731
outer membrane antigen XF1046 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82731
R;anonymus, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-784 <STM>
A;Cross-references: UNIPROT:Q9PEI2; GB:A8003941; GB:A8003849; NID:g91059978; PIDN:AAF8385
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrato, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Paciniani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1046
C;Superfamily: protective surface antigen D-15
Query Match 29.9%; Score 1241; DB 2; Length 784;
Best Local Similarity 33.7%; Pred. No. 1.4e-66; Indels 52; Gaps 10;
Matches 272; Conservative 163; Mismatches 319;
Qy 8 SALMLGIGSLAPADFTIODIRVEGLQRTPEPSVFVNYLPVKVGDYVNDTHGSAIIKSLYA 67
Db 15 AANFSLPVLTOAESFVANDIRVDGLQRTASGTVFYLPVNRGDTVDKADAIARLYR 74
Qy 68 TGFDDVRVETADGQLLLTVIERPTTGLSNIITGAKMLONDAIKNLESFGLAQSOYFNOA 127
Db 75 TGFENVIRDRQGNILVWVKERPAINKLTITGNKDIKSEELLKGLSEIGLSEGGTFDRL 134
Qy 128 TLNQAVAGLKEEYLRGKLNIOITPKVTKLARNRVDDITIDEGSKAKITDIEFEGNQVY 187
Db 135 SLDRVTEQLKQYNNRGYVQMTTTPLDNRVDTVTAKEGKAIRHINLIGTEKF 194
Qy 188 SDRKLQMSLTGGITWTLTNSQFNEQKPAQDKVKTDFYQNNGYDFPRLDTDTQTN 247
Db 195 NNDVMSANESKEHNWASVWRDDQYSKEKLSGDEKLNSWYLDGRVDFNIDSTQVSIS 254
Qy 248 EDKTKITIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMPKGRKYERQOMTAVLGE 307
Db 255 PEKHNFIAGVTEGQYKISSIKVTGNT-VLPQEKIEKLVIPKTDIPSKVLEYSAA 313
Qy 308 IQNRMSAGYAYSEISVQPLPNAETKTVDFVLHIEPGRKIYNEHIITGNKTRDEVVRR 367
Db 314 IINTLSNIGYAFSKVNPITANRADRTVAVNLHVPGRVTVRQILFKGNTRTSDVLR 373
Qy 368 ELRQMSAPYDTSKLORSKERVLLGYFDNVQFADVPLAGTDPKVDLNMSTLSTSGSLD 427
Db 374 EMQFNSWYQAIQDRSKIRLQRLGYFEADVSTPVGSDNQVDLVYTVKETTSGSFQ 433
Qy 428 LSAGWYQDPTGLVMSAGVQDNLFQGTGSAALRASRSTKTLNGLSFTDPYFTADGVSGLY 487
Db 434 VGLGSKTYGVTTSVQLSQNNFLGSGNRVSDASRSRYQDRYSFSYTNPFDTNGVSLGY 493
Qy 488 DVYKAFDPRKASTSIGKYKTTAGATIRMSVPVTEYDRVNFGLVAEHLTVNTY-NKAPK 546
Db 494 NLAYQKLD--YSDFNAAYNSKEMSGQITFGIPITENDTVSWVIGADSDNQITTFPGSTPK 551
Qy 547 HYADFTKYKGTGDTGSGPKGWLKGTGWRNKTDLSALWPTFGYLTGVNAEIALPCKSL 606
Db 552 AIIDYIDAVGQR-----TFRAW--RTELGWARTDRNDYFNPNGMYQRIQAEVTLPGSTI 604
Qy 607 QYYSATHNQWTFPPLSKTFTMLGGBGVAGYGRTE-----KEIPFFNFYFG 653
Db 605 KYKYNQISKYWPIIPALVNLTRLEVGYDGYKXSHTRILPDGTVATASGLPFFENFYA 664
Qy 654 GGLGVSRYGESGTLGPK--VYDEYGEKISYGGNKKANVSAAELFPMPGAKARTVRLSLF 711
Db 665 GGTVSVGRFRDNLGPRSEVLTALYNQOQPLGSGFKTVGSTEMYFPK--LPDPSARISAF 722
Qy 712 ADAGSVWDGKTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMK 771
Db 723 LDFGNVFNQY-----NNFKA---NELRASSGALLWRAPIGPIS 758
Qy 772 FRVAYPLKKKPEDEIQRFQFOLGTF 797
Db 759 ISYAFPIKKENDEIRLQTFFGQF 784

RESULT 5

AB0530

outer membrane protein precursor yaet [imported] - Salmonella enterica subsp. enterica serovar Typhimurium

C:Species: Salmonella enterica subsp. enterica serovar Typhi

C>Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C:Accession: AB0530

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AB0530

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-803 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD08682.1; PID:g16501505; GSPDB:GN00176

C:Genetics:

A:Gene: Yaet

C:Superfamily: protective surface antigen D-15

Query Match 29.2%; Score 1212; DB 2; Length 803;

Best Local Similarity 33.6%; Pred. No. 8e-65;

Matches 277; Conservative 154; Mismatches 345; Indels 48; Gaps 13;

Qy 1 M L K L Q I A S A L M M L G I S P L A F A D - F T I Q D I R V E G L Q R T E P S T V F N Y L P V K V G D T V N D T H G S 59

Db 1 M A M E K L L I A S L F S S A I V Y G A E G F V V K D I I F E G L O R V A V G A A L L S M P R T G D T V N D E D I S 60

Qy 60 A I I K S L V A T G F F D D R V R E T A D G O L L L T V I E R P T I G S L N I T G A K M L Q N D A I K K N L S F G L A 119

Db 61 N T I R A L P A T G N F E D R V L R D G T I L L V Q V K R P T I A S I T F S G N K S V K D M L K Q L N E A S G V R 120

Qy 120 Q S O Y F N Q A T L N Q A V A G L K E E V L G R G K L N I O I T P K V T K L A E R N V D I D I T I D E G S A K I T D I 179

Db 121 V G E S L D R T L L S D I E K G L E D F Y Y S G K Y S A S V A V T P L P R N R V D L K L V F O G E G S A K I Q I 180

Qy 180 E F E G N O V Y S D R K L M Q R M S L T E G G I T W L T R S N O F N E Q K F A Q D M E K V T D F Y Q N N G Y D F D R I 239

Db 181 N I V G N H A F S T E E L I S H F Q L R D E V P W N V G D R K Y Q K Q L A G D L E T L R S Y L D R G Y A R N I 240

Qy 240 L D T D I Q N E D K T Q T I K I T V H E G R F R W G K V S I E G D T N E V P K A E L K L T M K P G K W Y E R Q 299

Db 241 D S T Q V S I T P D K G I I T V N I T G E D Q Y K L S G V Q S G N L - A G H S A E I E K L T I E P G E L Y N G T 299

Qy 300 Q M T A V L G E I Q N R M G S A G Y A S E L S V Q P L P N A E T K T V D F V L H I B P G R K I Y V N E I H I T G N K 359

Db 300 K V T Q W E D D I I K K L G R Y G T A P R V Q S Q E I N D A D K T V K L R V N V D A G N R F Y R K I R F E G N D T 359

Qy 360 T R D E V V R R E L R Q M E S A P Y D T S K L O R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K Y D L N M S L T 419

Db 360 S K D S V L R R E M R Q E G A M G S D L V D Q G K E R L N R L G F F E T V D T D T Q R V P G S P D Q V D V V Y K V 419

Qy 420 E R S T G S L D L S A G W Q D T G L V M S A G V S O D N I F G T G K S A A L R A S R K T T L N G S L F T D P Y F T 479

Db 420 E R N T G S F N F I G Y G T E S G V S F Q A G V Q O D N M L G T G Y S V G I N G T K N D Y Q T Y S E L S V T N P Y F T 479

Qy 480 A D G V S L G D V V Y K A F D P R K A S T S I K O Y K T T T A G A G I R M S V P T V E Y D R V N F G L V A E H L T V N 539

Db 480 V D G V S L G R I F Y N D F E A D D A D L S - - D Y T N K S Y G T D V T L G F P I N E Y N T L R A G L G Y V N K U S 537

Qy 540 T Y N K A P K H Y A D - F I K K Y G K T D T G D S F K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E 598

Db 538 - - N M Q P I A M D R V L E S M G D P A S D F A A D F T F - - N Y G W T Y N K L D R G Y F P T D G S R V N L T G K 593

Qy 599 I A L P G S K L O Y S A T H Q T W F P P L S K T F T L M L G G E V - - G I A G G Y G R T K E I P F P F N F Y G G L 656

Db 594 V T I P G S N E Y Y K V S L D T A T V P I D N D H K W V L G R T R W Y G D G L G - G K E M P F Y E N F Y A G S 652

Qy 657 G S V R G Y E S G T L G P K V Y D E Y G E K I S Y - - - - - G G N K K A N V S A E L L F 695

[illegible]

Qy 536 LTVNTYNKAPKHADFTKKYKGTGDTGSGPKGMILYKGTGVGWRNKNTDSALWPRGYLTGV 595
Db 536 LSDMLPQVMWRVLYESGERPGYDREG-FTTDDFTLNLGWTTNNLDGRGFPTSGVKSSV 594
Qy 596 NAEIALPGSKLOYYSAATHNOTWPPLS--KTFTLMLGGEVGCIAGGYGRTKEIPFENFYG 653
Db 595 NTKLITPGSDNEFFKYVTFDISAQLPNEDRSWLLGRGLRGYGDGIG-SKEMPFYENFYA 653
Qy 654 GGLGSVRGYSBGTGLPKPV--YDEYGEKI-----SYGNKKKANVSAAELLPMP--GAKDAR 704
Db 654 GGSSTVRGPRSNNGIPKAAYANGATVTNSTDAVGGNAMAVASIELIITTPPISEKYSN 713
Qy 705 TVRLSLPADAGSVWDGTYTDNDSSSATG----GRVQNIYAGNTHKSTFTNEIRYSAGGA 760
Db 714 SVRTSIFIDSGTVDWTWENTAKTRAAGIDPYGKASNI-----RVSAAGA 758
Qy 761 VTWLSPGLGPWKERYAVPLKKKPDEIKORFOQLGTTF 797
Db 759 LQMNSPLGPLVFSTAPEVKOYEGDKSQOFNIGKTW 795

RESULT 7
A64742
hypothetical protein b0177 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: A64742
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CO
A.: Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; UID:97426617; PMID:9278503
A;Accession: A64742
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-810 <BLAST>
A;Cross-references: UNIPROT:P39170; GB:A5000127; GB:U000096; NID:g1786370; PIDN:AAC73288.
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: protective surface antigen D-15

Query Match 28.4%; Score 1178.5; DB 2; Length 810;
Best Local Similarity 32.8%; Pred. No. 8.3e-63;
Matches 273; Conservative 154; Mismatches 348; Indels 57; Gaps 15;

Qy 1 MKLKQIASALMGLGISPLAFAD-FTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYNDTHGS 59
Db 1 MAMKULLIASLLPSSATVYGAGFVVKDIIIEGLQRYAVAGVAALLSPVRTGDTVDEDIS 60
Qy 60 AIKLSLYATGFFDDRVRVETADGOLLTVIERPTIGSLNITGAKMKLONDAIKKNLESFGLA 119
Db 61 NTIRALPATGNFEDVRVLRDGDTLLVQVKERTPTIASITFGSNKSVKDDMLKQNLEASGVR 120
Qy 120 QSQYFNQATLNQAVAGLKEYLGRGKLNIQTTPKVTKLARNVDIDITIDEHKSAKITDI 179
Db 121 VGESLDRHTTIADIEKGLEDFPYVSGKYSASVKAIVTLPENRVDLKLVPQEGVSABEQI 180
Qy 180 EFEQNOVYSRDKLRQMSLTGEGGIWTLTRSNQNEOKFAQDMKEKVTFDFQNNNGYFDRI 239
Db 181 NIYGNHAFTDELISHPOLREDEVPMNVGDYKQKLAGDLETLSYLDRGYARFNI 240
Qy 240 LTDIDIQTNEDKTKQITIKITHVEGGRFRWGKVSIEGDTNEVPKAELEKLLTMFKPKWYERQ 299
Db 241 DSTQVSLTPDKKGIYVTVNITEGDQYKLSGVEVSGNL-AGHSAEIEQLTKIEPGELYNGT 299
Qy 300 QMTAVLGEIQNRMGSAAYASETSVQPLPAEYKTVDFVLHIIEGRKIYVNEHIITGNKK 359
Db 300 KVTQMEDDIKILLGRYGYAVPRVQSMEINADAKTVKLRVNVDAGNRFYRKIRFEGNDT 359
Qy 360 TRDBVRRRELROMESAIFYDYSKQRSKERVELLYGFQNFQVDAVPLAGTDPDKVDLNMSLT 419
Db 360 SKDAVLRERNQMEAGWLGSDLVDQGERLNRLGFFETVDTDQRPVPSQPQDVVYKVK 419
Qy 420 ERSTGSLDLASAGWWQDTGLVMSAGVSODNIEFGTGKSAALRASRSKTTINGSLGFTDOPYFT 479

```

Db      420 ERNTGTFNFGIGYGTSGVSFQAGVQQDNWMLGTGYAVGNGTKNDQTYAELSVTPNPYFT 479
Qy      480 ADGVSIGVDVYGKAF--DPRKASTSIQYKTTTACAGIRMSVPVTEYDRVNPGLVAEHLT 537
Db      480 VDGVSIG----GRLFYNDQFQADDADLSDYTNKSIVGTDTVLGFPINEYNSLRAGLGVVHNS 535
Qy      538 VNTYNKAPK----HYADPIKKYKTDGDFGSPKGLWLYKGTGVGWRNKDTSALWPTRGYLT 593
Db      536 LS--NMQPOQVAMWRYLYSMGHPSTSDQDNSFKTDDFTFNYGWTYNKLDRGYFPTDGSRV 593
Qy      594 GVNAEIALPGSKLOYYSATHNQWTFPLPSKTFITLMLGGEV--GIAGGVGRTKEIPFFENF 651
Db      594 NLTKGVTPGSDNBYKVTLDATYVPIDDHKWVVLGRTRWGYGDGLG--GKEMPFFYENF 652
Qy      652 YGGGLGVRGYESGTGPK-VY-----DEYGEKISY-----CGNKKA 687
Db      653 YAGSSTVRGFSQNTIGPKAVYFPHQASNYDPDYECATQDGAKDLCKSDDDAVGNGNA 712
Qy      688 NVSAELLFPMGAKD--ARTVRLSLFADAGSVWGDKTYDDNSSSATGGRVQNIYAGNTH 745
Db      713 VASLEFITPTPFISKVANSVRTFFWDMGTWVD--TNWDSQYS-----GYPD 759
Qy      746 KSTFTNELRYSAGGAVTWLSPGLGPMKFRYAYPLKKKPEDEIQRPQFQLTGTF 797
Db      760 YSDPSN--IRMSAGIALQWMSPLGVLVSYAOPFKYDGDKAEOQFQNGIKTW 810

RESULT 8
C90651
hypoetical protein ECs0179 [imported] - Escherichia coli (strain O157:H7, substrain RIN
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: C90651
R:Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90651
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-810 <HAY>
A:Cross-references: UNIPROT:P39170; GB:BA000007; PIDN:BA333602.1; PID:g13359635; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIND 0509952
C:Genetics:
A:Gene: ECs0179
C:Superfamily: protective surface antigen D-15

Query Match      28.4%; Score 1178.5; DB 2; Length 810;
Best Local Similarity 32.8%; Pred. No. 8.3e-63;
Matches 273; Conservative 154; Mismatches 348; Indels 57; Gaps 15;

Qy      1  MKLQIASALMLGISPLAFAD-FTIODIRVEGLQRTPEPSTVFNYLPVKVGQYNDTHGS 59
Db      1  MAMKLLIASLFPSSATVYGAGFVVKDIHPEGIQRVAVGAALLSMVPTGDTVNDSDIS 60
Qy      60  AITKSLVATGFDDRVRETADGQLLLTVIERPTTGSLNITGAKMLQNDAIKKNLSFGLA 119
Db      61  NTRALPATGNFEDRVRLRDGDTLLVQVKERTIASITFSGNKS VKDMLKQNLASGVR 120
Qy      120  QSQYFNQATLNQAVAGLKEEVLGRKLNQIQITPKVTKLARNRVDIDITIDECKSAKITDI 179
Db      121  VGBSLDRTTIADIEKGLDFYYSVGKYSASVAVVTPLPNRVLDLKI VFOEGVSABEQI 180
Qy      180  EFEGNQVYSDRKLQRMQSLTEGGIWTWLTTRSNQFNQEQFAQDMKVDTDFYQNNGYDFDRI 239
Db      181  NIVGNHAFTTDELISHFQLRDEVPMNVGVGRKYQKQKLAGDLETLSYLDRGYARFNI 240
Qy      240  LDDTIQNEKDKTQTIKIVTVEGGRFRWGVKSVIEGDTNEVPKAELEKLLTMKPGKWYERQ 299
Db      241  DSTQVSLTPPKKGYVTVNTIEGQYKLSGVVEVSGNL--AGHSABEQITKIPGSLYNGT 299

```

```
QY 300 QMTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKK 359
Db 300 KVTXMEDDIKLLGRYGYAYPRVQSMPEINDADKTVKLRVNVNDAGRFYVRKIRFEGNDT 359
QY 360 TRDEVVRELRQMESAPYDTSKLQSRKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLT 419
Db 360 SKDAVLRREMRQMEGAWLGSDLVDQGERLNRLGFFETVDTQTVQVPSDPQDVVYKVK 419
QY 420 ERSTGSLDLGAGVQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGSLSTFTDPYFT 479
Db 420 ERNTGSFNGIGYGTESGVFQAGVQDQNLWLTGTYAVGINGTKNDYQTYAELSVTNPYFT 479
QY 480 ADGVSGLGYDVYKAF--DPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLT 537
Db 480 VDGVSGLG---GRLFYNDQFQADDADLSYTNKSYGTDVTLGFPINEYNSLRAGLGYVHNS 535
QY 538 VNTYNKAPK---HYADFIKKYKTKDGTGSGFKGWLKGTGVGGRNKTDSALMPTRGYLT 593
Db 536 LS--NMQPQVAMRWYLSYMGHEPSTSDQNSFKTDDFTFNYGWTYNKLDRGYFPTDGSRV 593
QY 594 GVNAEIALPGSKLOYYSATHNQWFFPLSKTFTMLMGGEV--GIAGGYGRTEKIEPFENF 651
Db 594 NLATKVITPGSDNEYKVTLDATYVPIDDHKVWVLGRTFWGVDGLG--GKEMPFYENF 652
QY 652 YGGGLGSRVGYESTGLGPK-VY-----DEYGEKISY-----GKNKKA 687
Db 653 YAGGSSTVRGFSQNTIGPKAVYVPHOASNYDPDYDECATQDQAKOLCKSDDDAVGNGNAMA 712
QY 688 NVSAELLFPMGAKD--ARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGAGNTH 745
Db 713 VASLEFITTPTFISDKYANSVRTSFFMDMGTVMD--TNWSSSQYS-----GYPD 759
QY 746 KSTFTNELRYSGAGVATWLSPLGPKMFRYAYPLKKPDEIQRFPQFOLGTTFF 797
Db 760 YSDPSN-IRMSAGIALQWMSPLGLVFSYAQPFKKYDGDKAQEQFQFNIGKTW 810

RESULT 9
C85502
hypothetical protein yaeT [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85502
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-810 <STO>
A;Cross-references: UNIPROT:P39170; GB:AE005174; NID:g12512902; PIDN:AAG54479.1; GSPDB:C
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yaeT
C;Superfamily: protective surface antigen D-15

Query Match 28.4%; Score 1178.5; DB 2; Length 810;
Best Local Similarity 32.8%; Pred. No. 8.3e-63;
Matches 273; Conservative 154; Mismatches 348; Indels 57; Gaps 15;

QY 1 MLKKQTASALMLMGLISPLAFAD-FTIQDIRVEGLQRTEPSTVFNYLPVKVGDYNTDTHGS 59
Db 1 MANKULLIASLLPSSATVYGAEGFVVKDTHFEGLRQVAVGAALLSHPVRTGDTVNDSDIS 60
QY 60 AI1KSLYATGFFDDVRVETADGOLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLA 119
Db 61 NTIRALFATGNFEDVRVLRGDTLLVQVKERPTIASITFSGNKSXKVDMLKQNLASGVR 120
QY 120 QSQYFNQATLNQAVAGLKEEYLRGKLNIOITPKVTKLANRVVDIDITIDEGSAKITDI 179
Db 121 VGSLSORTTIADIEKGLDFYYSVGKYSASVKAIVTPLPRNRVDLKLVFQEGVSABIQI 180
```

```
QY 180 EPEGNQVSDRKLRMQMSLTBGGIWTWLTSRNQFNBQKFAQDMKEKVTDFYQNNGYDFRI 239
Db 181 NIVGNHAFITDELISHFQLRDEVPWNVVVDKRYQKQKLAGDLETLSRYVLDGRYARFNI 240
QY 240 LQDTQITNEDKTKQTIKITVHEGGRFRWGVKSIEGDTNEVPKAELEKLLTMKPGKKYERQ 299
Db 241 DSTQVSLTTPDKKGIYVTVNITEGDQYKLSGVEVSGNL-AGHSAEIRBQTKIEFELYNGT 299
QY 300 QMTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKK 359
Db 300 KVTXMEDDIKLLGRYGYAYPRVQSMPEINDADKTVKLRVNVNDAGRFYVRKIRFEGNDT 359
QY 360 TRDEVVRELRQMESAPYDTSKLQSRKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLT 419
Db 360 SKDAVLRREMRQMEGAWLGSDLVDQGERLNRLGFFETVDTQTVQVPSDPQDVVYKVK 419
QY 420 ERSTGSLDLGAGVQDTGLVMSAGVSQDNLFGTGKSAALRASRKTTLNGSLSTFTDPYFT 479
Db 420 ERNTGSFNGIGYGTESGVFQAGVQDQNLWLTGTYAVGINGTKNDYQTYAELSVTNPYFT 479
QY 480 ADGVSGLGYDVYKAF--DPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLT 537
Db 480 VDGVSGLG---GRLFYNDQFQADDADLSYTNKSYGTDVTLGFPINEYNSLRAGLGYVHNS 535
QY 538 VNTYNKAPK---HYADFIKKYKTKDGTGSGFKGWLKGTGVGGRNKTDSALMPTRGYLT 593
Db 536 LS--NMQPQVAMRWYLSYMGHEPSTSDQNSFKTDDFTFNYGWTYNKLDRGYFPTDGSRV 593
QY 594 GVNAEIALPGSKLOYYSATHNQWFFPLSKTFTMLMGGEV--GIAGGYGRTEKIEPFENF 651
Db 594 NLATKVITPGSDNEYKVTLDATYVPIDDHKVWVLGRTFWGVDGLG--GKEMPFYENF 652
QY 652 YGGGLGSRVGYESTGLGPK-VY-----DEYGEKISY-----GKNKKA 687
Db 653 YAGGSSTVRGFSQNTIGPKAVYVPHOASNYDPDYDECATQDQAKOLCKSDDDAVGNGNAMA 712
QY 688 NVSAELLFPMGAKD--ARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGAGNTH 745
Db 713 VASLEFITTPTFISDKYANSVRTSFFMDMGTVMD--TNWSSSQYS-----GYPD 759
QY 746 KSTFTNELRYSGAGVATWLSPLGPKMFRYAYPLKKPDEIQRFPQFOLGTTFF 797
Db 760 YSDPSN-IRMSAGIALQWMSPLGLVFSYAQPFKKYDGDKAQEQFQFNIGKTW 810

RESULT 10
B82099
surface antigen VC2252 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82099
R;Heidelberg, J.P.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathavan, J.; Babs, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-803 <HEI>
A;Cross-references: UNIPROT:Q9KPW0; GB:AE004297; GB:AE003852; NID:g9656810; PIDN:AAF95396
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2252
C;Superfamily: protective surface antigen D-15

Query Match 28.1%; Score 1168; DB 2; Length 803;
Best Local Similarity 32.4%; Pred. No. 3.5e-62;
Matches 285; Conservative 166; Mismatches 352; Indels 34; Gaps 13;
```

QY 1 MKLQKQIASA-LMWLGISPIAFADFTIQDIRVEGLQRTPEFTVFNVLPVKVGDTNDTHGS 59
 Db 1 MAMQKQILLATLATSVSANGAEKFFVODIQIDGLQVALGAALKMPVRVGDSDVSDQDA 60
 QY 60 AIIKSXYATGTFDDVRVETADQQLLTVERPTTGLSNIITCAKMLONDAIKKNLESFCLA 119
 Db 61 NIIRKALYSSGNFEDKVLNDGNTLWVQKERTPTASVSFGNKAKEQOLKQNLSEASIR 120
 QY 120 OSQVFNQATLNOAVAGLKEEYLRGKQLNIQTTPKTKLARNRVIDITIDEGKSAKITDI 179
 Db 121 VGEALDRITLNSIEKGLDFYISGVKYNATKAVVUTPLPRNRADLKFFVTEGVSAKIQOI 180
 QY 180 EFEGNOVYSDRKLAKRQMSLTGGGIWTWLTGRNQFNEQKFAODMEKVTDIFYONNYSFDPRI 239
 Db 181 NFIQNOVFSDELLSRFNLDVAVWNLADDKYKKQVLADGIEALRTYILDRGLYLFQV 240
 QY 240 LDTDIQTNEDTKOTIKITIVHEGGRFRWKVYSIEGDTNEVPKAELEKLLTMKPKQWYERQ 299
 Db 241 DSTQVAISPPKGGVYITLINNEGEPTVTSVKQFRGELMG-KEAEFTSLIPEIGETNGS 299
 QY 300 QMTAVLGEIQNRMSGAGVAYSEISVQPLPNAETKTVDVLHIEPRKLYVNEIHTGNK 359
 Db 300 AVTLRESVKVKGESGAYPQVARTIEFDDEKQCVSLVHVEAGKVVYRDIRFVGNS 359
 QY 360 TRDEVVRRELQMSAPYDTSKLORSKERVLELLGYFQNVQFVDAVPLAGTDPKVDLNMSLT 419
 Db 360 TRDEVLRREMEQMSWLNSKDIETGKTRLNRLGFFETVEVQTVRVPGSEDOVDLVYSK 419
 QY 420 ERSTGSLDSAGVQDVTGLVMSAGVSDQNLFGTKSAALRASRKTTLNGSLSTDPYFT 479
 Db 420 EANSNGVNFVGYGYESGVSPQVGLQDNFLGSGNRVGVNAMIINDYOKNLTLEVRDPYN 479
 QY 480 ADGVSLGVDVYKAFDPKPKASTSIKQYKTTAGAGIRMSVPVTEYDVRNFGVLAHLTVN 539
 Db 480 LDGYSLGKGFYNOFEASEA--GIVDTNYESYGHSLTWGPPFDLNFPEFGIYTHNKIG 537
 QY 540 TYNKAP-KHYADFIKKYKTDGTGDSFGKMLYKGTGVGMRNKTDLSALPTRGYLTGVNAE 598
 Db 538 --NLTPYLQVENFLAAQASNIDSGNLLTDDFDNLGSRNLLNSYFPTAGNHORAPYK 595
 QY 599 IALPGSKLOYYSATHNQTWEPPLSK--TFTLMLGGEVGIAGGYCRT---KEITPFENFY 652
 Db 596 MTPVGSQAQYFKLOYDVRQYFPLTKHEFTLLLRGLRYGNGYQGTGDKONLFPFYENFY 655
 QY 653 GGGGLSVRGYESGTLGPK-VYDEY-----GEKISYGKNKANYSAELLFMP-GAK 701
 Db 656 AGGFTSLRGFGNSAGFKAVYRYSNGNSGDTATDSDVSGNAIALASVELIYPTPASE 715
 QY 702 DART-VRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSAGGA 760
 Db 716 EARNQIRTSIFYDMASVWDTE-FDYRKADYGNQYYDYSDPTNYRSSY-----GVA 766
 QY 761 VTWLSPLGPKMKFRYAYPLKKPEDEIQRFQGLGTF 797
 Db 767 LOWVSPMGPLVFLSLAKPIKKYEGDDEFFFTIGRTF 803

RESULT 11
 JC4078
 C:Species: Haemophilus influenzae
 A:Variety: type b
 C:Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
 C:Accession: JC4078
 R:Flack, F.S.; Loosmore, S.; Chong, P.; Thomas, W.R.
 Gene 156, 97-99, 1995

Gene 100, 97-99, 1993
A:Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influenzae
A:Reference number: JC4078; MUID:95255676; PMID:7737523
A:Accession: JC4078
A:Molecule type: DNA
A:Residues: 1-797 <FLA>
A:Cross-references: UNIPROT:P46024; GB:U13961; NID:G537447; PIDN:AAA85645.1; PID:G5374448
A:Experimental source: type b

C:Superfamily: protective surface antigen D-15
 C:Keywords: surface antigen
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-797/Product: protective surface antigen D-15 #status predicted <MAT>

	Query Match	27.4%	Score 1136;	DB 2;	Length 797;															
	Best Local Similarity	31.6%	Pred. No. 2.9e-60;																	
	Matches 263;	Conservative 166;	Mismatches 332;	Indels 70;	Gaps 19;															
Qy	3	LKQFASALMLG	ISPLAF-A	DFTIQDIRVGLQ	TEPSTVFNVL	PKVKVGDYNDTHGSAI	61													
Db	1	MKKLLIASL	LFGGTTT	FAAFVAKD	IRVDGVQGDLE	EQIRASL	FPVAGQRTVDNDVANI	60												
Qy	62	IKSLYATG	FFDDVRVET	ADGQLLIT	VIERTPTIG	SLNITGAK	MLQNDAIKKNLSEFGLAQS	121												
Db	61	VRSLFVS	GRPDDVKA	HQEGDVL	VSVVAKSII	SDVKIKG	NSVIPTEALKQNL	DANGFKVKG	120											
Qy	122	QYFNQAT	LNAQVAGL	KEBYLGR	KLNIQIT	TPKVT	KLARNVDI	ITIDEGKSAKITDIEF	181											
Db	121	DVLIRE	KLNEFAK	SVKESV	GRYNATVE	PIVNTLP	NNRAEILI	QINEDDKAKLASLTF	180											
Qy	182	EGNQVSD	RKLMEQ	MSLITE	GIIW-TW	ITRSQ	FNQNEK	FPADMEK	VTDFYQNGYFDFRIL	240										
Db	181	KGNESV	SSSTLQ	EQMELQ	PDSSWKLW	--GNK	FEQAQF	EKDLQ	SIRDYILNNGYAKAQIT	237										
Qy	241	DTDIQ	TWEDKT	KOTIKIT	TVHGEGR	FRWKV	IS	EGDTN	VEPKAELEKLLT-MKPGK	WYERQ	299									
Db	238	KTDVQL	NDEKTK	KNVTI	DVNEG	LQYD	LRSARI	IGNLGM-SAE	LEPPLLSAHLNDT	FPFRS	296									
Qy	300	QMTAVL	GEIQNR	MGSGA	YAYSEIS	VOPL	NAETKT	VDVLHI	BPGRKI	YVNEIHITGNKK	359									
Db	297	DIADVEN	AIKAKL	GERGY	GSATV	NSVP	DDPDD	ANKLT	AILTV	VDAGR	ELTVRQLR	FEQNTV	356							
Qy	360	TRDEV	VRRELR	OMESAP	YDTSK	LQSK	ERV	VELLYG	FDNVQ	FADVPL	AGTDPK	VDLNNSLT	419							
Db	357	SADSTL	FAQENR	QOEGT	WYNSQ	LVGL	KIRL	DRTC	FFET	VENR	IDPINGS	DEVDVYVVKV	416							
Qy	420	ERSTG	SILDSAG	VQDTGL	VMSAG	VDNLF	GTGK	SAALRS	SKTTLN	GLSFTD	PDYFT	479								
Db	417	ERNTS	INF	GIGYGT	SEGISY	QASV	QDNFL	GTGAA	VSTAGT	KNDYGT	SVNLG	YTEPTEYF	476							
Qy	480	ADGVSL	GDYVYG	KAFPP	RKASTSI	KYKVT	TAGAG	IRMSVP	VTEDY	RNVF	GLVAEHL	TVN	539							
Db	477	KDGVSL	GNGV	FFENY	DNSK	SDTS-SNY	KRTY	SGNS	VTLGF	PNENNS	YYVGL-----GH	529								
Qy	540	TYNKAP	KPH-----	YADP	IKKYG---	KTDG	TGSG	FKGWL	YKGT	VGWGR	NKTD	SALWPT	588							
Db	530	TYNKIS	NFALE	YRN	LYIQSM	KPKG	NGIK	TNDF	DFSF-----	GWNYS	LN	RGVFPY	580							
Qy	589	RGYLT	GVNAE	IALPG	SKLQ	YYSATH	QNTW	FPPL	SKTFTL	MLGGE--	VGIAGG	YGR	KEIP	646						
Db	581	KGKAS	LGG	RVTT	TPGSD	NKYKL	SADV	QGFY	PLDR	DHLMV	VS	SAKASAG	YANGFG-NKRLP	639						
Qy	647	FFENFY	GGGLGS	VRGYES	GTLPK	-V	VEYGV	-----	EKIS--	--YGG	NKAN	VSAELL	694							
Db	640	FYQTY	TAG	IGSUR	GFAYG	ISG	IGNAI	YAE	VNGSG	TGTF	KKIS	SDVIG	GNAT	TA	GAELI	699				
Qy	695	FPMP--	-GAKD	ARTV	RLSL	FADAG	SVWD	GKTY	DDN	SSS	TGGR	VQNT-----	YCAG	NTHK	746					
Db	700	VPTP	FFVSD	KSQNT	VRTSL	FL	VD	AA	SVN	TKW	SKDN----	GLESD	VL	KRL	PDY	GK-----	749			
Qy	747	STTNE	LR	YSAG	AVTW	LSP	LG	MPK	FRY	APL	KKK	PEDEI	QR	FQ	Q	L	TTF	797		
Db	750	---SS	R	AST	GVGF	QWQ	SP	IG	PLV	FSY	AKPI	IKKY	END	D	VEQ	F	Q	SIG	FSF	997

RESULT 12
F64102
protective surface antigen D-15 - Haemophilus influenzae (strain Rd KW20)
C_Species: Haemophilus influenzae
C_Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998
C_Accession: F64102
R_Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirtress, P.E.

Db 646 NLLVDFQKFGG-RQVRGFKNDGIGPRIGSD-----SIGGTTTFAASAEVTAAMPQGVPE 699
QY 704 RTVRLSLFADAGSVDGKTVDNNSSSATGGRVQNIYAGNTHKSTFTNLRYSAGGAVTW 763
Db 700 FGLRLAGFVDAWTGMYGNKV-----STGTVKD-----DNSIRASAGIGVMM 740
QY 764 LSPGLPMKFRYAYPLKKKPEDEIQRFQOLGTTTF 797
Db 741 ASPFGPIRVDAIPIAKEDYDEQRFQMSNTF 774

RESULT 14
AE2746
group 1 outer membrane protein precursor omp1 [imported] - Agrobacterium tumefaciens (sb
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2746
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2746
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-774 <KUR>
A;Cross-references: UNIPROT:OBUFL6; GB:AE008688; PIDN:AAL42387.1; PID:g17739796; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: omp1
A;Map position: circular chromosome
C;Superfamily: protective surface antigen D-15

Query Match 21.8%; Score 906; DB 2; Length 774;
Best Local Similarity 28.5%; Pred. No. 1.7e-46;
Matches 232; Conservative 161; Mismatches 341; Indels 80; Gaps 18;

QY 7 ASALMMLGISPLAFADF-----TIQDIRVEGLQRTPESTVFNYLPVKVGTVDYNDTHGSAII 62
Db 18 AGVSSVAGLVLASAGVANAASVSKIDVRCAESGADSVRSNITIAPKNFNSDIDESV 77

QY 63 KSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDIAKKNLESFGLAQSQ 122
Db 78 KRLYATGYFSGVSMRVSGSLTAVTNENQLVQWFGNKRKIDDKLA-----GIVQIQ 131

QY 123 ---YFNOATLNOAVAGLKEEYLRGKLNITQITPKVTKLARNRVDIDITIDEGSAKITDI 179
Db 132 PMGPFNOAIVTADIAIRIKEAYSAGRSDBEITTTQTVSVOGGRVNIAPVINEGERTKIGRI 191

QY 180 EPEGNOVYSDRKLMRQMSLTGEGITWLTTRSNQFNQKPAQDMKEKVTDFYQNNGYDFDRI 239
Db 192 DFIGNNSYSDCLRAAVNTKSNMLFRLTKOVYNEKLRADAEALRQFYNNRGYADFRV 251

QY 240 LDTDIQTNEDKTKQTITKITVHEGGRFWGKVSIEGDTNEVPKAEKLLTMKPGKWERQ 299
Db 252 VSSDAVLDESKEVNTISITVEGKYDFGNVAVESTVPGVDSGLQGLVETROGASYSAK 311

QY 300 QMTAVLGEIQNRMGSAIYSEISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNK 359
Db 312 EVQOSMEAISKRVAGEGYPARPVTRGRDMSGNTIGVTIVDQGERAVVERIEIRGNTR 371

QY 360 TRDEVVRRELROMESAPYDTSKLQSKERVLLGYFDNQFQDAVPLAG---TPDKVDLMS 417
Db 372 TRDYVIRREFDISEGDAFNQITIAKRLAELGYSKVN---ISTAGSAPORVVIYVD 428

QY 418 LTERSTGSLDSAGVQDITGLVMSAGVSDNLFPTGKSAALRASRKTLLNG--SLSFDP 476
Db 429 VEDQSTGSGFAGYQNDGVLEASVEENKFLGRQYIRVAGACEDDARTVLSFTEP 488

QY 477 YFTADGVSIGDYVYGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHL 536

Db 489 YFLGYLAGFDLP-----KNQKSEDIYNYDEQGFALRVTAPIYE-----NLSTFKY - 537
QY 537 TVNTYNKAPKHYADFIKKYKTKTDGDSFGKMLYKGTV-----GWGR-----NKTDSA 584
Db 538 ---TYKQ-----INVEGKGDQNNANLAEPYQALIRGEDWTQSILSNTLNVNTLDDR 586
QY 585 LMPTRGYLTGVNAEIALPGSKLOYYSATHNQIWFPLSKTFTLMLGGEVGIAGGYRTKE 644
Db 587 NMPREGQQAALTNEFAGLGDSEYKIKYAKARYITLSDIYD-VIGSLTGQAGHVMPGTG 645
QY 645 -IPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKISYGNKKKANYSAELLFMPGAKDA 703
Db 646 NLLVDFQKFGG-RQVRGFKNDGIGPRIGSD-----SIGGTTTFAASAEVTAAMPQGVPE 699
QY 704 RTVRLSLFADAGSVDGKTVDNNSSSATGGRVQNIYAGNTHKSTFTNLRYSAGGAVTW 763
Db 700 FGLRLAGFVDAWTGMYGNKV-----STGTVKD-----DNSIRASAGIGVMM 740
QY 764 LSPGLPMKFRYAYPLKKKPEDEIQRFQOLGTTTF 797
Db 741 ASPFGPIRVDAIPIAKEDYDEQRFQMSNTF 774

RESULT 15
F87486
outer membrane protein CC1915 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87486
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: AB7249; MUID:21173698; PMID:11259647
A;Accession: F87486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-769 <STO>
A;Cross-references: UNIPROT:Q9A711; GB:AE005673; NID:g13423368; PIDN:AAK23890.1; GSPDB:G
C;Genetics:
A;Gene: CC1915
C;Superfamily: protective surface antigen D-15

Query Match 21.1%; Score 877.5; DB 2; Length 769;
Best Local Similarity 28.2%; Pred. No. 8.8e-45;
Matches 226; Conservative 157; Mismatches 369; Indels 49; Gaps 17;

QY 11 MMLGISPL-----AFADF-----TIQDIRVEGLQRTPESTVFNYLPVKVGTVDYNDTHGSAI 61
Db 3 LLLGSTALVAPQQAFAQAQTAQGVQKILVQGNRIEQGTVLSYLPQIGDVTDSQRLDLA 62

QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDIAKKNLESFGLAQ 121
Db 63 LKTLARTDLFADVKIEMLGGDLVWKVNPPIINQVVFEGNSLKDCKLQDEVQ---IRPR 119

QY 122 QYFNOATLNOAVAGLKEEYLRGKLNITQITPKVTKLARNRVDIDITIDEGSAKITDI 181
Db 120 GLFTRAKVQADVORIIEIYRRSGRISATVTPKVELPQKRVLDVFEINGAKSGVLGINF 179

QY 182 EGNQVYSDRKLMRQMSLTGEGIW-TWLTRSNQFNQKPAQDMKEKVTDFYQNNGYDFDRI 240
Db 180 LGNAEYSDNLD-RDVIIVTKESRWYKILTSNDNYDPRIDYEDREQLRKHYRNRGYDFRVI 238

QY 241 DTDIQTNEKTKQTITKITVHEGGRFWGKVSIEGDTNEVPKAEKLLTMKPGKWERQ 300
Db 239 SSVAEIAPDKNGFAVYITLEEGPKYKFGKITVETELKLDGNNLLAQILPVRTGQLYEDR 298

QY 301 MTAVLGEIQNRMGSAIYSEISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHTGNK 360
Db 299 ISQATDALTTAAGAAGFAEVDVPRVPRVNRKTKTVDDVVFQVREGPRVYVDRIIDVGNTR 358

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:22:47 ; Search time 170 Seconds
(without alignments)
1813.224 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLIGISPLAF.....LKKKPEDEIQRFQQLGTF 797

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : A Genesepc16Dec04:*

1: Genesepc1980s:*

2: Genesepc1990s:*

3: Genesepc2000s:*

4: Genesepc2001s:*

5: Genesepc2002s:*

6: Genesepc2003as:*

7: Genesepc2003bs:*

8: Genesepc2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	3	AAY84947 Amino aci
2	797	100.0	797	5	ABY79802 Neisseria
3	752	94.4	797	4	AU03959 Neisseria
4	752	94.4	797	4	AU03957 Neisseria
5	752	94.4	797	4	AU04451 Neisseria
6	752	94.4	797	4	AU04451 Neisseria
7	752	94.4	797	4	ABY23788 Neisseria
8	752	94.4	797	4	ABY23784 Neisseria
9	752	94.4	797	4	ABY84746 Amino aci
10	210	26.3	792	4	ABY84744 Amino aci
11	210	26.3	792	4	AU03958 Neisseria
12	210	26.3	792	4	ABY23786 Neisseria
13	210	26.3	792	6	ABY84745 Amino aci
14	210	26.3	792	6	ABY80499 N. gonorr
15	157	19.7	792	3	ABY79748 N. gonorr
16	157	19.7	792	5	AAY84946 Amino aci
17	157	19.7	792	5	ABY79801 Neisseria
18	37	4.6	37	4	AU03997 Neisseria
19	32	4.0	32	4	AU04410 Neisseria
20	29	3.6	29	4	AU03987 Neisseria
21	25	3.1	25	4	AU04412 Neisseria
22	25	3.1	25	4	AU04000 Neisseria
23	23	2.9	23	4	AU03971 Neisseria
24	22	2.8	22	4	AU04401 Neisseria
25	21	2.6	21	4	ABY23787 Neisseria

26	19	2.4	19	4	AAU03988	Aau03988 Neisseria
27	19	2.4	21	4	ABY23785	Aab23785 Neisseria
28	18	2.3	18	4	AAU04428	Aau04428 Neisseria
29	18	2.3	18	4	AAU04434	Aau04434 Neisseria
30	18	2.3	18	4	AAU04425	Aau04425 Neisseria
31	18	2.3	18	4	AAU03990	Aau03990 Neisseria
32	16	2.0	16	4	AAU04427	Aau04427 Neisseria
33	16	2.0	16	4	AAU04435	Aau04435 Neisseria
34	16	2.0	16	4	AAU03992	Aau03992 Neisseria
35	16	2.0	16	4	AAU04430	Aau04430 Neisseria
36	15	1.9	15	4	AAU04442	Aau04442 Neisseria
37	15	1.9	15	4	AAU04404	Aau04404 Neisseria
38	15	1.9	15	4	ABY84743	Aab84743 N-termina
39	14	1.8	14	4	AAU04438	Aau04438 Neisseria
40	14	1.8	14	4	AAU03980	Aau03980 Neisseria
41	14	1.8	14	4	AAU03984	Aau03984 Neisseria
42	13	1.6	13	4	AAU03985	Aau03985 Neisseria
43	12	1.5	12	4	AAU04423	Aau04423 Neisseria
44	12	1.5	12	4	AAU04424	Aau04424 Neisseria
45	12	1.5	12	4	AAU04416	Aau04416 Neisseria
46	12	1.5	12	4	AAU04418	Aau04418 Neisseria
47	12	1.5	12	4	AAU03986	Aau03986 Neisseria
48	11	1.4	11	4	AAU03981	Aau03981 Neisseria
49	11	1.4	11	4	AAU03999	Aau03999 Neisseria
50	11	1.4	21	4	ABY23789	Aab23789 Neisseria
51	10	1.3	10	4	AAU03993	Aau03993 Neisseria
52	10	1.3	10	4	AAU03982	Aau03982 Neisseria
53	10	1.3	10	4	AAU03975	Aau03975 Neisseria
54	10	1.3	10	4	AAU04413	Aau04413 Neisseria
55	10	1.3	10	4	AAU03974	Aau03974 Neisseria
56	10	1.3	10	4	AAU04411	Aau04411 Neisseria
57	10	1.3	10	4	AAU04450	Aau04450 Neisseria
58	10	1.3	10	4	AAU04405	Aau04405 Neisseria
59	10	1.3	10	4	AAU04408	Aau04408 Neisseria
60	10	1.3	10	4	AAU04439	Aau04439 Neisseria
61	10	1.3	10	4	AAU04403	Aau04403 Neisseria
62	10	1.3	10	4	AAU03965	Aau03965 Neisseria
63	9	1.1	9	4	AAU04448	Aau04448 Neisseria
64	9	1.1	9	4	AAU03961	Aau03961 Neisseria
65	9	1.1	9	4	AAU04414	Aau04414 Neisseria
66	9	1.1	9	4	AAU03994	Aau03994 Neisseria
67	9	1.1	9	4	AAU03967	Aau03967 Neisseria
68	9	1.1	9	4	AAU04420	Aau04420 Neisseria
69	9	1.1	9	4	AAU03995	Aau03995 Neisseria
70	9	1.1	9	4	AAU03991	Aau03991 Neisseria
71	9	1.1	9	4	AAU03998	Aau03998 Neisseria
72	9	1.1	9	4	AAU04447	Aau04447 Neisseria
73	9	1.1	12	4	AAU03964	Aau03964 Neisseria
74	9	1.1	185	3	AGY21459	Ag21459 Arabidops
75	9	1.1	334	3	AGY21458	Ag21458 Arabidops
76	9	1.1	362	3	AGY21457	Ag21457 Arabidops
77	9	1.1	798	6	ABY67563	Abm67563 Phototrab
78	9	1.1	1035	8	ADJ50326	Adj50326 O11-assoc
79	8	1.0	8	4	AAU04436	Aau04436 Neisseria
80	8	1.0	8	4	AAU03996	Aau03996 Neisseria
81	8	1.0	8	4	AAU04422	Aau04422 Neisseria
82	8	1.0	8	4	AAU04445	Aau04445 Neisseria
83	8	1.0	8	4	AAU04402	Aau04402 Neisseria
84	8	1.0	8	4	AAU04426	Aau04426 Neisseria
85	8	1.0	8	4	AAU03970	Aau03970 Neisseria
86	8	1.0	8	4	AAU03973	Aau03973 Neisseria
87	8	1.0	94	7	ABY61646	Ab61646 Klebsiell
88	8	1.0	95	3	AGY25177	Ag25177 Arabidops
89	8	1.0	97	4	ABY51139	Ab51139 Human sec
90	8	1.0	97	6	ABY45396	Ab45396 Novel hum
91	8	1.0	97	7	ABY26876	Ab26876 Protein a
92	8	1.0	116	3	AGY7649	Ag7649 Arabidops
93	8	1.0	117	3	AGY49893	Ag49893 Arabidops
94	8	1.0	126	3	AGY25176	Ag25176 Arabidops
95	8	1.0	201	3	AGY57648	Ag57648 Arabidops
96	8	1.0	202	3	AGY49892	Ag49892 Arabidops
97	8	1.0	214	3	AGY57647	Ag57647 Arabidops
98	8	1.0	214	3	AGY57647	Ag57647 Arabidops

99	8	1.0	215	3	AAG49891	Rag49891 Arabidops	172	7	0.9	96	4	AAU64929	Aau64929 Propionib
100	8	1.0	216	5	ADN21670	Adn21670 Bacterial	173	7	0.9	96	6	ABM61448	Abm61448 Propionib
101	8	1.0	217	8	ABG60322	Yeast dyn	174	7	0.9	97	7	ABO69614	AbO69614 Pseudomon
102	8	1.0	266	4	ABG15869	Novel hum	175	7	0.9	101	4	ABBI17344	Abb17344 Human ner
103	8	1.0	266	7	ADC32990	Adc32990 Human nov	176	7	0.9	102	7	ADM27054	Adm27054 Hyperther
104	8	1.0	289	3	AAG49003	Arabidops	177	7	0.9	110	3	AAG02520	Aag02520 Human sec
105	8	1.0	299	4	AAG90486	C glutami	178	7	0.9	110	4	AAO06467	Aao06467 Human pol
106	8	1.0	315	8	ADS24860	Bacterial	179	7	0.9	119	5	ABP07824	Abp07824 Human ORF
107	8	1.0	335	4	AAB96813	Putative	180	7	0.9	120	4	AAU40749	Aau40749 Propionib
108	8	1.0	336	8	ADN47487	Thermococ	181	7	0.9	120	6	ABM37268	Abm37268 Propionib
109	8	1.0	349	3	AAG49002	Arabidops	182	7	0.9	121	3	AAG14889	Aag14889 Arabidops
110	8	1.0	349	3	AAG48988	Arabidops	183	7	0.9	122	4	AAM86629	Aam86629 Human imm
111	8	1.0	397	3	AAG48988	Arabidops	184	7	0.9	122	6	AAM69954	Aam69954 Photorhab
112	8	1.0	409	3	AAG49001	Arabidops	185	7	0.9	126	4	ABG69082	Abg69082 Drosophil
113	8	1.0	422	8	ADS23854	Bacterial	186	7	0.9	129	7	ADF04752	Adf04752 Bacterial
114	8	1.0	426	3	RAG48987	Arabidops	187	7	0.9	132	4	ABBI1237	Abbi1237 Human pho
115	8	1.0	426	5	ABB93220	Herbicida	188	7	0.9	143	3	AAG14888	Aag14888 Arabidops
116	8	1.0	428	3	AAG14941	Arabidops	189	7	0.9	150	6	ABU26587	Abu26587 Protein e
117	8	1.0	438	3	AAG14940	Arabidops	190	7	0.9	157	7	ADF07373	Adf07373 Bacterial
118	8	1.0	445	4	ABG17863	Novel hum	191	7	0.9	170	3	AAG21405	Aag21405 Arabidops
119	8	1.0	451	3	AAG06359	Arabidops	192	7	0.9	171	6	ABU01664	Abu01664 S. pneumo
120	8	1.0	454	3	RAG14939	Arabidops	193	7	0.9	178	2	AAY45288	Aay45288 Human sec
121	8	1.0	461	3	AAG06358	Arabidops	194	7	0.9	178	2	AAY30708	Aay30708 Amino aci
122	8	1.0	479	3	AAG06357	Arabidops	195	7	0.9	179	7	ABQ75778	Abq75778 Pseudomon
123	8	1.0	494	8	ADS24095	Bacterial	196	7	0.9	182	3	AAG22490	Aag22490 Arabidops
124	8	1.0	583	8	ADS14924	Pseudomon	197	7	0.9	189	4	ABG23074	Abg23074 Novel hum
125	8	1.0	648	7	ABO75882	Pseudomon	198	7	0.9	193	7	ABO69082	AbO69082 Pseudomon
126	8	1.0	745	4	ABG03852	Novel hum	199	7	0.9	194	4	ADM20062	Adm20062 Protein e
127	8	1.0	745	4	ABG09109	Novel hum	200	7	0.9	195	5	ABU52193	Abu52193 Helicobac
128	8	1.0	745	4	ABG10367	Novel hum	201	7	0.9	195	8	ADF30464	Adf30464 Human sec
129	8	1.0	745	4	ABG14890	Novel hum	202	7	0.9	196	3	AAG22489	Aag22489 Arabidops
130	8	1.0	897	8	ADP98989	C. albica	203	7	0.9	200	8	ADP30686	Adp30686 Human sec
131	8	1.0	1577	6	ABU41145	Protein e	204	7	0.9	208	4	ABE88565	AbE88565 Drosophil
132	8	1.0	1589	7	ADF04713	Bacterial	205	7	0.9	213	7	ABO68534	AbO68534 Pseudomon
133	7	0.9	7	4	AAU04432	Neisseria	206	7	0.9	213	8	ABO60429	AbO60429 Human gen
134	7	0.9	7	4	AAU04441	Neisseria	207	7	0.9	221	8	ADN25744	Adn25744 Bacterial
135	7	0.9	7	4	AAU04446	Neisseria	208	7	0.9	226	4	ABB67771	Abb67771 Drosophil
136	7	0.9	7	4	AAU03969	Neisseria	209	7	0.9	226	8	ABM68435	Abm68435 Photorhab
137	7	0.9	7	4	AAU04437	Neisseria	210	7	0.9	228	6	ADs42499	AdS42499 Bacterial
138	7	0.9	7	4	AAU04419	Neisseria	211	7	0.9	232	4	AAU59216	Aau59216 Propionib
139	7	0.9	7	4	AAU04429	Neisseria	212	7	0.9	232	6	ABM55735	Abm55735 Propionib
140	7	0.9	7	4	AAU04443	Neisseria	213	7	0.9	233	5	ABU51725	Abu51725 Helicobac
141	7	0.9	7	4	AAU04433	Neisseria	214	7	0.9	234	2	AAW98579	Aaw98579 H. pylori
142	7	0.9	23	3	AAV65830	Mismatch	215	7	0.9	243	4	ABG24253	Abg24253 Novel hum
143	7	0.9	50	4	AAW20158	Peptide #	216	7	0.9	244	6	ABM70306	Abm70306 Photorhab
144	7	0.9	50	4	ABB40395	Peptide #	217	7	0.9	244	7	ABO67562	AbO67562 Klebsiell
145	7	0.9	50	4	ABM34301	Peptide #	218	7	0.9	250	4	ABBS9528	AbBS9528 Drosophil
146	7	0.9	50	4	ABB24767	Protein #	219	7	0.9	253	8	ADL04906	Adl04906 M. catarr
147	7	0.9	50	4	AAW73922	Human bon	220	7	0.9	255	6	ABU02460	AbU02460 S. pneumo
148	7	0.9	50	4	ABG55674	Human liv	221	7	0.9	255	8	ADM92238	Adm92238 S. pneumon
149	7	0.9	50	4	ABG55674	Human liv	222	7	0.9	257	7	ABO82478	AbO82478 Pseudomon
150	7	0.9	56	5	ABG43810	Human pep	223	7	0.9	263	7	ABO77554	AbO77554 Pseudomon
151	7	0.9	56	8	ADN46996	Thermococ	224	7	0.9	268	3	AAV95697	Aay95697 Cosmid ch
152	7	0.9	58	2	AAW48931	Schwannom	225	7	0.9	268	7	ABO74392	AbO74392 Pseudomon
153	7	0.9	60	3	AAU03150	Human sec	226	7	0.9	268	7	ABO83252	AbO83252 Pseudomon
154	7	0.9	61	4	AAU65753	Protonib	227	7	0.9	268	7	ABO74393	AbO74393 Pseudomon
155	7	0.9	61	6	ABM62272	Protonib	228	7	0.9	270	7	ABO74440	AbO74440 Pseudomon
156	7	0.9	69	4	ABM88690	Human imm	229	7	0.9	277	2	AAV37752	Aay37752 Amino aci
157	7	0.9	75	7	ADC00302	Enterohae	230	7	0.9	277	8	ADQ81750	Adq81750 Trypanoso
158	7	0.9	76	6	ABU15436	Protein e	231	7	0.9	280	5	ABP26998	Abp26998 Streptoco
159	7	0.9	78	4	AAU90288	Human imm	232	7	0.9	280	6	ABU46897	Abu46897 Protein e
160	7	0.9	82	5	ABP33075	Human ORF	233	7	0.9	282	6	ADA54528	Ada54528 Human pro
161	7	0.9	83	4	AAU60561	Protonib	234	7	0.9	282	7	ADC95911	AdC95911 E. faeciu
162	7	0.9	83	6	ABM57080	Protonib	235	7	0.9	285	6	ABU45032	Abu45032 Protein e
163	7	0.9	85	8	ADS42710	Bacterial	236	7	0.9	288	2	AAR22996	Aar22996 Yeast pro
164	7	0.9	86	6	ADA34965	Acinetoba	237	7	0.9	288	6	AAR53144	Abr53144 Protein s
165	7	0.9	86	7	ABO63968	Klebsiell	238	7	0.9	288	7	ADK63118	Adk63118 Disease t
166	7	0.9	87	4	AAU17729	Novel hum	239	7	0.9	288	8	ADS44003	AdS44003 Bacterial
167	7	0.9	87	7	ADG41109	Human res	240	7	0.9	290	4	ABB10987	Abb10987 Human WD-
168	7	0.9	87	7	ADI96883	Human res	241	7	0.9	290	4	ABM79660	Aam79660 Human pro
169	7	0.9	88	3	AAV86404	Human gen	242	7	0.9	291	7	ABO79608	AbO79608 Pseudomon
170	7	0.9	88	6	ABO53551	Novel hum	243	7	0.9	292	6	ABU29077	Abu29077 Protein e
171	7	0.9	92	7	ADE08224	Novel pro	244	7	0.9	293	8	ADS24291	AdS24291 Bacterial

245	7	0.9	294	7	ADC94620	Adc94620 E. faeciu	318	7	0.9	416	6	ABM72077	Abm72077 Staphyloc
246	7	0.9	300	7	ABO63156	AbO63156 Klebsiell	319	7	0.9	417	4	ABG03334	Abg03334 Novel hum
247	7	0.9	305	8	ADN17987	Adn17987 Bacterial	320	7	0.9	418	5	ABP27080	Abp27080 Streptoco
248	7	0.9	307	3	AAG22488	Aag22488 Arabidops	321	7	0.9	420	4	ABP27080	Abp27080 Streptoco
249	7	0.9	310	8	ADS23653	Ads23653 Bacterial	322	7	0.9	420	4	ABG62035	Abg62035 P. furios
250	7	0.9	314	3	AAG21404	Aag21404 Arabidops	323	7	0.9	420	8	ADN47143	Adn47143 Thermococ
251	7	0.9	315	4	AAG74783	Aag74783 Human col	324	7	0.9	423	4	ABG28086	Abg28086 Novel hum
252	7	0.9	315	5	ABB91630	Abb91630 Herbicida	325	7	0.9	423	3	AY444389	Yay444389 Zea may
253	7	0.9	318	6	ABM67272	Abm67272 Phototrab	326	7	0.9	426	8	ADN21982	Adn21982 Bacterial
254	7	0.9	320	2	AAR33279	Aar33279 43 KD end	327	7	0.9	429	6	ABM23542	Abm23542 Protein e
255	7	0.9	324	4	ABU38302	Au38302 Salmonell	328	7	0.9	430	6	ABM68699	Abm68699 Phototrab
256	7	0.9	324	6	ABU48397	Abu48397 Protein e	329	7	0.9	432	4	ABP96771	Abp96771 Putative
257	7	0.9	325	4	ABG79630	Abg79630 Coryneb	330	7	0.9	433	6	ABU21968	Abu21968 Protein e
258	7	0.9	325	4	AAG91087	Aag91087 C glutami	331	7	0.9	434	7	ABO78489	AbO78489 Pseudomon
259	7	0.9	327	5	ABB89542	Abb89542 Human pol	332	7	0.9	434	8	ADN24740	Adn24740 Bacterial
260	7	0.9	327	5	ABO81872	AbO81872 Pseudomon	333	7	0.9	436	5	ABU50710	Abu50710 Helicobac
261	7	0.9	328	5	ABU51082	Abu51082 Helicobac	334	7	0.9	437	5	AAH47762	Aah47762 RNA bindi
262	7	0.9	329	3	ABAS2512	Abas2512 Helicobac	335	7	0.9	441	7	ADH86636	Adh86636 Enterococ
263	7	0.9	335	5	AAU93075	Aau93075 Arabidops	336	7	0.9	442	5	ABP72317	Abp72317 Rat prote
264	7	0.9	335	7	ADD30801	Add30801 Plant yie	337	7	0.9	444	4	AAU03821	Aau03821 G protein
265	7	0.9	335	8	ADI141831	Adi141831 Plant tra	338	7	0.9	444	4	ABG08390	Abg08390 Novel hum
266	7	0.9	336	8	ADI27927	Adi27927 Murine pr	339	7	0.9	444	8	ADN24258	Adn24258 Bacterial
267	7	0.9	337	3	AAU96738	Aau96738 Streptoco	340	7	0.9	448	4	AAU20358	Aau20358 Human sec
268	7	0.9	337	5	ABP26971	Abp26971 Streptoco	341	7	0.9	448	7	ADN76885	Adn76885 A. gossyp
269	7	0.9	337	5	ABP26970	Abp26970 Streptoco	342	7	0.9	448	8	ADN21452	Adn21452 Bacterial
270	7	0.9	337	5	ABB90355	Abb90355 Human pol	343	7	0.9	456	8	ADP31476	Adp31476 Human sec
271	7	0.9	337	6	ABU46738	Abu46738 Protein e	344	7	0.9	456	8	ADS41854	Ads41854 Bacterial
272	7	0.9	341	4	ABG65050	Abg65050 Drosophil	345	7	0.9	458	5	ABU42209	Abu42209 Protein e
273	7	0.9	341	4	ABG17128	Abg17128 Novel hum	346	7	0.9	459	6	ABU42209	Abu42209 Protein e
274	7	0.9	342	5	ADN19670	Adn19670 Human dru	347	7	0.9	459	6	ABU42209	Abu42209 Protein e
275	7	0.9	349	6	ABU23963	Abu23963 Protein e	348	7	0.9	460	4	AAU41439	Aau41439 Pseudomon
276	7	0.9	351	7	ABO62898	AbO62898 Klebsiell	349	7	0.9	460	4	AAU41439	Aau41439 Pseudomon
277	7	0.9	351	8	ADS73568	Ads73568 Glycopept	350	7	0.9	464	3	AAU51524	Aau51524 E. coli p
278	7	0.9	351	8	ADN21155	Adn21155 Bacterial	351	7	0.9	464	6	ABU4689	Abu4689 Protein e
279	7	0.9	352	8	ABM83397	Abm83397 Human dia	352	7	0.9	464	6	ABU4689	Abu4689 Protein e
280	7	0.9	353	8	ABM83396	Abm83396 Human dia	353	7	0.9	465	7	ABO80641	AbO80641 Pseudomon
281	7	0.9	353	8	ABM83395	Abm83395 Human dia	354	7	0.9	466	4	AAU62912	Aau62912 Propionib
282	7	0.9	355	2	AAR74758	Aar74758 Beta-keto	355	7	0.9	466	6	ABM59431	Abm59431 Propionib
283	7	0.9	355	2	AAR31945	Aar31945 Polynhydro	356	7	0.9	469	8	ADS24348	Ads24348 Bacterial
284	7	0.9	355	6	ABM73087	Abm73087 Staphyloc	357	7	0.9	469	8	ADS24348	Ads24348 Bacterial
285	7	0.9	355	6	ABM73087	Abm73087 Staphyloc	358	7	0.9	472	3	ABU18420	Abu18420 Amino aci
286	7	0.9	355	6	ADA34127	Ada34127 Acinetoba	359	7	0.9	473	6	ADA33992	Ada33992 Acinetoba
287	7	0.9	356	6	ABU24320	Abu24320 Protein e	360	7	0.9	478	4	ABG66297	Abg66297 Drosophil
288	7	0.9	357	7	ABO84393	AbO84393 Pseudomon	361	7	0.9	478	5	ABR38839	AbR38839 A. niger
289	7	0.9	357	6	ABO84393	AbO84393 Pseudomon	362	7	0.9	482	4	ADN19812	Adn19812 Protein e
290	7	0.9	359	8	ADP55871	Adp55871 Human col	363	7	0.9	485	5	ADU33852	Adu33852 Protein o
291	7	0.9	366	2	AAW69392	Aaw69392 Aspergill	364	7	0.9	490	6	ADA28694	Ada28694 Plasmid p
292	7	0.9	366	8	ADN18365	Adn18365 Bacterial	365	7	0.9	490	6	ADA28694	Ada28694 Plasmid p
293	7	0.9	367	7	ADI60171	Adi60171 Secreted	366	7	0.9	497	4	AAU37751	Aau37751 Streptoco
294	7	0.9	382	2	AAU45261	Aau45261 Human sec	367	7	0.9	497	6	ABU01284	Abu01284 S. pneumo
295	7	0.9	383	4	AAG91116	Aag91116 C glutami	368	7	0.9	497	8	ADK48573	Adk48573 Streptoco
296	7	0.9	386	4	ABG21113	Abg21113 Novel hum	369	7	0.9	497	8	ADN92139	Adn92139 S pneumon
297	7	0.9	386	8	ADN26073	Adn26073 Bacterial	370	7	0.9	504	8	ADR95097	Adr95097 Novel S.
298	7	0.9	387	7	ADI60400	Adi60400 Secreted	371	7	0.9	514	6	ABJ20237	Abj20237 Human IG
299	7	0.9	387	8	ADP31368	Adp31368 Human sec	372	7	0.9	517	3	AAU32390	Aau32390 Harpevir
300	7	0.9	390	6	ABU20261	Abu20261 Protein e	373	7	0.9	517	5	AAE23294	Aae23294 Human nec
301	7	0.9	392	8	ADP29346	Adp29346 Human sec	374	7	0.9	518	8	ABG77170	Abg77170 Prostata
302	7	0.9	393	7	ABO68025	AbO68025 Pseudomon	375	7	0.9	518	8	ADS29669	Ads29669 Bacterial
303	7	0.9	397	2	AAW29659	Aaw29659 Homo sapi	376	7	0.9	521	6	ABU35710	Abu35710 Protein e
304	7	0.9	399	4	AAU32410	Aau32410 Novel hum	377	7	0.9	522	6	ABU22090	Abu22090 Protein e
305	7	0.9	399	7	ABO69686	AbO69686 Pseudomon	378	7	0.9	527	6	ABU19551	Abu19551 Protein e
306	7	0.9	399	8	ADP31313	Adp31313 Human sec	379	7	0.9	528	4	ABB71669	Abb71669 Drosophil
307	7	0.9	405	4	AAU93419	Aau93419 Human pro	380	7	0.9	529	7	ADG61129	Adg61129 Baeyer-Vi
308	7	0.9	405	8	ADN25996	Adn25996 Bacterial	381	7	0.9	531	8	ADP30594	Adp30594 Human sec
309	7	0.9	405	8	ADS42259	Ads42259 Bacterial	382	7	0.9	531	8	ADP31696	Adp31696 Human sec
310	7	0.9	406	4	AAU39653	Aau39653 Human pol	383	7	0.9	544	2	AAW03943	Aaw03943 LKT-GNRH
311	7	0.9	409	6	ABU96684	Abu96684 Human nuc	384	7	0.9	544	2	AAW79570	Aaw79570 LKT-GNRH
312	7	0.9	410	5	ABP29775	Abp29775 Streptoco	385	7	0.9	551	8	ADQ65217	Adq65217 Novel hum
313	7	0.9	410	5	ABP30545	Abp30545 Streptoco	386	7	0.9	559	7	ABO75946	AbO75946 Pseudomon
314	7	0.9	411	8	ADS23906	Ads23906 Bacterial	387	7	0.9	560	4	AAU78929	Aau78929 Human pro
315	7	0.9	413	4	AAU41340	Aau41340 Propionib	388	7	0.9	562	4	ABB64878	Abb64878 Drosophil
316	7	0.9	413	6	ABU37859	Abu37859 Propionib	389	7	0.9	564	6	ABJ37094	Abj37094 Low-affin
317	7	0.9	416	6	ABU42300	Abu42300 Protein e	390	7	0.9	566	6	AAE35922	Aae35922 Human All

391	7	0.9	568	5	ABU51967	Abu51967 Helicobac	464	7	0.9	792	8	ADH12911	Adh12911 Francisel
392	7	0.9	568	5	ABP74083	Abp74083 Candida a	465	7	0.9	797	8	ADS23447	Ads23447 Bacterial
393	7	0.9	572	6	ABJ37095	Abj37095 Low-affin	466	7	0.9	799	3	AAy92061	Aay92061 Human APC
394	7	0.9	572	7	ADC07800	Adc07800 Rice prot	467	7	0.9	809	2	AAy29672	Aay29672 Human cer
395	7	0.9	572	7	ADF74126	Adf74126 Human nov	468	7	0.9	816	8	ADP31581	Adp31581 Human sec
396	7	0.9	573	4	ABB60673	Abb60673 Drosophil	469	7	0.9	818	4	AAG92737	Aag92737 C glutami
397	7	0.9	576	7	ABO74500	Abp74500 Pseudomon	470	7	0.9	821	7	ABO72267	Abp72267 Pseudomon
398	7	0.9	578	8	ADP03592	Adp03592 Infection	471	7	0.9	823	4	ABB71484	Abb71484 Drosophil
399	7	0.9	579	4	ABG24250	Abg24250 Novel hum	472	7	0.9	827	7	ADF06140	Adf06140 Bacterial
400	7	0.9	580	5	AAG66008	Aag66008 F. necrop	473	7	0.9	850	4	ABBS2809	Abbs2809 Escherich
401	7	0.9	580	8	ADO47877	Ado47877 Alpha-Her	474	7	0.9	851	8	ADP31340	Adp31340 Human sec
402	7	0.9	581	8	ADP03590	Adp03590 Infection	475	7	0.9	870	8	ADP30646	Adp30646 Human sec
403	7	0.9	584	6	ABU19765	Abu19765 Protein e	476	7	0.9	874	6	ABU33564	Abu33564 Protein e
404	7	0.9	587	4	AAU78928	Aam78928 Human pro	477	7	0.9	892	8	ADP31578	Adp31578 Human sec
405	7	0.9	587	5	AAU82982	Aau82982 Human hom	478	7	0.9	897	4	ABBG2261	Abbg2261 Drosophil
406	7	0.9	587	5	AAU10799	Aau10799 Polymorph	479	7	0.9	908	6	ABU08492	Abu08492 Alpha-hel
407	7	0.9	587	5	AAU10796	Aau10796 Reference	480	7	0.9	914	6	ABU08604	Abu08604 Neisseria
408	7	0.9	587	5	AAU10797	Aau10797 Polymorph	481	7	0.9	921	2	AAW72033	Aaw72033 HSV-2 str
409	7	0.9	587	5	AAU10798	Aau10798 Polymorph	482	7	0.9	924	2	AAU10889	Aar10889 Leukotoxi
410	7	0.9	587	8	ADL17020	Adl17020 Human Ran	483	7	0.9	924	2	AAU42378	Aar42378 Recombina
411	7	0.9	587	8	ADQ88017	Adq88017 Human Ran	484	7	0.9	924	2	AAU42380	Aar42380 Recombina
412	7	0.9	587	8	ABM82366	Abm82366 Tumour-as	485	7	0.9	924	2	AAU42385	Aar42385 Recombina
413	7	0.9	589	7	ADB85263	Adb85263 Mouse RNA	486	7	0.9	925	5	AAO14246	Aao14246 Human pre
414	7	0.9	596	8	ADN99873	Adn99873 Novel hum	487	7	0.9	926	2	AAU14482	Aar14482 LKT352. 1
415	7	0.9	596	8	ADN99872	Adn99872 Novel hum	488	7	0.9	926	2	AAU34545	Aar34545 Leukotoxi
416	7	0.9	609	3	AAU73487	Aay73487 Human sec	489	7	0.9	926	2	AAU50291	Aar50291 Recombina
417	7	0.9	614	6	ADA33217	Ada33217 Acinetoba	490	7	0.9	926	2	AAU03945	P. haemol
418	7	0.9	614	8	ADH48376	Adh48376 Human KPP	491	7	0.9	926	2	AAU79568	Aaw79568 Leukotoxi
419	7	0.9	619	8	ADN23202	Adn23202 Bacterial	492	7	0.9	932	8	ADR08677	Adr08677 Human pro
420	7	0.9	620	2	AAU77275	Aar77275 ORC2 subu	493	7	0.9	933	7	ABM85855	Abm85855 Human pro
421	7	0.9	620	2	AAW22225	Aaw22225 S. cerevi	494	7	0.9	933	8	ADN03759	Adn03759 AntipOri
422	7	0.9	620	5	AAU82999	Aau82999 S. cerevi	495	7	0.9	934	2	AAW07637	Aaw07637 P. suis 1
423	7	0.9	620	6	ABR53643	AbR53643 Protein s	496	7	0.9	936	2	AAU34547	Aar34547 GnrH-Leuk
424	7	0.9	620	7	ADR64130	Adr64130 Disease t	497	7	0.9	937	8	ADH13664	Adh13664 Human ENZ
425	7	0.9	620	8	ADN18789	Adn18789 Bacterial	498	7	0.9	943	2	AAU34546	Aar34546 Somatosta
426	7	0.9	621	7	ABO70379	Abp70379 Pseudomon	499	7	0.9	949	4	AAU68553	Aab68553 Human GTP
427	7	0.9	622	5	ABP61455	Abp61455 Human NF-	500	7	0.9	950	4	AAU73355	Aab73355 Human mes
428	7	0.9	622	6	ABR41026	AbR41026 Human MAP	501	7	0.9	951	2	AAU34548	Aar34548 Rotavirus
429	7	0.9	623	4	AAU79912	Aam79912 Human pro	502	7	0.9	951	4	AAU73356	Aab73356 Rat meg-1
430	7	0.9	623	4	AAU79913	Aam79913 Human pro	503	7	0.9	951	4	AAU79261	Aam79261 Human pro
431	7	0.9	625	8	ADS44452	Ads44452 Bacterial	504	7	0.9	953	2	AAU07167	Aar07167 105kD PTX
432	7	0.9	627	4	ABG18262	Abg18262 Novel hum	505	7	0.9	953	2	AAU15159	Aar15159 Leukotoxi
433	7	0.9	628	4	ABG23677	Abg23677 Novel hum	506	7	0.9	953	2	AAU43865	Aar43865 Leukotoxi
434	7	0.9	632	5	AAO19378	Aao19378 Human pal	507	7	0.9	953	2	AAU60072	Aar60072 PtxA prot
435	7	0.9	632	5	ABP61456	Abp61456 Human NF-	508	7	0.9	953	4	AAU04638	Aae04638 Pasteurel
436	7	0.9	649	4	ABG61237	Abg61237 Drosophil	509	7	0.9	956	6	AAU08602	Abu08602 Neisseria
437	7	0.9	663	6	ABU24491	Abu24491 Protein e	510	7	0.9	963	4	AAU78880	Aam78880 Human pro
438	7	0.9	665	4	AAU78876	Aam78876 Human pro	511	7	0.9	963	7	ADB67089	Kinesin h
439	7	0.9	666	4	AAU79657	Aab79657 Corynebac	512	7	0.9	963	7	ADB67091	Kinesin h
440	7	0.9	666	4	AAU71885	Aau71885 C. glutam	513	7	0.9	964	8	ADL99362	Adl99362 Nanostruc
441	7	0.9	667	4	ABG16901	Abg16901 Novel hum	514	7	0.9	964	8	ADL99360	Adl99360 Nanostruc
442	7	0.9	667	4	AAU32908	Aau32908 Novel hum	515	7	0.9	967	4	AAU80245	Aam80245 Human pro
443	7	0.9	671	2	AAU38505	Aaw38505 Streptoco	516	7	0.9	969	6	AAU34448	Aae34448 Human lip
444	7	0.9	671	2	AAU85917	Aay85917 S. pneumo	517	7	0.9	977	2	AAU03942	Aaw03942 LKT-GnrH
445	7	0.9	671	8	ADK47127	Adk47127 Streptoco	518	7	0.9	977	2	AAU79569	Aaw79569 LKT-GnrH
446	7	0.9	673	5	AAE25082	Aae25082 Human kin	519	7	0.9	978	7	ADM05468	Adm05468 Human pro
447	7	0.9	676	8	ADR95463	Adr95463 Novel S.	520	7	0.9	979	4	AAU79864	Aam79864 Human pro
448	7	0.9	686	6	ABU39853	Abu39853 Protein e	521	7	0.9	983	5	ABU77509	Abb77509 Trameaes
449	7	0.9	692	8	ADN26147	Adn26147 Bacterial	522	7	0.9	998	2	AAU38822	Aay38822 Neisseria
450	7	0.9	695	3	AAU79573	Aaw79573 LKT-GnrH	523	7	0.9	1004	8	ADL18816	Adol18816 Human lip
451	7	0.9	695	3	AAU58361	Aay58361 Leukotoxi	524	7	0.9	1016	4	AAG90609	Aag90609 C glutami
452	7	0.9	695	3	AAU58133	Aay58133 Gonadotro	525	7	0.9	1016	6	ABU41567	Abu41567 Protein e
453	7	0.9	699	7	ABO68327	Abp68327 Pseudomon	526	7	0.9	1017	8	ADP31268	Adp31268 Human sec
454	7	0.9	702	5	ABP65679	Abp65679 Bifidobac	527	7	0.9	1019	7	ADJ69855	Adj69855 Human hea
455	7	0.9	705	4	AAU79860	Aam79860 Human pro	528	7	0.9	1050	8	ADP31376	Adp31376 Human sec
456	7	0.9	710	8	ADP30746	Adp30746 Human sec	529	7	0.9	1054	5	ABU79311	Abb79311 Human ova
457	7	0.9	717	4	ABG61609	Abb61609 Drosophil	530	7	0.9	1069	2	AAU52748	Aar52748 Bovine IF
458	7	0.9	717	8	ADO07924	Ado07924 Fly polyp	531	7	0.9	1069	2	AAU13867	Aaw13867 Chimeric
459	7	0.9	731	5	ABU52070	Abu52070 Helicobac	532	7	0.9	1069	3	ABU21074	Abb21074 Bovine ga
460	7	0.9	741	6	ABU42146	Abu42146 Protein e	533	7	0.9	1076	5	ABP69070	Abp69070 Human pol
461	7	0.9	761	5	ABU77431	Abb77431 Human tum	534	7	0.9	1078	4	ABU61597	Abb61597 Drosophil
462	7	0.9	792	4	ABG15703	Novel hum	535	7	0.9	1088	4	AAU78676	Aam78676 Human pro
463	7	0.9	792	7	ABM85854	Abm85854 Mouse pro	536	7	0.9	1098	2	AAU22103	Aar22103 Bovine IL

537	7	0.9	1098	2	AAR52747	Aar52747 Bovine IL	610	7	0.9	1628	4	ABG02195	Abg02195 Novel hum
538	7	0.9	1098	2	AAR52747	Aar52747 Bovine IL	611	7	0.9	1686	2	AAW70991	Aaw70991 Human cla
539	7	0.9	1098	2	AAR52747	Aar52747 Bovine IL	612	7	0.9	1686	6	ABJ19811	Abj19811 Androgen-
540	7	0.9	1116	8	ADP31692	Adp31692 Human sec	613	7	0.9	1725	8	ADP30654	Adp30654 Human sec
541	7	0.9	1121	5	AAE20419	Aae20419 Human cdc	614	7	0.9	1833	8	ADP30642	Adp30642 Human sec
542	7	0.9	1121	8	ADJ66576	Adj66576 WD-repeat	615	7	0.9	1846	6	ABR39833	AbR39833 Human sca
543	7	0.9	1129	7	ABO79806	AbO79806 Pseudomon	616	7	0.9	1896	2	AAW72095	Aaw72095 HSV-2 str
544	7	0.9	1132	2	AAR77417	Aar77417 Human cel	617	7	0.9	1912	7	ADC26223	Adc26223 Human NOV
545	7	0.9	1132	2	AAR77417	Aar77417 Human int	618	7	0.9	1912	6	ABU30826	Abu30826 Protein e
546	7	0.9	1136	6	ABU08605	Abu08605 Neisseria	619	7	0.9	1956	8	ADN00371	Adn00371 Novel hum
547	7	0.9	1139	5	ABG97360	Abg97360 Human CGD	620	7	0.9	1974	2	AAW98391	Aaw98391 H. pylori
548	7	0.9	1156	3	ABAI0104	Abi010104 Feline fo	621	7	0.9	1984	4	ABG01338	Abg01338 Novel hum
549	7	0.9	1161	5	ABG97354	Abg97354 Human CGD	622	7	0.9	2274	4	AAO50674	Aao50674 Mouse APC
550	7	0.9	1178	6	ABU08603	Abu08603 Neisseria	623	7	0.9	2274	8	ADO08047	Ado08047 Mouse pol
551	7	0.9	1187	8	ADJ49198	Adj49198 Oil-assoc	624	7	0.9	2303	6	ABR58648	AbR58648 Human can
552	7	0.9	1197	8	ADP31342	Adp31342 Human sec	625	7	0.9	2303	8	ADO08045	Ado08045 Human pol
553	7	0.9	1216	5	AAE22860	Aae22860 Human pho	626	7	0.9	2338	8	ABO58348	AbO58348 Human sec
554	7	0.9	1268	4	ABBG1314	AbB61314 Drosophil	627	7	0.9	2349	8	ADP30959	Adp30959 Human sec
555	7	0.9	1269	8	ADP31500	Adp31500 Human sec	628	7	0.9	2382	8	ADP31341	Adp31341 Human sec
556	7	0.9	1296	2	AAW47157	Aaw47157 Nevoid ba	629	7	0.9	2431	2	AAR25138	Aar25138 SFV4 non-
557	7	0.9	1320	5	AAW47603	Aaw47603 Drosophil	630	7	0.9	2732	4	ABR52855	AbR52855 Escherich
558	7	0.9	1334	2	AAR14481	Aar14481 LkTA:lacZ	631	7	0.9	2834	5	ABG97576	Abg97576 Haemagglu
559	7	0.9	1334	2	AAR50290	Aar50290 lktA::lac	632	7	0.9	2834	7	ADH80652	Adh80652 Escherich
560	7	0.9	1336	7	ADJ92014	Adj92014 Semliki f	633	7	0.9	3119	2	AAW72204	Aaw72204 HSV-2 str
561	7	0.9	1390	6	ABP60436	Abp60436 Human and	634	7	0.9	3122	7	ADG75178	Adg75178 Human her
562	7	0.9	1396	8	ADN01130	Adn01130 Human cel	635	7	0.9	3122	7	ADG75129	Adg75129 Human her
563	7	0.9	1403	2	AAR10890	Aar10890 lktA::lac	636	7	0.9	3194	6	ABU31122	Abu31122 Protein e
564	7	0.9	1403	2	AAW79574	Aaw79574 Leukotoxi	637	7	0.9	3339	8	ADP31219	Adp31219 Human sec
565	7	0.9	1419	5	ABU65081	Abu65081 Human NOV	638	7	0.9	3407	8	ADP31060	Adp31060 Human sec
566	7	0.9	1419	8	ADH42427	Adh42427 Novel hum	639	7	0.9	3407	8	ADP31062	Adp31062 Human sec
567	7	0.9	1419	8	ADN61813	Adn61813 Human nov	640	7	0.9	3477	8	ADP30704	Adp30704 Human sec
568	7	0.9	1423	5	ABU65083	Abu65083 Human NOV	641	7	0.9	3579	8	ADP31098	Adp31098 Human sec
569	7	0.9	1423	8	ADH42431	Adh42431 Novel hum	642	7	0.9	4106	4	ABG99872	Abg99872 S. cinnam
570	7	0.9	1423	8	ADN61817	Adn61817 Human nov	643	7	0.9	4752	8	ADP30585	Adp30585 Human sec
571	7	0.9	1433	8	ADO18815	Ado18815 Human lip	644	7	0.9	4752	5	AAO22158	Aao22158 Ramoplani
572	7	0.9	1434	2	AAR94380	Aar94380 Mouse pat	645	7	0.9	4999	5	AAO22158	Aao22158 Ramoplani
573	7	0.9	1434	2	AAW52199	Aaw52199 Mouse pat	646	7	0.9	5304	8	ADP30706	Adp30706 Human sec
574	7	0.9	1434	2	AAW72968	Aaw72968 Mouse pat	647	7	0.9	5304	8	ADP30705	Adp30705 Human sec
575	7	0.9	1434	4	AAW67159	Aaw67159 Murine pa	648	7	0.9	8026	6	AAE35489	Aae35489 Streptomy
576	7	0.9	1434	5	AAW79572	Aaw79572 Mouse pat	649	7	0.9	8976	8	ADP31425	Adp31425 Human sec
577	7	0.9	1434	7	ABU62271	Abu62271 Mouse pat	650	7	0.9	9195	8	ADP31494	Adp31494 Human sec
578	7	0.9	1434	7	ADH94215	Adh94215 Murine pt	651	7	0.9	10944	8	ADP31311	Adp31311 Human sec
579	7	0.9	1434	7	ADH62722	Adh62722 Mouse pat	652	7	0.9	11328	8	ADP31310	Adp31310 Human sec
580	7	0.9	1434	8	ADE48980	Ade48980 Mouse pat	653	6	0.8	6	4	AAU03972	Aau03972 Neisseria
581	7	0.9	1439	4	AAW7557	Aaw7557 Neisseria	654	6	0.8	6	4	AAU03989	Aau03989 Neisseria
582	7	0.9	1447	2	AAR75375	Aar75375 Human pat	655	6	0.8	6	4	AAU04415	Aau04415 Neisseria
583	7	0.9	1447	2	AAW52200	Aaw52200 Human pat	656	6	0.8	6	4	AAU03962	Aau03962 Neisseria
584	7	0.9	1447	2	AAW72969	Aaw72969 Human pat	657	6	0.8	6	4	AAU03968	Aau03968 Neisseria
585	7	0.9	1447	4	AAW67163	Aaw67163 Human pat	658	6	0.8	6	4	AAU04431	Aau04431 Neisseria
586	7	0.9	1447	5	AAE19830	Aae19830 Human pat	659	6	0.8	6	4	AAU03983	Aau03983 Neisseria
587	7	0.9	1447	5	ABJ10931	Abj10931 TRC8 rela	660	6	0.8	7	2	AAW44781	Aaw44781 Sequence
588	7	0.9	1447	5	AAW79571	Aaw79571 Human pat	661	6	0.8	7	2	AAW44782	Aaw44782 Sequence
589	7	0.9	1447	7	ABU62275	Abu62275 Human pat	662	6	0.8	7	4	AAW62826	Aaw62826 Fibrinoge
590	7	0.9	1447	7	ADH46678	Adh46678 Human Pro	663	6	0.8	7	4	AAW62823	Aaw62823 Fibrinoge
591	7	0.9	1447	7	ADH46678	Adh46678 Human Pro	664	6	0.8	7	5	AAO21220	Aao21220 Absorptio
592	7	0.9	1447	7	ADH62731	Adh62731 Human pat	665	6	0.8	8	2	AAW73428	Aaw73428 Human TSH
593	7	0.9	1447	8	ADE48989	Ade48989 Human pat	666	6	0.8	8	5	AAO21222	Aao21222 Absorptio
594	7	0.9	1449	2	AAW38824	Aaw38824 Neisseria	667	6	0.8	9	2	AAW25260	Aaw25260 HIV Env g
595	7	0.9	1449	6	ABU37787	Abu37787 Protein e	668	5	0.8	9	5	ABW94918	Abw94918 CTL epito
596	7	0.9	1454	3	AAW56621	Aaw56621 Neisseria	669	6	0.8	9	5	ABW94587	Abw94587 CTL epito
597	7	0.9	1457	2	AAW38823	Aaw38823 Neisseria	670	6	0.8	9	5	ABW95084	Abw95084 CTL epito
598	7	0.9	1457	3	AAW25662	Aaw25662 N. mening	671	6	0.8	9	5	ABW94690	Abw94690 CTL epito
599	7	0.9	1457	3	AAW56622	Aaw56622 Neisseria	672	6	0.8	9	5	AAO21237	Aao21237 Absorptio
600	7	0.9	1457	3	AAW58592	Aaw58592 N. mening	673	6	0.8	9	8	ADP25609	Adp25609 Plasmodiu
601	7	0.9	1457	4	AAW27556	Aaw27556 Neisseria	674	6	0.8	10	2	AAW33824	Aaw33824 Selectin
602	7	0.9	1457	5	ABU08601	Abu08601 Neisseria	675	6	0.8	10	2	AAW33825	Aaw33825 Selectin
603	7	0.9	1458	5	ABW09556	Abw09556 Human lip	676	6	0.8	10	2	AAW33833	Aaw33833 Selectin
604	7	0.9	1458	5	ABW09555	Abw09555 Human lip	677	6	0.8	10	2	AAW33834	Aaw33834 Selectin
605	7	0.9	1458	6	ADP31440	Adp31440 Human lip	678	6	0.8	10	2	AAW50817	Aaw50817 Cyclic pe
606	7	0.9	1464	6	ADP31437	Adp31437 Human sec	679	6	0.8	10	4	AAW94318	Aaw94318 Human com
607	7	0.9	1468	2	AAW38825	Aaw38825 Neisseria	680	6	0.8	10	4	AAW85396	Aaw85396 Saccharom
608	7	0.9	1468	6	ABP77279	Abp77279 N. gonorr	681	6	0.8	10	4	AAW85682	Aaw85682 Saccharom
609	7	0.9	1468	6	ABU37103	Abu37103 Protein e	682	6	0.8	10	5	ABW95044	Abw95044 CTL epito

683	6	0.8	10	5	ABB94737	Abb94737 CTL epit	756	6	0.8	34	2	AAM65997	Aaw65997 Parathyro
684	6	0.8	10	5	ABB94739	Abb94739 CTL epit	757	6	0.8	34	2	AAM65997	Aaw65997 Parathyro
685	6	0.8	10	5	ABB94944	Abb94944 CTL epit	758	6	0.8	34	2	AAM65997	Aaw65997 Parathyro
686	6	0.8	10	5	ABB94629	Abb94629 CTL epit	759	6	0.8	34	2	AAM65997	Aaw65997 Parathyro
687	6	0.8	10	8	ADK06129	Adk06129 Hepatitis	760	6	0.8	34	5	AAB73134	Aab73134 Human sec
688	6	0.8	12	2	AAU731275	Aau731275 Human sem	761	6	0.8	34	5	AAB73134	Aab73134 Human sec
689	6	0.8	12	2	ABP98955	Abp98955 ErbB2 cel	762	6	0.8	34	5	AAB73134	Aab73134 Human sec
690	6	0.8	13	2	AAW3015	Aaw3015 R4 recept	763	6	0.8	34	5	AAB73134	Aab73134 Human sec
691	6	0.8	13	6	ABP98589	Abp98589 Beta-barr	764	6	0.8	34	8	ABU42245	Abu42245 Protein e
692	6	0.8	14	4	ABBS6739	Abbs6739 Human SNP	765	6	0.8	34	8	ABU42245	Abu42245 Protein e
693	6	0.8	15	5	ABPA6959	Abpa6959 Human BLY	766	6	0.8	34	8	ADH35571	Adh35571 Human par
694	6	0.8	15	7	ADF32583	Adf32583 Clostridi	767	6	0.8	34	8	ADH35571	Adh35571 Human par
695	6	0.8	15	7	ADG97786	Adg97786 scfV VHCD	768	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
696	6	0.8	18	2	AAW40133	Aaw40133 Delta'S s	769	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
697	6	0.8	18	2	AAW36080	Aaw36080 E. coli D	770	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
698	6	0.8	18	8	ADL15120	Adl15120 E. coli D	771	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
699	6	0.8	19	2	AAW46341	Aaw46341 Amino aci	772	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
700	6	0.8	19	5	ABB07414	Abb07414 Plasmid p	773	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
701	6	0.8	19	5	AAO19110	Aao19110 Human cir	774	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
702	6	0.8	20	2	AAW22332	Aaw22332 HIV-1 cli	775	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
703	6	0.8	20	2	AAW62895	Aaw62895 Peptide s	776	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
704	6	0.8	21	3	AAW56865	Aaw56865 B. catarr	777	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
705	6	0.8	21	3	ABW07415	Abw07415 Plasmid p	778	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
706	6	0.8	21	7	ADC73122	Adc73122 Domain li	779	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
707	6	0.8	22	4	AAW83929	Aaw83929 Antigenic	780	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
708	6	0.8	23	6	ADA11828	Ada11828 Human nov	781	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
709	6	0.8	24	5	AAU73141	Aau73141 Parathyro	782	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
710	6	0.8	24	5	AAU73142	Aau73142 Parathyro	783	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
711	6	0.8	24	8	ADQ75456	Adq75456 PTH/PTHrP	784	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
712	6	0.8	24	8	ADQ75457	Adq75457 PTH/PTHrP	785	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
713	6	0.8	26	4	AAW99735	Aaw99735 Human exc	786	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
714	6	0.8	26	4	AAW42550	Aaw42550 Human kid	787	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
715	6	0.8	28	2	AAW54400	Aaw54400 MAGE-10 t	788	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
716	6	0.8	28	3	AAW5042	Aaw5042 Human 5'	789	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
717	6	0.8	28	3	AAW99875	Aaw99875 Human MAG	790	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
718	6	0.8	28	4	AAO13828	Aao13828 Human pol	791	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
719	6	0.8	28	5	AAU73105	Aau73105 Parathyro	792	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
720	6	0.8	28	5	AAU73106	Aau73106 Parathyro	793	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
721	6	0.8	28	8	ADQ75421	Adq75421 PTH/PTHrP	794	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
722	6	0.8	28	8	ADQ75420	Adq75420 PTH/PTHrP	795	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
723	6	0.8	29	6	ABJ26817	Abj26817 Endotheli	796	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
724	6	0.8	30	5	ABP29400	Abp29400 Streptoco	797	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
725	6	0.8	30	5	AAU73170	Aau73170 Parathyro	798	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
726	6	0.8	30	5	AAU73136	Aau73136 Parathyro	799	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
727	6	0.8	30	5	AAU73137	Aau73137 Parathyro	800	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
728	6	0.8	30	8	ADQ75451	Adq75451 PTH/PTHrP	801	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
729	6	0.8	30	8	ADQ75485	Adq75485 PTH/PTHrP	802	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
730	6	0.8	30	8	ADQ75452	Adq75452 PTH/PTHrP	803	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
731	6	0.8	31	2	AAU04222	Aau04222 Human par	804	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
732	6	0.8	31	5	ABBS7410	Abbs7410 Human sec	805	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
733	6	0.8	31	7	ADI24798	Adi24798 Parathyro	806	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
734	6	0.8	32	3	AAW58650	Aaw58650 Calluna v	807	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
735	6	0.8	32	3	AAW33972	Aaw33972 Human sec	808	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
736	6	0.8	32	3	AAW44807	Aaw44807 Calluna v	809	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
737	6	0.8	32	4	AAW60746	Aaw60746 Human sec	810	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
738	6	0.8	33	4	AAW80170	Aaw80170 MiSP1-der	811	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
739	6	0.8	33	4	AAW16134	Aaw16134 Peptide #	812	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
740	6	0.8	33	4	AAW28628	Aaw28628 Peptide #	813	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
741	6	0.8	33	4	AAW83228	Aaw83228 Human imm	814	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
742	6	0.8	33	4	ABW29945	Abw29945 Peptide #	815	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
743	6	0.8	33	4	ABW20544	Abw20544 Protein #	816	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
744	6	0.8	33	4	AAW68319	Aaw68319 Human bon	817	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
745	6	0.8	33	4	ABW49983	Abw49983 Human liv	818	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
746	6	0.8	33	4	AAW03864	Aaw03864 Peptide #	819	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
747	6	0.8	33	5	ABW77069	Abw77069 Prostate	820	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
748	6	0.8	33	5	ABW37869	Abw37869 Human pep	821	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
749	6	0.8	33	8	ABO59958	Abos9958 Human gen	822	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
750	6	0.8	34	2	AAW45483	Aaw45483 Parathyro	823	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
751	6	0.8	34	2	AAW80175	Aaw80175 MiSP1-der	824	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
752	6	0.8	34	2	AAW69009	Aaw69009 PTH analo	825	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
753	6	0.8	34	2	AAW13300	Aaw13300 Truncated	826	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
754	6	0.8	34	2	AAW12179	Aaw12179 Parathyro	827	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
755	6	0.8	34	2	AAW61677	Aaw61677 Parathyro	828	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP

829	6	0.8	51	4	AAM76570	Aam76570 Human bon	902	6	0.8	60	5	ABJ10575	Abj10575 Galanin-1
830	6	0.8	51	4	AAM63756	Aam63756 Human bra	903	6	0.8	60	5	ABR44366	Abr44366 Rat antib
831	6	0.8	51	4	AM63058	Aam63058 Human bra	904	6	0.8	60	8	ADM97216	Adm97216 Rat galan
832	6	0.8	51	4	ABG58269	Abg58269 Human liv	905	6	0.8	60	8	ADO80860	Ado80860 Rat galan
833	6	0.8	51	4	ABG57603	Abg57603 Human liv	906	6	0.8	62	2	AAW26187	Aaw26187 Fragment
834	6	0.8	51	4	ABG90451	Abg90451 C glutami	907	6	0.8	62	4	AAU51462	Aau51462 Propionib
835	6	0.8	51	5	ABP02926	Abp02926 Human ORF	908	6	0.8	62	4	ABU15048	Abu15048 Human ner
836	6	0.8	51	5	ABG45818	Abg45818 Human pep	909	6	0.8	62	4	AU20999	Au20999 Human nov
837	6	0.8	52	3	AA826169	Aa826169 Rat GBX2	910	6	0.8	62	5	ABP09466	Abp09466 Human ORF
838	6	0.8	52	4	AAU86739	Aau86739 Novel hum	911	6	0.8	62	6	ABM47981	Abm47981 Propionib
839	6	0.8	52	4	AAU52328	Aau52328 Propionib	912	6	0.8	63	2	AAW26188	Aaw26188 Fragment
840	6	0.8	52	6	ABM48847	Abm48847 Propionib	913	6	0.8	63	2	AAW60203	Aaw60203 Human end
841	6	0.8	52	7	ADB60073	Adb60073 Connectiv	914	6	0.8	63	4	AAU17736	Aau17736 Novel hum
842	6	0.8	52	8	ABO59052	Abos9052 Human gen	915	6	0.8	63	4	AAW70726	Aaw70726 Human bon
843	6	0.8	53	7	ADF59117	Adf59117 Human pol	916	6	0.8	63	4	AAU66861	Aau66861 Propionib
844	6	0.8	53	7	AB334069	Abp334069 Human sec	917	6	0.8	63	4	AAU51025	Aau51025 Propionib
845	6	0.8	54	5	ABP08116	Abp08116 Human ORF	918	6	0.8	63	4	AAU51025	Aau51025 Propionib
846	6	0.8	55	4	AA80177	Aar80177 MiSP1-der	919	6	0.8	63	6	AAU51025	Aau51025 Propionib
847	6	0.8	55	4	ABM43693	Abm43693 Peptide #	920	6	0.8	63	6	ABM63380	Abm63380 Propionib
848	6	0.8	55	4	AA82838	Aam82838 Human imm	921	6	0.8	63	6	ABM47544	Abm47544 Propionib
849	6	0.8	55	4	AAU40171	Aau40171 Propionib	922	6	0.8	63	7	ADG41116	Adg41116 Human res
850	6	0.8	55	4	AAU52709	Aau52709 Propionib	923	6	0.8	63	7	ADI96890	Adi96890 Human res
851	6	0.8	55	4	ABG59065	Abg59065 Human liv	924	6	0.8	64	4	AAU21216	Aau21216 Human nov
852	6	0.8	55	4	ABM36690	Abm36690 Propionib	925	6	0.8	64	5	ABP11025	Abp11025 Human ORF
853	6	0.8	55	6	ABM49228	Abm49228 Propionib	926	6	0.8	65	3	ABP16790	Abp16790 Bacteriop
854	6	0.8	55	6	ABU56878	Abu56878 BONT/A Hc	927	6	0.8	65	3	ABG32555	Abg32555 Eucalyptu
855	6	0.8	55	6	ABU56877	Abu56877 BONT/A Hc	928	6	0.8	65	3	ABG32555	Abg32555 Zea may
856	6	0.8	56	2	AAW77572	Aaw77572 Staphyloc	929	6	0.8	65	4	ABM40266	Abm40266 Peptide #
857	6	0.8	56	3	AA833881	Aam33881 Human sec	930	6	0.8	65	4	ABM33947	Abm33947 Peptide #
858	6	0.8	56	4	ABM19289	Abm19289 Peptide #	931	6	0.8	65	4	ABM24683	Abm24683 Protein #
859	6	0.8	56	4	ABM38566	Abm38566 Peptide #	932	6	0.8	65	4	AAW73760	Aaw73760 Human bon
860	6	0.8	56	4	ABM32017	Abm32017 Peptide #	933	6	0.8	65	4	AAU57533	Aau57533 Propionib
861	6	0.8	56	4	ABM32694	Abm32694 Protein #	934	6	0.8	65	4	AAU54889	Aau54889 Propionib
862	6	0.8	56	4	AAW71725	Aaw71725 Human bon	935	6	0.8	65	4	AAU61425	Aau61425 Propionib
863	6	0.8	56	4	AAO10744	Aao10744 Human pol	936	6	0.8	65	4	ABG55505	Abg55505 Human bra
864	6	0.8	56	4	AAU59190	Aau59190 Human bra	937	6	0.8	65	4	ABG55505	Abg55505 Human liv
865	6	0.8	56	4	ABG53410	Abg53410 Human liv	938	6	0.8	65	5	ABP05332	Abp05332 Human pep
866	6	0.8	56	5	ABP10151	Abp10151 Human ORF	939	6	0.8	65	5	ABG43644	Abg43644 Human pep
867	6	0.8	56	5	ABG41539	Abg41539 Human pep	940	6	0.8	65	5	ABG66811	Abg66811 Human pro
868	6	0.8	57	2	AAI12580	Aai12580 Human 5'	941	6	0.8	65	6	ABM51408	Abm51408 Propionib
869	6	0.8	57	4	AAU63871	Aau63871 Propionib	942	6	0.8	65	6	ABM54052	Abm54052 Propionib
870	6	0.8	57	4	ABM32669	Abm32669 Peptide #	943	6	0.8	65	6	ABM57944	Abm57944 Propionib
871	6	0.8	57	4	ABM89887	Abm89887 Human imm	944	6	0.8	66	3	ABM12794	Abm12794 Clostridi
872	6	0.8	57	4	ABG47522	Abg47522 Human liv	945	6	0.8	66	3	ABM51481	Abm51481 Human sec
873	6	0.8	58	4	ABM5135	Abm5135 Rat physl	946	6	0.8	66	3	ABM51477	Abm51477 Human sec
874	6	0.8	58	4	AA899036	Aa899036 Human imm	947	6	0.8	66	4	AAO07490	Aao07490 Human pol
875	6	0.8	58	4	AAU63871	Aau63871 Propionib	948	6	0.8	66	4	AAU31514	Aau31514 Novel hum
876	6	0.8	58	4	ABG22198	Abg22198 Novel hum	949	6	0.8	66	6	ABG36900	Abg36900 Spider (P
877	6	0.8	58	2	AAW26186	Aaw26186 Fragment	950	6	0.8	66	6	ABG25158	Abg25158 Novel hum
878	6	0.8	59	4	ABM6390	Abm6390 Propionib	951	6	0.8	68	4	AAW91587	Aaw91587 Human imm
879	6	0.8	59	4	ABM6390	Abm6390 Propionib	952	6	0.8	68	5	ABP08088	Abp08088 Human ORF
880	6	0.8	59	4	ABM6390	Abm6390 Propionib	953	6	0.8	68	7	ABO81828	Abos1828 Pseudomon
881	6	0.8	59	4	ABM66647	Abm66647 Human bon	954	6	0.8	68	7	ABO64949	Abos64949 Klebsiell
882	6	0.8	59	4	AAO12589	Aao12589 Human pol	955	6	0.8	68	8	ADN99417	Adn99417 Novel hum
883	6	0.8	59	4	AAU55699	Aau55699 Propionib	956	6	0.8	68	8	ADF31694	Adf31694 Human sec
884	6	0.8	59	4	AAU54254	Aau54254 Human bra	957	6	0.8	69	2	AAU15052	Aau15052 N-terminu
885	6	0.8	59	6	ABM52218	Abm52218 Propionib	958	6	0.8	69	4	AAU43578	Aau43578 Propionib
886	6	0.8	60	2	AAU5924	Aau5924 Thermophi	959	6	0.8	69	4	AAU56797	Aau56797 Propionib
887	6	0.8	60	2	AAU45146	Aau45146 Rat ligan	960	6	0.8	69	4	AAU21518	Aau21518 Human nov
888	6	0.8	60	4	AAU16802	Aau16802 Peptide #	961	6	0.8	69	5	ABP08792	Abp08792 Human ORF
889	6	0.8	60	4	ABG5132	Abg5132 Rat physl	962	6	0.8	69	5	ABF04965	Abf04965 Human ORF
890	6	0.8	60	4	AAU74452	Aau74452 Human col	963	6	0.8	69	5	ABM53316	Abm53316 Propionib
891	6	0.8	60	4	ABM35785	Abm35785 Peptide #	964	6	0.8	69	6	ABM40097	Abm40097 Propionib
892	6	0.8	60	4	AAU29284	Aau29284 Peptide #	965	6	0.8	69	7	ADN88751	Adn88751 Ribosomal
893	6	0.8	60	4	ABM30620	Abm30620 Peptide #	966	6	0.8	69	8	ABO56109	Abos6109 Human gen
894	6	0.8	60	4	ABM21207	Abm21207 Protein.#	967	6	0.8	69	8	ADP30715	Adp30715 Human sec
895	6	0.8	60	4	AAU88973	Aau88973 Human bon	968	6	0.8	70	1	AAU70992	Aau70992 Sequence
896	6	0.8	60	4	AAU88973	Aau88973 Human bra	969	6	0.8	70	2	AAU92243	Aau92243 N-terminu
897	6	0.8	60	4	ABG50636	Abg50636 Human liv	970	6	0.8	70	5	ABP42746	Abp42746 Human ova
898	6	0.8	60	4	AAU04518	Aau04518 Peptide #	971	6	0.8	70	7	ADN88630	Adn88630 Ribosomal
899	6	0.8	60	5	ABG38561	Abg38561 Human pep	972	6	0.8	71	4	AAU21309	Aau21309 Peptide #
900	6	0.8	60	5	ABM76804	Abm76804 Rat GALP-	973	6	0.8	71	4	AAU91991	Aau91991 Human dig
901	6	0.8	60	5	AAU68222	Aau68222 Rat galan	974	6	0.8	71	4	ABM43642	Abm43642 Peptide #

975 6 0.8 71 4 AAM37537 Peptide #
 976 6 0.8 71 4 AAM38586 Human col
 977 6 0.8 71 4 AAM77385 Human bon
 978 6 0.8 71 4 AAO10378 Human pol
 979 6 0.8 71 4 AAU43958 Propionib
 980 6 0.8 71 4 AAM64586 Human bra
 981 6 0.8 71 4 ABG59013 Human liv
 982 6 0.8 71 5 ABG46399 Human pep
 983 6 0.8 71 5 ABG97638 Human col
 984 6 0.8 71 6 ABM40477 Propionib
 985 6 0.8 71 7 ABU39720 Protein e
 986 6 0.8 71 6 ADB92894 Human col
 987 6 0.8 71 7 ADC87840 Ribosomal
 988 6 0.8 72 2 AAW59265 Human Fan
 989 6 0.8 72 3 AAG35300 Zea mays
 990 6 0.8 72 4 AAM14285 Peptide #
 991 6 0.8 72 4 ABB33232 Peptide #
 992 6 0.8 72 4 AAM26695 Peptide #
 993 6 0.8 72 4 ABB28058 Human pep
 994 6 0.8 72 4 ABB18695 Protein #
 995 6 0.8 72 4 AAM66415 Human bon
 996 6 0.8 72 4 AAU48612 Propionib
 997 6 0.8 72 4 AAM54025 Human bra
 998 6 0.8 72 4 ABG48081 Human liv
 999 6 0.8 72 4 AAM02014 Peptide #
 1000 6 0.8 72 5 AAO22519 Small aci

ALIGNMENTS

RESULT 1
 AAY84947 ID AAY84947 standard; protein; 797 AA.
 AC AAY84947;
 XX
 XX 21-AUG-2000 (first entry)
 DT
 DE Amino acid sequence of outer membrane protein (omp) 85.
 XX
 XX Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
 KW meningococcal infection; protective immune response; vaccine.
 KW
 XX Neisseria meningitidis.
 OS
 XX
 XX W0200023595-A1.
 PN
 XX
 XX 27-APR-2000.
 PD
 XX
 XX 22-OCT-1998; 98WO-US022352.
 PF
 XX
 XX 22-OCT-1998; 98WO-US022352.
 PR
 XX
 XX (UTMO-) UNIV MONTANA.
 PA
 XX
 XX Judd RC, Manning SD;
 PI
 XX
 XX WPI; 2000-339694/29.
 DR
 XX
 XX N-PSDB; AAA15156.
 DR
 XX
 XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
 PT meningitidis useful for vaccine, therapeutic and diagnostic compositions
 PT for gonococcal or meningococcal infections.
 PT
 XX
 XX Claim 41; Page 89-92; 98pp; English.
 PS
 XX
 XX The present sequence represents an outer membrane protein (omp) 85 of
 CC Neisseria meningitidis. The omp polypeptides and polynucleotides are
 CC useful in compositions for use in the prevention, treatment and diagnosis
 CC of non-symptomatic gonococcal infection or meningococcal infection and
 CC symptomatic disease. They are also useful for the detection of
 CC hybridisation complexes. Antigens and antibodies specific omp proteins

CC also provide diagnostic, therapeutic and prophylactic compositions for
 CC the treatment or prevention of the infections described above. The
 CC antibodies are useful for inducing a protective immune response in humans
 CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
 CC species. The proteins, antibodies and polynucleotide sequences of the
 CC present invention may also be used in the screening and development of
 CC chemical compounds such as drugs or vaccines
 XX
 SQ Sequence 797 AA;
 Query Match 100.0%; Score 797; DB 3; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGILQRTPESTVFNYLPVKVGDYVNDTHGSA 60
 DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGILQRTPESTVFNYLPVKVGDYVNDTHGSA 60
 QY 61 IIKSLVATGFFDDVRVETADGQILLTVIERPTIGSLNITGAKMLQNDAIKONLESFGLAQ 120
 DB 61 IIKSLVATGFFDDVRVETADGQILLTVIERPTIGSLNITGAKMLQNDAIKONLESFGLAQ 120
 QY 121 SOYFNOATLNQAVAGLKEEVLGRGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITDIE 180
 DB 121 SOYFNOATLNQAVAGLKEEVLGRGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITDIE 180
 QY 181 FEGNQVYSRDKLMRQMSLTEGGIWTLTRSNQFNEQKFAQDMKVKTDFFYQNNGYFDFRIL 240
 DB 181 FEGNQVYSRDKLMRQMSLTEGGIWTLTRSNQFNEQKFAQDMKVKTDFFYQNNGYFDFRIL 240
 QY 241 DTDIQNEDKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGWTEROQ 300
 DB 241 DTDIQNEDKTKQTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGWTEROQ 300
 QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDFVLHIEPGRKIYNEIHTGNKKT 360
 DB 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDFVLHIEPGRKIYNEIHTGNKKT 360
 QY 361 RDEVVRRELQMESAPYDTSKLQSKERVVELLYGFDNVQFADAVPLAGTDPKVDLNMSLTE 420
 DB 361 RDEVVRRELQMESAPYDTSKLQSKERVVELLYGFDNVQFADAVPLAGTDPKVDLNMSLTE 420
 QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDTDPYFTA 480
 DB 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDTDPYFTA 480
 QY 481 DGVSLGYDYVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 DB 481 DGVSLGYDYVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPKHYADFIKKYKTDGTDGSPKGLYKGTGVMGRNKTDSALWPTTRGYLTGVNAEIA 600
 DB 541 YNKAPKHYADFIKKYKTDGTDGSPKGLYKGTGVMGRNKTDSALWPTTRGYLTGVNAEIA 600
 QY 601 LPGSKLQYYSATHNQTFWPFPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
 DB 601 LPGSKLQYYSATHNQTFWPFPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
 QY 661 GYESGTLGPKVYDVEYGEKLSYGNKKANYSAEILLFPMPCGAKDARTVRLSLFADAGSVWDG 720
 DB 661 GYESGTLGPKVYDVEYGEKLSYGNKKANYSAEILLFPMPCGAKDARTVRLSLFADAGSVWDG 720
 QY 721 KYDDNSSSATGGRVQNIYCAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
 DB 721 KYDDNSSSATGGRVQNIYCAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
 QY 781 KPDEIQRFQFQLGTTTF 797
 DB 781 KPDEIQRFQFQLGTTTF 797

RESULT 2
 ABB79802

ID ABB79802 standard; protein; 797 AA.
AC ABB79802;
XX
XX 15-NOV-2002 (first entry)
XX
XX Neisseria meningitidis outer membrane protein Omp85.
XX
XX Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
XX antibacterial.
XX
XX Neisseria meningitidis.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX /label= Signal_peptide
XX Protein 22..797
XX /label= Mature_protein
XX
XX US2002086028-A1.
XX
XX 04-JUL-2002.
XX
XX 26-NOV-2001; 2001US-00994192.
XX
XX 22-OCT-1998; 98US-00177039.
XX
XX (JUDD/) JUDD R C.
XX (MANN/) MANNING D S.
XX
XX JUDD RC, Manning DS;
XX
XX WPI; 2002-642234/69.
XX
XX Novel immunogenic composition for vaccinating against meningococcal or
XX gonococcal infection, comprises Omp85 protein of Neisseria meningitidis
XX or Neisseria gonorrhoeae, or nucleic acid encoding the protein.
XX
XX Claim 13; Fig 5; 30pp; English.
XX
XX The present sequence is that of the Neisseria meningitidis strain HH
XX outer membrane protein 85 (Omp85), as predicted from a gene that was
XX obtained from a genomic DNA by PCR amplification using primers based on
XX the gonococcal omp85 gene. The meningococcal Omp85 protein is 95%
XX identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed
XX immunogenic compositions comprise N. meningitidis Omp85, its fragments,
XX fusion proteins including the Omp85, or nucleic acids encoding them,
XX which induce a protective immune response in a subject. The immunogenic
XX compositions may also include an antigen from a heterologous or
XX homologous pathogen, or a nucleic acid encoding it. They are used in a
XX claimed method of vaccinating a human or animal against non-symptomatic
XX meningococcal infection or symptomatic disease. A kit for diagnosing
XX infection with N. meningitidis comprising labelled Omp85 is also claimed.
XX The Omp85 polypeptides and polynucleotides are also useful in drug
XX screening and development
XX
XX Sequence 797 AA;
XX
XX Query Match 100.0%; Score 797; DB 5; Length 797;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 MKLQKIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFVYLPVKVGDTYNDTHGSA 60
XX
XX 1 MKLQKIASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFVYLPVKVGDTYNDTHGSA 60
XX
XX 61 IIKSLYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
XX
XX 61 IIKSLYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
XX
XX 121 SQVFNQATLQNAVAGLKEEYLGKLNQIQTPKVKTLARNRVDITIDITDEGKSAKITDIE 180
XX
XX 121 SQVFNQATLQNAVAGLKEEYLGKLNQIQTPKVKTLARNRVDITIDITDEGKSAKITDIE 180

QY 181 FEGNQVYSRDKLMRQMSLTGGIWTWLTTRSNQFNQKFAQDMKQVTDYQNNGYFDFRIL 240
DB 181 FEGNQVYSRDKLMRQMSLTGGIWTWLTTRSNQFNQKFAQDMKQVTDYQNNGYFDFRIL 240
QY 241 DTDIQTNEDKTKQTIKITVHEGGRFRWGVKISIEGDTNEVPKAELEKLLTWKPGKWYERQQ 300
DB 241 DTDIQTNEDKTKQTIKITVHEGGRFRWGVKISIEGDTNEVPKAELEKLLTWKPGKWYERQQ 300
QY 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELROMESAPYDTSKQRSKERVELLGYFDNVQFQDAVPLAGTPDKVDLNSLTE 420
DB 361 RDEVVRRELROMESAPYDTSKQRSKERVELLGYFDNVQFQDAVPLAGTPDKVDLNSLTE 420
QY 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFGTGCKSAALRASRSKTTTLNGSLSTFDTPYFTA 480
DB 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFGTGCKSAALRASRSKTTTLNGSLSTFDTPYFTA 480
QY 481 DGVSLGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKTKDTGDSFGKWLKYGTVGGRNKTDTSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKTKDTGDSFGKWLKYGTVGGRNKTDTSALWPTRGYLTGVNAEIA 600
QY 601 LPSGLQYYSATHNQTFWEPFLSKTFTMLGSGEYGIAGGYGRTEKEIPFFENFYGGGLGSVR 660
DB 601 LPSGLQYYSATHNQTFWEPFLSKTFTMLGSGEYGIAGGYGRTEKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYAGGAVTWLSPGLPKMFPRIAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYAGGAVTWLSPGLPKMFPRIAYPLKK 780
QY 781 KPEDEIQRFQFQLGTTTF 797
DB 781 KPEDEIQRFQFQLGTTTF 797
XX
XX RESULT 3
XX AAU03959
XX ID AAU03959 standard; protein; 797 AA.
XX
XX AC AAU03959;
XX
XX DT 23-OCT-2001 (first entry)
XX
XX DE Neisseria gonorrhoeae antigenic protein.
XX
XX Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
XX bacterial infection; baculovirus; yeast; Neisseria meningitidis.
XX
XX OS Neisseria gonorrhoeae.
XX
XX XX Key Location/Qualifiers
XX Peptide 1..21
XX /note= "Signal peptide"
XX Protein 22..797
XX /note= "Mature N. gonorrhoeae antigen"
XX
XX WO200138350-A2.
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WO-IB001851.
XX

PR 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 PA (CHIR-) CHIRON SPA.
 PA (STAT-) STATENS INST FOLKEHELSE.
 XX
 PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.
 DR N-PSDB; AAS07279.
 XX
 PT Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX
 PS Claim 1; Page 37-39; 92pp; English.
 XX
 CC The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.
 CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the
 CC pharynx, causing meningitis and, occasionally, septicaemia in the absence
 CC of meningitis. This antigenic protein is useful in the manufacture of a
 CC medicament for treating or preventing infection due to Neisseria
 CC bacteria, such as meningitis and septicaemia. It is also useful as a
 CC diagnostic reagent for detecting the presence of Neisseria bacteria or
 CC antibodies raised against Neisseria, and as a reagent for raising the
 CC antibodies. The Neisserial nucleotide sequences can be expressed in a
 CC variety of different expression systems, for example, mammalian cells,
 CC baculoviruses, plants, bacteria and yeast
 CC
 SQ Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPEPSTVFNFVLPVKVGTNDYTHGSAIIKSLYATGFFDVRVETAD 80
 Db 21 ADFTIQDIRVEGLQRTPEPSTVFNFVLPVKVGTNDYTHGSAIIKSLYATGFFDVRVETAD 80
 Qy 81 GOLLTVIERPTTGSNITGAKMLQNDIAIKNLESFGLAQSVFNOATLNOAVAGLKEEY 140
 Db 81 GOLLTVIERPTTGSNITGAKMLQNDIAIKNLESFGLAQSVFNOATLNOAVAGLKEEY 140
 Qy 141 LGRGKLNITQPKVKTLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
 Db 141 LGRGKLNITQPKVKTLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
 Qy 201 GGIWTWLTNRNQFNEQFAQDMKVTFYQNGVYDFPRILDTDIQTNEDTKTQIKITVH 260
 Db 201 GGIWTWLTNRNQFNEQFAQDMKVTFYQNGVYDFPRILDTDIQTNEDTKTQIKITVH 260
 Qy 261 EGGFRFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQTAVLGEIQNRMSAGYAYS 320
 Db 261 EGGFRFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQTAVLGEIQNRMSAGYAYS 320
 Qy 321 EISVQPLPNAETKTVDVFLVIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
 Db 321 EISVQPLPNAETKTVDVFLVIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
 Qy 381 KLQSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTRSTGSLDSAGVQDTGLVM 440
 Db 381 KLQSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTRSTGSLDSAGVQDTGLVM 440
 Qy 441 SAGVQDNLFCTGKSAALRASRTKTLNGSISFTDPTADGVSGLGYDVVKGKAFDPRKAS 500
 Db 441 SAGVQDNLFCTGKSAALRASRTKTLNGSISFTDPTADGVSGLGYDVVKGKAFDPRKAS 500
 Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFIKKYKGTG 560
 Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFIKKYKGTG 560
 Qy 561 TDGSFKWLYKGTVGWRNKTDTSALWTRGVLTCVNAEIALPGSKLOYYSATHNQTWFFP 620

Db 561 TDGSFKWLYKGTVGWRNKTDTSALWTRGVLTCVNAEIALPGSKLOYYSATHNQTWFFP 620
 Qy 621 LSKTFTMLGGEVGIAGGYGRTKETIPEFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
 Db 621 LSKTFTMLGGEVGIAGGYGRTKETIPEFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
 Qy 681 YGKNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
 Db 681 YGKNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
 Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
 Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

RESULT 4
 AAU03957
 ID AAU03957 standard; protein; 797 AA.
 XX
 AC AAU03957;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 XX Neisseria meningitidis serogroup B antigenic protein.
 XX
 XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein 22..797 /note= "Signal peptide"
 FT Binding-site 715..722 /note= "Mature N. meningitidis serogroup B antigen"
 FT /note= "ATP/GTP-binding site motif A (P-loop)"
 XX
 PN WO200138350-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 28-NOV-2000; 2000WO-IB001851.
 XX
 PR 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 XX
 XX (CHIR-) CHIRON SPA.
 PA (STAT-) STATENS INST FOLKEHELSE.
 XX
 PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.
 DR N-PSDB; AAS07277.
 XX
 XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX
 PS Claim 1; Fig 1; 92pp; English.
 XX
 CC The sequence represents a Neisseria meningitidis serogroup B 85 kDa
 CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
 CC meningitis and, occasionally, septicaemia in the absence of meningitis.
 CC This antigenic protein is useful in the manufacture of a medicament for
 CC treating or preventing infection due to Neisseria bacteria, such as
 CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
 CC detecting the presence of Neisseria bacteria or antibodies raised against
 CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
 CC nucleotide sequences can be expressed in a variety of different
 CC expression systems, for example, mammalian cells, baculoviruses, plants,
 CC bacteria and yeast
 XX

SQ Sequence 797 AA;
 Query Match 94.4%; Score 752; DB 4; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	21	ADPTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
DB	21	ADPTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
QY	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSOYFNQATLNOAVAGLKEEY	140
DB	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSOYFNQATLNOAVAGLKEEY	140
QY	141	LGRGKLNIIQITPKVTKLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE	200
DB	141	LGRGKLNIIQITPKVTKLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE	200
QY	201	GGIWTWLTSSNQFNEQKFAQDMKEKVTDFYQNGGYDFRILDTDIQTNEDEKTKQITKIVH	260
DB	201	GGIWTWLTSSNQFNEQKFAQDMKEKVTDFYQNGGYDFRILDTDIQTNEDEKTKQITKIVH	260
QY	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQOMTAVLGEIQNRMGSAAYYS	320
DB	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQOMTAVLGEIQNRMGSAAYYS	320
QY	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS	380
DB	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS	380
QY	381	KLQSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
DB	381	KLQSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
QY	441	SAGVSODNLFQGTGKSAALRASRSKTTLNGSLSPDTPYTAGVSLGVDYVYKAPDPRKAS	500
DB	441	SAGVSODNLFQGTGKSAALRASRSKTTLNGSLSPDTPYTAGVSLGVDYVYKAPDPRKAS	500
QY	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTWNTYNKAPKHVADFIKKYKGTG	560
DB	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTWNTYNKAPKHVADFIKKYKGTG	560
QY	561	TGSPFGWLYKGTGVGWRNKTDLSALWPRGYLTGVNABIALPGSKLQYYSATHNQWTFPP	620
DB	561	TGSPFGWLYKGTGVGWRNKTDLSALWPRGYLTGVNABIALPGSKLQYYSATHNQWTFPP	620
QY	621	LSKFTPLMLGGVGTAGGVRKTEIPFENFVGGLGSVRGYESGTGPKVYDEYGEKIS	680
DB	621	LSKFTPLMLGGVGTAGGVRKTEIPFENFVGGLGSVRGYESGTGPKVYDEYGEKIS	680
QY	681	YGGNKANVSABLLPMPGAKDARVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYG	740
DB	681	YGGNKANVSABLLPMPGAKDARVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYG	740
QY	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772
DB	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772

RESULT 5
 AAU04451
 ID AAU04451 standard; protein; 797 AA.
 XX AC AAU04451;
 XX DT 23-OCT-2001 (first entry)
 XX DE Neisseria meningitidis serogroup A antigenic protein #2.
 XX KW Serogroup B antigen; pharynx; meningitis; septicemia; mammalian cell;
 XX BW bacterial infection; baculovirus; yeast.
 XX QS Neisseria meningitidis.

Key Peptide 1..21
 Location/Qualifiers
 /note= "Signal peptide"
 Protein 22..797
 /note= "Mature N. meningitidis serogroup A antigen"
 WO200138350-A2.
 31-MAY-2001.
 28-NOV-2000; 2000WO-IB001951.
 29-NOV-1999; 99GB-00028197.
 09-MAR-2000; 2000GB-00005698.
 (CHIR-) CHIRON SPA.
 (STAT-) STATENS INST FOLKEHELSE.
 Giuliani MM, Pizza M, Rappuoli R, Holst J;
 WPI; 2001-381289/40.
 Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection.
 Claim 1; Page 39-40; 92pp; English.
 The sequence represents a Neisseria meningitidis serogroup A 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants, bacteria and yeast. Note: There are two versions of this sequence displayed in the specification (see AAU03958)

Query Match 94.4%; Score 752; DB 4; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	21	ADPTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
DB	21	ADPTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
QY	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSOYFNQATLNOAVAGLKEEY	140
DB	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQSOYFNQATLNOAVAGLKEEY	140
QY	141	LGRGKLNIIQITPKVTKLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE	200
DB	141	LGRGKLNIIQITPKVTKLARNRVDIITIDEGKSAKITDIEFEGNQVYSDRKLQMSLSTE	200
QY	201	GGIWTWLTSSNQFNEQKFAQDMKEKVTDFYQNGGYDFRILDTDIQTNEDEKTKQITKIVH	260
DB	201	GGIWTWLTSSNQFNEQKFAQDMKEKVTDFYQNGGYDFRILDTDIQTNEDEKTKQITKIVH	260
QY	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQOMTAVLGEIQNRMGSAAYYS	320
DB	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGKWERQOMTAVLGEIQNRMGSAAYYS	320
QY	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS	380
DB	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS	380
QY	381	KLQSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
DB	381	KLQSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
QY	441	SAGVSODNLFQGTGKSAALRASRSKTTLNGSLSPDTPYTAGVSLGVDYVYKAPDPRKAS	500
DB	441	SAGVSODNLFQGTGKSAALRASRSKTTLNGSLSPDTPYTAGVSLGVDYVYKAPDPRKAS	500
QY	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTWNTYNKAPKHVADFIKKYKGTG	560
DB	501	TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTWNTYNKAPKHVADFIKKYKGTG	560
QY	561	TGSP	

RESULT 5

AAU04451

TD AALL

XX

AC
AAU

XX

DT 23-

XX

DE **Nei**

KW Ser

KW bac

XX

OS Nei

Db 381 KQSKERVLLGYFDNVQFVDAVFLAGTDPKVDLNNLSLTERSTGSLDSAGWQDITGLVM 440
Qy 441 SAGVSQDNLFGTGSAAALRASRSKTTILNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500
Db 441 SAGVSQDNLFGTGSAAALRASRSKTTILNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFICKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFICKYKGTG 560
Qy 561 TDGSFKWLYKGTGCGRNKTDLSALWTRGVLTVGNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSFKWLYKGTGCGRNKTDLSALWTRGVLTVGNAEIALPGSKLOYYSATHNQWTFPP 620
Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYSGTLPKVDYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYSGTLPKVDYDEYGEKIS 680
Qy 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIY 740
Db 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIY 740
Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 6

AAB23788
ID AAB23788 standard; protein; 797 AA.

AC AAB23788;

XX 12-JAN-2001 (first entry)

DE Neisseria meningitidis serogroup A amino acid sequence.

XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.

XX Neisseria meningitidis.

XX WO2000050075-A2.

XX 31-AUG-2000.

XX 09-FEB-2000; 2000WO-IB000176.

XX 26-FEB-1999; 99US-0121792P.

XX (CHIR-) CHIRON SPA.

XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;

XX WPI; 2001-015529/02.

XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.

XX Claim 22; Page 33; 39pp; English.

XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response

CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup A amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention

XX SQ Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADPTIQDIRVEGIQRTPESTVFVNYLPVKVGDYVNDTHGSAIKSLYATGFFDDVRVETAD 80

Db 21 ADPTIQDIRVEGIQRTPESTVFVNYLPVKVGDYVNDTHGSAIKSLYATGFFDDVRVETAD 80

Qy 81 GQLLLTVIERPTIGSINITGAKMLQNDAIKKNLSEFLAQSOYFNQATLNQAVAGLKEEY 140

Db 81 GQLLLTVIERPTIGSINITGAKMLQNDAIKKNLSEFLAQSOYFNQATLNQAVAGLKEEY 140

Qy 141 LGRGKLNIOITPKVTKLARNVDIDITIDEGSAKITDIEFEGNOVYSRDKLMRQSLTE 200

Db 141 LGRGKLNIOITPKVTKLARNVDIDITIDEGSAKITDIEFEGNOVYSRDKLMRQSLTE 200

Qy 201 GGIWTWLTNRSNQFNEQFAQDMKVDFYQNNGYFDFRILDTDIQTNEOKTKQIKITVH 260

Db 201 GGIWTWLTNRSNQFNEQFAQDMKVDFYQNNGYFDFRILDTDIQTNEOKTKQIKITVH 260

Qy 261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKWTYERQOMTAVLGEIQNRMGSAAYYS 320

Db 261 EGGFRFWGKVSIEGDTNEVPKAELEKLLTMKPGKWTYERQOMTAVLGEIQNRMGSAAYYS 320

Qy 321 EISVQPLPNAETKTVDVFLHIIEPRKIYVNEIHTGNNTKTRDEVVRELRQMESAPYDTS 380

Db 321 EISVQPLPNAETKTVDVFLHIIEPRKIYVNEIHTGNNTKTRDEVVRELRQMESAPYDTS 380

Qy 381 KLQSKERVVLLGYFDNVQFVDAVFLAGTDPKVDLNNLSLTERSTGSLDSAGWQDITGLVM 440

Db 381 KLQSKERVVLLGYFDNVQFVDAVFLAGTDPKVDLNNLSLTERSTGSLDSAGWQDITGLVM 440

Qy 441 SAGVSQDNLFGTGSAAALRASRSKTTILNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500

Db 441 SAGVSQDNLFGTGSAAALRASRSKTTILNGSLSFDPYFTADGVSGLGYDVYKGFADPRKAS 500

Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFICKYKGTG 560

Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFICKYKGTG 560

Qy 561 TDGSFKWLYKGTGCGRNKTDLSALWTRGVLTVGNAEIALPGSKLOYYSATHNQWTFPP 620

Db 561 TDGSFKWLYKGTGCGRNKTDLSALWTRGVLTVGNAEIALPGSKLOYYSATHNQWTFPP 620

Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYSGTLPKVDYDEYGEKIS 680

Db 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYSGTLPKVDYDEYGEKIS 680

Qy 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIY 740

Db 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIY 740

Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 7

AAB23784
ID AAB23784 standard; protein; 797 AA.

XX AAB23784;

XX 12-JAN-2001 (first entry)

XX Neisseria meningitidis serogroup B amino acid sequence.

XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;

KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;

KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;

KW immune response.

XX Neisseria meningitidis.

XX WO2000050075-A2.

PN 31-AUG-2000.

XX 09-FEB-2000; 2000WO-IB000176.

PF 26-FEB-1999; 99US-0121792P.

XX (CHIR-) CHIRON SPA.

XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;

PI WPI; 2001-015529/02.

DR Immunogenic composition useful for stimulating an immune response in a

XX mammal against Neisseria infection, comprises Neisseria antigen and an

PT adjuvant composition comprising an oligonucleotide with a CG motif.

PT Claim 22; Page 32; 39pp; English.

XX The present invention describes an immunogenic composition (I) comprising

CC a Neisseria antigen and an adjuvant composition comprising an

CC oligonucleotide comprising at least 1 CG motif. Also described is an

CC adjuvant composition (II) comprising an oligonucleotide which comprises

CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the

CC oligonucleotide preferably comprises at least one phosphorothioate bond.

CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of

CC the present invention. (I) is useful for stimulating an immune response

CC in a mammal, preferably a human, against Neisseria infection, preferably

CC Neisseria meningitidis infection and in the manufacture of a medicament

CC for inducing a protective immune response in a mammal. The present

CC sequence represents the claimed Neisseria meningitidis serogroup B amino

CC acid sequence disclosed in GB-9928197.4, which is given in the present

CC invention

XX Query Match 94.4%; Score 752; DB 4; Length 797;

XX Best Local Similarity 100.0%; Pred. No. 0;

XX Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPEFTVFNYPVKVGTNDTHGSAIIKSLYATGFFDDVRVETAD 80

Db 21 ADFTIQDIRVEGLQRTPEFTVFNYPVKVGTNDTHGSAIIKSLYATGFFDDVRVETAD 80

Qy 81 GOLLTVIERPTTGSNLITGAKMLQNDIAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140

Db 81 GOLLTVIERPTTGSNLITGAKMLQNDIAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140

Qy 141 LGRGLKNIQTTPKVTKLARNVDITDITDEGSAKITDIEFEGNOVYSDRKLQMSLTE 200

Db 141 LGRGLKNIQTTPKVTKLARNVDITDITDEGSAKITDIEFEGNOVYSDRKLQMSLTE 200

Qy 201 GGIWTWLTNRSNQFNEQFAQDMKRVTDYQNGGYFDFRILDTDITQTNEDKTKQITKIVH 260

Db 201 GGIWTWLTNRSNQFNEQFAQDMKRVTDYQNGGYFDFRILDTDITQTNEDKTKQITKIVH 260

Qy 261 EGGFRFGKVSIEGDTNEVPKAELEKLLTKMPGKWERQQTAVLGIQNRMSGAGVAYS 320

Db 261 EGGFRFGKVSIEGDTNEVPKAELEKLLTKMPGKWERQQTAVLGIQNRMSGAGVAYS 320

Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380

Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380

Qy 381 KLQRSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVQDTGLYM 440

Db 381 KLQRSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVQDTGLYM 440

Qy 441 SAGVSQDNLFQGTGSAALRASRKTTLNGSLSTFDYFTADGVSIGYDVYVKAFDPRKAS 500

Db 441 SAGVSQDNLFQGTGSAALRASRKTTLNGSLSTFDYFTADGVSIGYDVYVKAFDPRKAS 500

Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNNKAPKHADFIKKYKTDG 560

Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNNKAPKHADFIKKYKTDG 560

Qy 561 TDGSPFKGWLKGTGVRGNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620

Db 561 TDGSPFKGWLKGTGVRGNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620

Qy 621 LSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSRGYESGTLGPKVYDEYGEKIS 680

Db 621 LSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSRGYESGTLGPKVYDEYGEKIS 680

Qy 681 YGNNKKANVSARELLPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIY 740

Db 681 YGNNKKANVSARELLPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIY 740

Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

RESULT 8

AAB84746

ID AAB84746 standard; protein; 797 AA.

XX AAB84746;

XX 17-SEP-2001 (first entry)

XX Amino acid sequence of a Neisseria serogroup A protein.

DE Serogroup A protein; outer membrane protein; Neisserial infection;

KW vaccine.

XX Neisseria meningitidis.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "signal peptide"

FT /note= "mature protein"

XX WO200152885-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-IB000166.

XX 17-JAN-2000; 2000GB-00001067.

PR 09-MAR-2000; 2000GB-00005699.

XX (CHIR-) CHIRON SPA.

XX Pizza M, Rappuoli R, Giuliani M;

XX WPI; 2001-451895/48.

DR N-PSDB; AA42130.

XX Composition for treating or preventing infection to, detecting, or for

PT raising antibodies against Neisserial bacteria, comprises an N.

PT meningitidis serogroup B outer membrane preparation and an immunogenic

PT component.

XX

PS Disclosure; Page 71-74; 83pp; English.

XX The present sequence represents a Neisseria serogroup A protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisserial
CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria; or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX
SQ Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||
Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
Db |||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
Db |||||
Qy 141 LGRGKLNQITPQVTKLARNVDIDITDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
Db |||||
Qy 141 LGRGKLNQITPQVTKLARNVDIDITDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
Db |||||
Qy 201 GGIWTLTRSNORNEQFAQDMEKVTDFYQNGVYDFRILDTDIOTNEDTKTQIKITVH 260
Db |||||
Qy 201 GGIWTLTRSNORNEQFAQDMEKVTDFYQNGVYDFRILDTDIOTNEDTKTQIKITVH 260
Db |||||
Qy 261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOQMTAVLGIQNRMSAGVAYS 320
Db |||||
Qy 261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOQMTAVLGIQNRMSAGVAYS 320
Db |||||
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKNKTRDEVVRRELQMESAPYDTS 380
Db |||||
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKNKTRDEVVRRELQMESAPYDTS 380
Db |||||
Qy 381 KLQSKSERVELLYGFDNVQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVDQTLVM 440
Db |||||
Qy 381 KLQSKSERVELLYGFDNVQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVDQTLVM 440
Db |||||
Qy 441 SAGVSQDNLFGTKSAALRASRSKTTLLNGSLSFPTDYPFTADGVSIGYDVYVGKAFDPRKAS 500
Db |||||
Qy 441 SAGVSQDNLFGTKSAALRASRSKTTLLNGSLSFPTDYPFTADGVSIGYDVYVGKAFDPRKAS 500
Db |||||
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNAKPHYAFIKKYGKTDG 560
Db |||||
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNAKPHYAFIKKYGKTDG 560
Db |||||
Qy 561 TDGSKFGLYKVTGWGRNKTDLSALWPTRGVLTGVNAEIALPGSKLOYYSATHNQTFWFF 620
Db |||||
Qy 561 TDGSKFGLYKVTGWGRNKTDLSALWPTRGVLTGVNAEIALPGSKLOYYSATHNQTFWFF 620
Db |||||
Qy 621 LSKTFTLLMGEVGIAGYGRKTEIPEFFENFYGGGLSGVRGYSGLTGPVKVYDEYGEKIS 680
Db |||||
Qy 621 LSKTFTLLMGEVGIAGYGRKTEIPEFFENFYGGGLSGVRGYSGLTGPVKVYDEYGEKIS 680
Db |||||
Qy 681 YGKNKANVASLELLFPMGAKADARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
Db |||||
Qy 681 YGKNKANVASLELLFPMGAKADARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
Db |||||
Qy 741 AGNTHKSTFTNEURYSGAGVATWLSPLGPMKF 772
Db |||||
Qy 741 AGNTHKSTFTNEURYSGAGVATWLSPLGPMKF 772
Db |||||

RESULT 9
AAB84744
ID AAB84744 standard; protein; 797 AA.
XX
AC AAB84744;
XX
DT 17-SBP-2001 (first entry)
XX
DE Amino acid sequence of a Neisseria serogroup B protein.
XX
KW Serogroup B protein; outer membrane protein; Neisserial infection;
XX vaccine.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
FT Protein 22..797
FT Protein /note= "mature protein"
XX
PN WO200152885-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-IB000166.
XX
PR 17-JAN-2000; 2000GB-00001067.
XX
PR 09-MAR-2000; 2000GB-00005699.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Pizza M, Rappuoli R, Giuliani M;
XX
DR WPI; 2001-451895/48.
DR N-PSDB; AA442128.
XX
PT Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisserial bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX
PS Disclosure; Page 59-61; 83pp; English.
XX
CC The present sequence represents a Neisseria serogroup B protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisserial
CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria; or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX
SQ Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||
Qy 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
Db |||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
Db |||||

141 LGRGKLNIOITPKVTKLARNRVDIDITIDEKSAKITDIEPEGNOVYSDRKLMEQMSLTE 200
141 LGRGKLNIOITPKVTKLARNRVDIDITIDEKSAKITDIEPEGNOVYSDRKLMEQMSLTE 200
201 GGIWTLTRSNQFNEQKFAQDMEKVTDFYQNNGYDFRILDTDIQTNEDEKTKQIKITVH 260
201 GGIWTLTRSNQFNEQKFAQDMEKVTDFYQNNGYDFRILDTDIQTNEDEKTKQIKITVH 260
261 EGGFRGKVSIEGDTNEVPKAELEKLLTMKPGWYERQQTAVLGIQNRMGSAQVAYS 320
261 EGGFRGKVSIEGDTNEVPKAELEKLLTMKPGWYERQQTAVLGIQNRMGSAQVAYS 320
321 EISVQPLPNAETKTVDVFLHTEPGRKLYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380
321 EISVQPLPNAETKTVDVFLHTEPGRKLYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380
381 KLQSKERVVELLYGFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
381 KLQSKERVVELLYGFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
441 SAGVSQNLFGTGSAALRASRSKTTNLGSLSFDPYFTADGVSGLGYDVYKGFAPDKPKAS 500
441 SAGVSQNLFGTGSAALRASRSKTTNLGSLSFDPYFTADGVSGLGYDVYKGFAPDKPKAS 500
501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNEGLVAEHLTVNTYKAPKHVADFIKKYKGTG 560
501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNEGLVAEHLTVNTYKAPKHVADFIKKYKGTG 560
561 TDGSKFGLYKGTGWRGNKTDLSALWTRGYLTGVNAEIALPGSKLOYYSATHNQTWFFP 620
561 TDGSKFGLYKGTGWRGNKTDLSALWTRGYLTGVNAEIALPGSKLOYYSATHNQTWFFP 620
621 LSKTFTLMLGGEVGIAGGYRTKEIPFFENFYGGGLSVRGYESTGLGPKVYDEYGEKIS 680
621 LSKTFTLMLGGEVGIAGGYRTKEIPFFENFYGGGLSVRGYESTGLGPKVYDEYGEKIS 680
681 YGNKKANVAEALLFPMPGAKDARTVLSLFPADAGSVWDGKTYDDNSSATGGRVQNIY 740
681 YGNKKANVAEALLFPMPGAKDARTVLSLFPADAGSVWDGKTYDDNSSATGGRVQNIY 740
741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

RESULT 10
AAU03958
ID AAU03958 standard; protein; 792 AA.
AC AAU03958;
XX
XX 23-OCT-2001 (first entry)
XX
XX Neisseria meningitidis serogroup A antigenic protein #1.
XX
XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.
XX
XX Neisseria meningitidis.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /note= "Signal peptide"
FT Protein 22..792
FT /note= "Mature N. meningitidis serogroup A antigen"
XX
PN WO200138350-A2.
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WO-IB001851.
XX

29-NOV-1999; 99GB-00028197.
09-MAR-2000; 2000GB-00005698.
(CHIR-) CHIRON SPA.
(STAT-) STATENS INST FOLKEHELSE.
Giuliani MM, Pizza M, Rappuoli R, Holst J;
WPI; 2001-381289/40.
N-PSDB; AAS07278.
Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection.
Claim 1; Page 66-68; 92pp; English.
The sequence represents a Neisseria meningitidis serogroup A 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants, bacteria and yeast. Note: There are two versions of this sequence displayed in the specification (see AAU04451)
Query Match 26.3%; Score 210; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 3.3e-201;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLKQITASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNLPVKVGDTYNDTHGSA 60
Db 1 MKLKQITASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNLPVKVGDTYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 FEGNQVYSRDKLRQMSLTGGIWTWLTSS 210
Db 181 FEGNQVYSRDKLRQMSLTGGIWTWLTSS 210
RESULT 11
AAB23786
ID AAB23786 standard; protein; 792 AA.
XX
XX AAB23786;
XX
XX 11-SEP-2003 (revised)
DT 12-JAN-2001 (first entry)
XX
XX Neisseria gonorrhoeae amino acid sequence.
XX
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
XX immune response.
XX
XX Neisseria gonorrhoeae.
XX
XX WO200050075-A2.
XX

PD 31-AUG-2000.
 XX
 PF 09-FEB-2000; 2000WO-IB000176.
 XX
 PR 26-FEB-1999; 99US-0121792P.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
 XX
 XX WPI; 2001-015529/02.
 DR
 XX
 XX Immunogenic composition useful for stimulating an immune response in a
 PT mammal against Neisseria infection, comprises Neisseria antigen and an
 PT adjuvant composition comprising an oligonucleotide with a CG motif.
 XX
 XX Claim 22; Page 32; 39pp; English.
 PS
 XX The present invention describes an immunogenic composition (I) comprising
 CC a Neisseria antigen and an adjuvant composition comprising an
 CC oligonucleotide comprising at least 1 CG motif. Also described is an
 CC adjuvant composition (II) comprising an oligonucleotide which comprises
 CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
 CC oligonucleotide preferably comprises at least one phosphorothioate bond.
 CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
 CC the present invention. (I) is useful for stimulating an immune response
 CC in a mammal, preferably a human, against Neisseria infection, preferably
 CC Neisseria meningitidis infection and in the manufacture of a medicament
 CC for inducing a protective immune response in a mammal. The present
 CC sequence represents the claimed Neisseria gonorrhoeae amino acid sequence
 CC disclosed in GB-9928197.4, which is given in the present invention.
 CC (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 4; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNQVYSDRKLMRQMSLTGGIWTWLTTRS 210
 DB 181 FEGNQVYSDRKLMRQMSLTGGIWTWLTTRS 210
 RESULT 12
 AAB84745
 ID AAB84745 standard; protein; 792 AA.
 XX
 AC AAB84745;
 AC
 XX
 DT 11-SEP-2003 (revised)
 DT 17-SEP-2001 (first entry)
 XX
 DE Amino acid sequence of a Neisseria gonorrhoeae protein.
 XX
 KW Serogroup B protein; outer membrane protein; Neisseria infection;
 KW vaccine.
 XX
 OS Neisseria gonorrhoeae.
 XX
 XX Key Location/Qualifiers
 FH

FT Peptide 1..21
 FT /note= "signal peptide"
 FT Protein 22..792
 FT /note= "mature protein"
 XX
 XX WO200152885-A1.
 DN
 XX 26-JUL-2001.
 PD
 XX 17-JAN-2001; 2001WO-IB000166.
 XX
 XX 17-JAN-2000; 2000GB-00001067.
 PR 09-MAR-2000; 2000GB-00005699.
 XX
 XX (CHIR-) CHIRON SPA.
 PA
 XX Pizza M, Rappuoli R, Giuliani M;
 PI
 XX WPI; 2001-451895/48.
 DR N-PSDB; AAH42129.
 CC Composition for treating or preventing infection to, detecting, or for
 CC raising antibodies against Neisseria bacteria, comprises an N.
 CC meningitidis serogroup B outer membrane preparation and an immunogenic
 CC component.
 PT
 XX Disclosure; Page 65-67; 83pp; English.
 PS
 XX The present sequence represents a Neisseria gonorrhoeae protein. The
 CC protein is used to produce the compositions of the invention. The
 CC specification describes a composition, comprising a Neisseria
 CC meningitidis serogroup B outer membrane preparation and an immunogenic
 CC component. The immunogenic component is protein disclosed in WO99/57280,
 CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
 CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
 CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
 CC medicament for treating or preventing infection due to Neisseria
 CC bacteria; a diagnostic reagent for detecting the presence of Neisseria
 CC bacteria or of antibodies raised against Neisseria bacteria; and/or a
 CC reagent which can raise antibodies against Neisseria bacteria. It may
 CC also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 4; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNQVYSDRKLMRQMSLTGGIWTWLTTRS 210
 DB 181 FEGNQVYSDRKLMRQMSLTGGIWTWLTTRS 210
 RESULT 13
 AAB80499
 ID AAB80499 standard; protein; 792 AA.
 XX
 AC AAB80499;
 AC
 XX
 DT 07-MAR-2003 (first entry)
 DT

XX DE N. gonorrhoeae amino acid sequence SEQ ID 7528.
 XX KW Antibacterial; infection; vaccine; gene therapy.
 XX OS Neisseria gonorrhoeae.
 XX PN WO200279243-A2.
 XX PD 10-OCT-2002.
 XX PF 12-FEB-2002; 2002WO-IB002069.
 XX PR 12-FEB-2001; 2001GB-00003424.
 XX PA (CHIR-) CHIRON SPA.
 XX PI Fontana MR, Pizza M, Massignani V, Monaci E;
 XX DR WPI; 2003-058415/05.
 XX DR N-PSDB; ABZ41469.
 XX PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 XX PT medicament for treating or preventing N. gonorrhoeae infection.
 XX PS Disclosure; Page 736; 815pp; English.
 XX CC The present invention relates to proteins from Neisseria gonorrhoeae.
 XX CC Also disclosed are the nucleic acid molecules encoding the proteins and
 XX CC antibodies that specifically bind to the proteins. The composition
 XX CC comprising the protein, nucleic acid or antibody is useful for the
 XX CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 XX CC infection, this may be in the form of a vaccine or gene therapy.
 XX CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 XX CC molecules of the invention
 XX SQ Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 6; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 DB 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNOVYSDRKLQMSLTGGIWTWLTTRS 210
 DB 181 FEGNOVYSDRKLQMSLTGGIWTWLTTRS 210
 RESULT 14
 ID ABP79748
 AC ABP79748;
 AC ABP79748;
 DT 07-MAR-2003 (first entry)
 DE N. gonorrhoeae amino acid sequence SEQ ID 6026.
 KW Antibacterial; infection; vaccine; gene therapy.
 OS Neisseria gonorrhoeae.

PN WO200279243-A2.
 XX 10-OCT-2002.
 XX 12-FEB-2002; 2002WO-IB002069.
 XX 12-FEB-2001; 2001GB-00003424.
 XX (CHIR-) CHIRON SPA.
 XX Fontana MR, Pizza M, Massignani V, Monaci E;
 XX WPI; 2003-058415/05.
 XX N-PSDB; ABZ40718.
 XX PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 XX PT medicament for treating or preventing N. gonorrhoeae infection.
 XX PS Disclosure; Page 628; 815pp; English.
 XX CC The present invention relates to proteins from Neisseria gonorrhoeae.
 XX CC Also disclosed are the nucleic acid molecules encoding the proteins and
 XX CC antibodies that specifically bind to the proteins. The composition
 XX CC comprising the protein, nucleic acid or antibody is useful for the
 XX CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 XX CC infection, this may be in the form of a vaccine or gene therapy.
 XX CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 XX CC molecules of the invention
 XX SQ Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 6; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 DB 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNOVYSDRKLQMSLTGGIWTWLTTRS 210
 DB 181 FEGNOVYSDRKLQMSLTGGIWTWLTTRS 210
 RESULT 15
 ID AAY84946
 ID AAY84946 standard; protein; 792 AA.
 AC AAY84946;
 AC AAY84946;
 DT 12-SEP-2003 (revised)
 DT 21-AUG-2000 (first entry)
 DE Amino acid sequence of outer membrane protein (omp) 85.
 DE Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
 KW meningococcal infection; protective immune response; vaccine.
 XX Neisseria gonorrhoeae.
 XX Key Location/Qualifiers
 XX Peptide 1..21
 XX /note= "signal peptide"
 XX WO200023595-A1.

XX 27-APR-2000.
XX PD
XX PF 22-OCT-1998; 98WO-US022352.
XX PR 22-OCT-1998; 98WO-US022352.
XX PA (UYMO-) UNIV MONTANA.
XX PI Judd RC, Manning SD;
XX WPI; 2000-339694/29.
XX N-PSDB; AAA15155.
XX
XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
XX meningitidis useful for vaccine, therapeutic and diagnostic compositions
XX for gonococcal or meningococcal infections.
XX
XX Claim 1; Fig 2; 98pp; English.
XX
XX The present sequence represents an outer membrane protein (omp) 85 of
XX Neisseria gonorrhoeae. The omp polypeptides and polynucleotides are
XX useful in compositions for use in the prevention, treatment and diagnosis
XX of non-symptomatic gonococcal infection or meningococcal infection and
XX symptomatic disease. They are also useful for the detection of
XX hybridisation complexes. Antigens and antibodies specific omp proteins
XX also provide diagnostic, therapeutic and prophylactic compositions for
XX the treatment or prevention of the infections described above. The
XX antibodies are useful for inducing a protective immune response in humans
XX or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
XX species. The proteins, antibodies and polynucleotide sequences of the
XX present invention may also be used in the screening and development of
XX chemical compounds such as drugs or vaccines. (Updated on 12-SEP-2003 to
XX standardise OS field)
XX
SQ Sequence 792 AA;

Query Match 19.7%; Score 157; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 5.4e-148;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSKLQSKERVEL 391
Db |||||
332 TKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTSKLQSKERVEL 391
Qy 392 LGYFDNVQFDAPVPLAGTPDKVDLNMSLTERSTGSLDLSAGWVQDTGLVMSAGVSQDNLFG 451
Db |||||
392 LGYFDNVQFDAPVPLAGTPDKVDLNMSLTERSTGSLDLSAGWVQDTGLVMSAGVSQDNLFG 451
Qy 452 TGKSAALRASRSKTTLNGSLSFDTDPYFTADGVSLGYD 488
Db |||||
452 TGKSAALRASRSKTTLNGSLSFDTDPYFTADGVSLGYD 488

Search completed: July 6, 2005, 15:47:37
Job time : 210 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:44:30 ; Search time 162 Seconds

(without alignments)

1898.018 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLGISPLAF.....LKKKPEDEIQRFQQLGTTTF 757

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1722976 seqs, 385795295 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	9	US-09-994-192-4
2	797	100.0	797	17	US-10-606-618-4
3	752	94.4	797	14	US-10-181-660-3
4	752	94.4	797	14	US-10-181-660-11
5	752	94.4	797	15	US-10-320-800-6
6	752	94.4	797	16	US-10-181-600-3
7	752	94.4	797	16	US-10-181-600-11
8	751	94.2	776	14	US-10-181-660-5
9	751	94.2	776	14	US-10-181-660-13
10	751	94.2	776	16	US-10-181-600-5
11	751	94.2	776	16	US-10-181-600-13

792	14	US-10-181-660-7	Sequence 7, Appli
792	16	US-10-181-600-7	Sequence 7, Appli
771	14	US-10-181-660-9	Sequence 9, Appli
771	16	US-10-181-600-9	Sequence 9, Appli
792	9	US-09-994-192-2	Sequence 2, Appli
792	16	US-10-467-534-92	Sequence 92, Appli
792	17	US-10-606-618-2	Sequence 2, Appli
792	14	US-10-181-660-8	Sequence 8, Appli
21	16	US-10-181-600-8	Sequence 8, Appli
21	14	US-10-181-660-4	Sequence 4, Appli
21	16	US-10-181-600-4	Sequence 4, Appli
15	14	US-10-181-660-1	Sequence 1, Appli
15	16	US-10-181-600-1	Sequence 1, Appli
11	14	US-10-181-660-12	Sequence 12, Appli
11	16	US-10-181-600-12	Sequence 12, Appli
177	15	US-10-425-114-63291	Sequence 149837, A
9	1.1	US-10-424-599-149837	Sequence 149837, A
28	9	US-10-424-599-154779	Sequence 154779, A
31	9	US-10-425-114-72370	Sequence 72370, A
30	9	US-10-425-115-266878	Sequence 266878, A
31	9	US-10-424-599-147939	Sequence 147939, A
32	9	US-10-389-566-2330	Sequence 2330, Ap
33	9	US-09-933-767-1092	Sequence 1092, Ap
34	8	US-10-004-860-1092	Sequence 1092, Ap
35	8	US-10-023-282-1092	Sequence 1092, Ap
36	8	US-10-437-963-168144	Sequence 168144, A
37	8	US-10-424-599-217994	Sequence 217994, A
38	8	US-10-369-493-4323	Sequence 4323, Ap
39	8	US-10-425-114-51162	Sequence 51162, A
40	8	US-09-738-626-4240	Sequence 4240, Ap
41	8	US-10-369-493-13893	Sequence 13893, A
42	8	US-10-437-963-146233	Sequence 146233, A
43	8	US-10-369-493-12887	Sequence 12887, A
44	8	US-10-369-493-13128	Sequence 13128, A
45	8	US-10-389-647-479	Sequence 479, App
46	8	US-10-437-963-201769	Sequence 201769, A
47	8	US-10-437-963-118138	Sequence 118138, A
48	8	US-10-741-849-7164	Sequence 7164, Ap
49	8	US-10-282-122A-69069	Sequence 69069, A
50	8	US-10-732-923-13991	Sequence 13991, A
51	8	US-10-776-224-147	Sequence 147, App
52	7	US-10-425-115-275165	Sequence 275165, A
53	7	US-10-425-115-352701	Sequence 352701, A
54	7	US-09-864-761-40065	Sequence 40065, A
55	7	US-10-425-115-215004	Sequence 215004, A
56	7	US-10-767-701-50935	Sequence 50935, A
57	7	US-10-425-115-341846	Sequence 341846, A
58	7	US-10-425-115-196424	Sequence 196424, A
59	7	US-10-424-599-14303	Sequence 14303, A
60	7	US-10-424-599-203518	Sequence 203518, A
61	7	US-10-767-701-53260	Sequence 53260, A
62	7	US-10-424-599-248374	Sequence 248374, A
63	7	US-10-424-599-190349	Sequence 190349, A
64	7	US-10-425-115-359285	Sequence 359285, A
65	7	US-10-424-599-249223	Sequence 249223, A
66	7	US-10-425-115-246828	Sequence 246828, A
67	7	US-10-424-599-189046	Sequence 189046, A
68	7	US-10-437-963-104699	Sequence 104699, A
69	7	US-10-437-963-156781	Sequence 156781, A
70	7	US-09-864-408A-4096	Sequence 40864, Ap
71	7	US-10-424-599-188471	Sequence 188471, A
72	7	US-10-425-115-219581	Sequence 219581, A
73	7	US-10-369-493-21140	Sequence 21140, A
74	7	US-09-764-860-347	Sequence 347, App
75	7	US-10-074-095-347	Sequence 347, App
76	7	US-10-212-872-347	Sequence 347, App
77	7	US-10-012-542-325	Sequence 325, App
78	7	US-10-115-123-325	Sequence 325, App
79	7	US-10-425-115-364770	Sequence 364770, A
80	7	US-10-424-599-174289	Sequence 174289, A
81	7	US-10-437-963-188438	Sequence 188438, A

85	7	0.9	93	15	US-10-424-599-146654	Sequence 146654,	158	7	0.9	308	14	US-10-156-761-14268	Sequence 14268, A
86	7	0.9	96	16	US-10-437-963-123593	Sequence 123593,	159	7	0.9	308	17	US-10-732-923-10057	Sequence 10057, A
87	7	0.9	101	16	US-10-425-115-258624	Sequence 258624,	160	7	0.9	310	15	US-10-369-493-12686	Sequence 12686, A
88	7	0.9	102	15	US-10-424-599-259123	Sequence 259123,	161	7	0.9	315	14	US-10-106-698-5557	Sequence 5557, Ap
89	7	0.9	105	15	US-10-424-599-227387	Sequence 227387,	162	7	0.9	324	9	US-09-815-242-13895	Sequence 13895, A
90	7	0.9	106	16	US-10-425-115-338480	Sequence 338480,	163	7	0.9	324	15	US-10-282-122A-76321	Sequence 76321, A
91	7	0.9	107	16	US-10-425-115-354503	Sequence 354503,	164	7	0.9	325	9	US-09-738-626-4841	Sequence 4841, Ap
92	7	0.9	110	14	US-10-291-851-93	Sequence 93, Appl	165	7	0.9	325	16	US-10-781-014-776	Sequence 776, App
93	7	0.9	113	16	US-10-425-115-258019	Sequence 258019,	166	7	0.9	327	15	US-10-264-237-1918	Sequence 1918, Ap
94	7	0.9	122	15	US-10-424-599-166965	Sequence 166965,	167	7	0.9	329	14	US-10-012-819-60	Sequence 60, Appl
95	7	0.9	122	15	US-10-424-599-256379	Sequence 256379,	168	7	0.9	335	10	US-09-934-455-226	Sequence 226, App
96	7	0.9	122	16	US-10-425-115-347287	Sequence 347287,	169	7	0.9	335	15	US-10-225-066A-834	Sequence 834, App
97	7	0.9	122	16	US-10-739-930-8036	Sequence 8036, Ap	170	7	0.9	335	15	US-10-374-780A-294	Sequence 294, App
98	7	0.9	123	16	US-10-425-115-235907	Sequence 235907,	171	7	0.9	336	14	US-10-146-733-20	Sequence 20, Appl
99	7	0.9	123	16	US-10-425-115-314619	Sequence 314619,	172	7	0.9	337	15	US-10-264-237-2731	Sequence 2731, Ap
100	7	0.9	125	16	US-10-767-701-32380	Sequence 32380, A	173	7	0.9	337	15	US-10-282-122A-74662	Sequence 74662, A
101	7	0.9	129	16	US-10-437-963-104429	Sequence 104429,	174	7	0.9	340	16	US-10-767-701-41329	Sequence 41329, A
102	7	0.9	132	15	US-10-276-774-1607	Sequence 1607, Ap	175	7	0.9	342	15	US-10-381-898-9	Sequence 9, Appli
103	7	0.9	133	16	US-10-425-115-239682	Sequence 239682,	176	7	0.9	349	15	US-10-282-122A-51887	Sequence 51887, A
104	7	0.9	145	16	US-10-425-115-366479	Sequence 366479,	177	7	0.9	351	15	US-10-369-493-3808	Sequence 3808, Ap
105	7	0.9	150	15	US-10-282-122A-54511	Sequence 54511, A	178	7	0.9	353	16	US-10-425-115-271431	Sequence 271431,
106	7	0.9	150	16	US-10-767-701-54531	Sequence 54531, A	179	7	0.9	355	15	US-10-357-521-4	Sequence 4, Appli
107	7	0.9	150	16	US-10-425-115-187306	Sequence 187306,	180	7	0.9	355	17	US-10-915-029-8	Sequence 8, Appli
108	7	0.9	150	16	US-10-425-115-331739	Sequence 331739,	181	7	0.9	356	15	US-10-282-122A-52244	Sequence 52244, A
109	7	0.9	151	16	US-10-424-599-171238	Sequence 171238,	182	7	0.9	359	14	US-10-225-486-54	Sequence 54, Appl
110	7	0.9	154	16	US-10-425-115-337169	Sequence 337169,	183	7	0.9	366	15	US-10-369-493-1018	Sequence 1018, Ap
111	7	0.9	157	15	US-10-424-599-257335	Sequence 257335,	184	7	0.9	381	15	US-10-633-680-49	Sequence 49, Appl
112	7	0.9	169	16	US-10-437-963-125771	Sequence 125771,	185	7	0.9	382	10	US-09-798-889-49	Sequence 49, Appl
113	7	0.9	171	17	US-10-472-928-2480	Sequence 2480, Ap	186	7	0.9	383	9	US-09-738-626-4870	Sequence 4870, Ap
114	7	0.9	176	15	US-10-425-114-49034	Sequence 49034, A	187	7	0.9	384	17	US-10-732-923-2861	Sequence 2861, Ap
115	7	0.9	176	17	US-10-732-923-5057	Sequence 5057, Ap	188	7	0.9	386	15	US-10-369-493-8726	Sequence 8726, Ap
116	7	0.9	177	15	US-10-633-680-76	Sequence 76, Appl	189	7	0.9	390	15	US-10-282-122A-48185	Sequence 48185, A
117	7	0.9	177	15	US-10-632-983-55	Sequence 55, Appl	190	7	0.9	391	16	US-10-437-963-189621	Sequence 189621,
118	7	0.9	178	10	US-09-798-889-76	Sequence 76, Appl	191	7	0.9	398	15	US-10-425-114-71531	Sequence 71531, A
119	7	0.9	182	16	US-10-767-701-52318	Sequence 52318, A	192	7	0.9	401	15	US-10-424-599-269452	Sequence 269452,
120	7	0.9	186	16	US-10-739-930-8997	Sequence 8997, Ap	193	7	0.9	405	15	US-10-369-493-8649	Sequence 8649, Ap
121	7	0.9	191	16	US-10-437-963-133805	Sequence 133805,	194	7	0.9	405	15	US-10-369-493-20689	Sequence 20689, A
122	7	0.9	194	15	US-10-424-599-173855	Sequence 173855,	195	7	0.9	411	15	US-10-425-115-192417	Sequence 192417,
123	7	0.9	197	15	US-10-425-114-42546	Sequence 42546, A	196	7	0.9	411	15	US-10-369-493-12939	Sequence 12939, A
124	7	0.9	199	15	US-10-424-599-192625	Sequence 192625,	197	7	0.9	416	15	US-10-282-122A-70224	Sequence 70224, A
125	7	0.9	199	16	US-10-767-701-46512	Sequence 46512, A	198	7	0.9	425	14	US-10-117-015-8	Sequence 8, Appli
126	7	0.9	200	16	US-10-425-115-279847	Sequence 279847,	199	7	0.9	425	17	US-10-946-424-8	Sequence 8, Appli
127	7	0.9	213	14	US-10-029-386-34063	Sequence 34063, A	200	7	0.9	426	15	US-10-369-493-4635	Sequence 4635, Ap
128	7	0.9	213	16	US-10-425-115-185030	Sequence 185030,	201	7	0.9	426	16	US-10-425-115-368617	Sequence 368617,
129	7	0.9	217	15	US-10-425-114-39820	Sequence 39820, A	202	7	0.9	428	17	US-10-732-923-10735	Sequence 10735, A
130	7	0.9	220	16	US-10-437-963-187087	Sequence 187087,	203	7	0.9	429	15	US-10-282-122A-51466	Sequence 51466, A
131	7	0.9	221	15	US-10-369-493-8397	Sequence 8397, Ap	204	7	0.9	432	16	US-10-437-963-182668	Sequence 182668
132	7	0.9	221	16	US-10-425-115-337161	Sequence 337161,	205	7	0.9	433	15	US-10-282-122A-49892	Sequence 49892, A
133	7	0.9	228	15	US-10-369-493-20929	Sequence 20929, A	206	7	0.9	434	15	US-10-369-493-7393	Sequence 7393, Ap
134	7	0.9	228	15	US-10-424-599-171239	Sequence 171239,	207	7	0.9	442	10	US-09-866-050A-641	Sequence 641, App
135	7	0.9	234	10	US-09-882-227-24	Sequence 24, Appl	208	7	0.9	444	15	US-10-369-493-6911	Sequence 6911, Ap
136	7	0.9	234	16	US-10-335-977-8510	Sequence 8510, Ap	209	7	0.9	448	15	US-10-369-493-4105	Sequence 4105, Ap
137	7	0.9	234	16	US-10-425-115-185029	Sequence 185029,	210	7	0.9	456	15	US-10-369-493-20284	Sequence 20284, A
138	7	0.9	245	16	US-10-425-115-351748	Sequence 351748,	211	7	0.9	458	10	US-09-972-268-21	Sequence 21, Appl
139	7	0.9	254	15	US-10-395-607-127	Sequence 127, App	212	7	0.9	458	15	US-10-299-636-99	Sequence 99, Appl
140	7	0.9	254	16	US-10-799-870-127	Sequence 127, App	213	7	0.9	459	15	US-10-282-122A-70133	Sequence 70133, A
141	7	0.9	255	17	US-10-472-928-4076	Sequence 4076, Ap	214	7	0.9	464	9	US-09-912-020-281	Sequence 281, App
142	7	0.9	260	16	US-10-425-115-249662	Sequence 249662,	215	7	0.9	464	14	US-10-287-274-441	Sequence 441, App
143	7	0.9	262	15	US-10-424-599-232524	Sequence 232524,	216	7	0.9	464	15	US-10-282-122A-42613	Sequence 42613, A
144	7	0.9	263	15	US-10-424-599-189044	Sequence 189044,	217	7	0.9	464	16	US-10-771-241-281	Sequence 281, App
145	7	0.9	272	16	US-10-437-963-201475	Sequence 201475,	218	7	0.9	465	17	US-10-904-588-18	Sequence 18, Appl
146	7	0.9	273	16	US-10-437-963-127798	Sequence 127798,	219	7	0.9	469	15	US-10-369-493-13381	Sequence 13381, A
147	7	0.9	274	16	US-10-437-963-116008	Sequence 116008,	220	7	0.9	472	9	US-09-870-162A-33	Sequence 3, Appli
148	7	0.9	280	15	US-10-282-122A-74821	Sequence 74821, A	221	7	0.9	478	17	US-10-469-204-141	Sequence 141, App
149	7	0.9	282	15	US-10-094-749-2096	Sequence 2096, Ap	222	7	0.9	488	16	US-10-437-963-180174	Sequence 180174,
150	7	0.9	285	15	US-10-282-122A-72956	Sequence 72956, A	223	7	0.9	490	14	US-10-074-152-26	Sequence 26, Appl
151	7	0.9	288	15	US-10-369-493-22433	Sequence 22433, A	224	7	0.9	497	9	US-09-815-242-13344	Sequence 13344, A
152	7	0.9	290	15	US-10-776-774-1357	Sequence 1357, Ap	225	7	0.9	497	15	US-10-282-122A-73912	Sequence 73912, A
153	7	0.9	292	15	US-10-282-122A-57001	Sequence 57001, A	226	7	0.9	497	17	US-10-472-928-1718	Sequence 1718, Ap
154	7	0.9	293	15	US-10-369-493-13324	Sequence 13324, A	227	7	0.9	504	18	US-10-617-320-3732	Sequence 3732, Ap
155	7	0.9	301	14	US-10-156-761-13367	Sequence 13367, A	228	7	0.9	510	17	US-10-732-923-13923	Sequence 13923, A
156	7	0.9	305	15	US-10-369-493-640	Sequence 640, App	229	7	0.9	514	14	US-10-161-572-60	Sequence 60, Appl
157	7	0.9	307	15	US-10-424-599-224191	Sequence 224191,	230	7	0.9	517	10	US-09-972-268-20	Sequence 20, Appl

231	7	0.9	518	9	US-09-919-172-20	Sequence 20, Appl	304	7	0.9	953	10	US-09-884-696-3	Sequence 3, Appl
232	7	0.9	518	15	US-10-369-493-18702	Sequence 18702, A	305	7	0.9	953	16	US-10-148-884-5	Sequence 5, Appl
233	7	0.9	518	16	US-10-752-986-20	Sequence 20, Appl	306	7	0.9	959	16	US-10-428-115-37013	Sequence 37013, A
234	7	0.9	521	15	US-10-282-122A-63634	Sequence 63634, A	307	7	0.9	963	14	US-10-080-608A-20	Sequence 20, Appl
235	7	0.9	522	15	US-10-282-122A-50014	Sequence 50014, A	308	7	0.9	963	14	US-10-080-608A-22	Sequence 22, Appl
236	7	0.9	527	15	US-10-282-122A-47475	Sequence 47475, A	309	7	0.9	963	15	US-10-370-685-109	Sequence 109, App
237	7	0.9	529	9	US-09-954-314-22	Sequence 22, Appl	310	7	0.9	963	15	US-10-370-685-111	Sequence 111, App
238	7	0.9	529	14	US-10-230-562-22	Sequence 22, Appl	311	7	0.9	969	16	US-10-478-245-9	Sequence 9, Appl
239	7	0.9	529	14	US-10-230-026-16	Sequence 16, Appl	312	7	0.9	978	15	US-10-108-260A-4153	Sequence 4153, Ap
240	7	0.9	529	16	US-10-739-930-9550	Sequence 9550, Ap	313	7	0.9	992	16	US-10-425-115-194052	Sequence 194052, A
241	7	0.9	529	16	US-10-486-307-16	Sequence 16, Appl	314	7	0.9	1016	9	US-09-738-626-4363	Sequence 4363, Ap
242	7	0.9	539	15	US-10-424-599-227399	Sequence 227399, A	315	7	0.9	1016	15	US-10-283-122A-69491	Sequence 69491, A
243	7	0.9	564	16	US-10-739-930-9713	Sequence 9713, Ap	316	7	0.9	1019	16	US-10-408-765A-1661	Sequence 1661, Ap
244	7	0.9	564	17	US-10-481-113-28	Sequence 28, Appl	317	7	0.9	1031	16	US-10-437-963-169433	Sequence 169433, A
245	7	0.9	568	14	US-10-032-585-7920	Sequence 7920, Ap	318	7	0.9	1034	15	US-10-001-885-108	Sequence 108, App
246	7	0.9	572	16	US-10-437-963-173191	Sequence 173191, A	319	7	0.9	1120	15	US-10-335-977-5265	Sequence 5265, Ap
247	7	0.9	572	17	US-10-481-113-104	Sequence 104, App	320	7	0.9	1120	16	US-10-437-963-152821	Sequence 152821, A
248	7	0.9	578	16	US-10-425-115-249810	Sequence 249810, A	321	7	0.9	1121	8	US-08-915-048A-2	Sequence 2, Appl
249	7	0.9	580	15	US-10-647-057-4	Sequence 4, Appl	322	7	0.9	1174	14	US-10-184-644-353	Sequence 353, App
250	7	0.9	581	16	US-10-767-701-46924	Sequence 46924, A	323	7	0.9	1174	14	US-10-184-634-333	Sequence 353, App
251	7	0.9	584	15	US-10-282-122A-47689	Sequence 47689, A	324	7	0.9	1187	15	US-10-389-566-1202	Sequence 1202, Ap
252	7	0.9	587	10	US-09-893-519A-42	Sequence 42, Appl	325	7	0.9	1248	16	US-10-437-963-188299	Sequence 188299, A
253	7	0.9	589	14	US-10-205-194-144	Sequence 144, App	326	7	0.9	1264	14	US-10-123-155-1	Sequence 1, Appl
254	7	0.9	589	16	US-10-437-963-127286	Sequence 127286, A	327	7	0.9	1264	14	US-10-146-731-1	Sequence 1, Appl
255	7	0.9	590	17	US-10-831-070-10	Sequence 10, Appl	328	7	0.9	1264	14	US-10-140-472-1	Sequence 1, Appl
256	7	0.9	604	9	US-09-862-027-17	Sequence 17, Appl	329	7	0.9	1264	14	US-10-141-761-1	Sequence 1, Appl
257	7	0.9	604	17	US-10-989-228-17	Sequence 17, Appl	330	7	0.9	1264	14	US-10-143-885-1	Sequence 1, Appl
258	7	0.9	619	15	US-10-369-493-5855	Sequence 5855, Ap	331	7	0.9	1264	14	US-10-158-790-1	Sequence 1, Appl
259	7	0.9	620	10	US-09-893-519A-59	Sequence 59, Appl	332	7	0.9	1264	15	US-10-137-871-1	Sequence 1, Appl
260	7	0.9	620	15	US-10-369-493-1442	Sequence 1442, Ap	333	7	0.9	1264	15	US-10-140-923-1	Sequence 1, Appl
261	7	0.9	622	14	US-10-197-666A-22	Sequence 22, Appl	334	7	0.9	1264	15	US-10-141-756-1	Sequence 1, Appl
262	7	0.9	622	14	US-10-024-298A-63	Sequence 63, Appl	335	7	0.9	1264	15	US-10-141-759-1	Sequence 1, Appl
263	7	0.9	622	14	US-10-042-211A-63	Sequence 63, Appl	336	7	0.9	1264	15	US-10-140-805-1	Sequence 1, Appl
264	7	0.9	622	15	US-10-617-217A-63	Sequence 63, Appl	337	7	0.9	1264	15	US-10-140-864-1	Sequence 1, Appl
265	7	0.9	622	16	US-10-024-298A-63	Sequence 63, Appl	338	7	0.9	1264	15	US-10-142-426-1	Sequence 1, Appl
266	7	0.9	625	15	US-10-369-493-22882	Sequence 22882, A	339	7	0.9	1296	14	US-10-302-279-60	Sequence 60, Appl
267	7	0.9	628	14	US-10-156-761-10990	Sequence 10990, A	340	7	0.9	1297	14	US-10-184-644-599	Sequence 599, App
268	7	0.9	632	14	US-10-024-298A-65	Sequence 65, Appl	341	7	0.9	1297	14	US-10-184-634-599	Sequence 599, App
269	7	0.9	632	14	US-10-042-211A-65	Sequence 65, Appl	342	7	0.9	1297	14	US-10-123-155-435	Sequence 435, App
270	7	0.9	632	15	US-10-617-217A-65	Sequence 65, Appl	343	7	0.9	1297	14	US-10-146-731-435	Sequence 435, App
271	7	0.9	632	16	US-10-024-298A-65	Sequence 65, Appl	344	7	0.9	1297	14	US-10-140-472-435	Sequence 435, App
272	7	0.9	640	16	US-10-425-115-317987	Sequence 317987, A	345	7	0.9	1297	14	US-10-141-761-435	Sequence 435, App
273	7	0.9	663	15	US-10-282-122A-52415	Sequence 52415, A	346	7	0.9	1297	14	US-10-142-885-435	Sequence 435, App
274	7	0.9	666	10	US-09-746-660A-46	Sequence 46, Appl	347	7	0.9	1297	14	US-10-158-790-435	Sequence 435, App
275	7	0.9	667	16	US-10-767-701-46248	Sequence 46248, A	348	7	0.9	1297	15	US-10-137-871-435	Sequence 435, App
276	7	0.9	673	15	US-10-433-794-2	Sequence 2, Appl	349	7	0.9	1297	15	US-10-140-923-435	Sequence 435, App
277	7	0.9	676	18	US-10-617-320-4098	Sequence 4098, Ap	350	7	0.9	1297	15	US-10-141-756-435	Sequence 435, App
278	7	0.9	684	16	US-10-437-963-11247	Sequence 11247, A	351	7	0.9	1297	15	US-10-141-759-435	Sequence 435, App
279	7	0.9	686	15	US-10-282-122A-67777	Sequence 67777, A	352	7	0.9	1297	15	US-10-140-805-435	Sequence 435, App
280	7	0.9	692	15	US-10-369-493-8800	Sequence 8800, Ap	353	7	0.9	1297	15	US-10-140-864-435	Sequence 435, App
281	7	0.9	695	10	US-09-305-924-13	Sequence 13, Appl	354	7	0.9	1297	15	US-10-142-426-435	Sequence 435, App
282	7	0.9	699	14	US-10-156-761-12338	Sequence 12338, A	355	7	0.9	1320	14	US-10-161-051-167	Sequence 167, App
283	7	0.9	705	15	US-10-425-114-46512	Sequence 46512, A	356	7	0.9	1320	14	US-10-184-644-339	Sequence 339, App
284	7	0.9	711	15	US-10-425-114-54901	Sequence 54901, A	357	7	0.9	1334	14	US-10-184-634-339	Sequence 339, App
285	7	0.9	711	16	US-10-425-115-317988	Sequence 317988, A	358	7	0.9	1336	14	US-10-224-999A-3482	Sequence 3482, Ap
286	7	0.9	717	15	US-10-267-502-250	Sequence 250, App	359	7	0.9	1355	16	US-10-437-963-110486	Sequence 110486, A
287	7	0.9	732	14	US-10-184-634-577	Sequence 577, App	360	7	0.9	1376	14	US-10-123-155-161	Sequence 161, App
288	7	0.9	732	14	US-10-184-634-577	Sequence 577, App	361	7	0.9	1376	14	US-10-146-731-161	Sequence 161, App
289	7	0.9	741	15	US-10-282-122A-70070	Sequence 70070, A	362	7	0.9	1376	14	US-10-140-472-161	Sequence 161, App
290	7	0.9	755	16	US-10-437-963-171603	Sequence 171603, A	363	7	0.9	1376	14	US-10-141-761-161	Sequence 161, App
291	7	0.9	761	16	US-10-416-330-35	Sequence 35, Appl	364	7	0.9	1376	14	US-10-142-885-161	Sequence 161, App
292	7	0.9	786	17	US-10-874-049-3	Sequence 3, Appl	365	7	0.9	1376	14	US-10-158-790-161	Sequence 161, App
293	7	0.9	789	17	US-10-874-049-5	Sequence 5, Appl	366	7	0.9	1376	15	US-10-137-871-161	Sequence 161, App
294	7	0.9	792	13	US-10-087-192-1977	Sequence 1977, Ap	367	7	0.9	1376	15	US-10-140-923-161	Sequence 161, App
295	7	0.9	797	15	US-10-369-493-12480	Sequence 12480, A	368	7	0.9	1376	15	US-10-141-756-161	Sequence 161, App
296	7	0.9	818	9	US-09-738-626-6491	Sequence 6491, Ap	369	7	0.9	1376	15	US-10-141-759-161	Sequence 161, App
297	7	0.9	822	16	US-10-437-963-104983	Sequence 104983, A	370	7	0.9	1376	15	US-10-140-805-161	Sequence 161, App
298	7	0.9	850	14	US-10-238-075-1021	Sequence 1021, Ap	371	7	0.9	1376	15	US-10-140-864-161	Sequence 161, App
299	7	0.9	874	15	US-10-282-122A-61488	Sequence 61488, A	372	7	0.9	1376	15	US-10-142-426-161	Sequence 161, App
300	7	0.9	902	14	US-10-184-644-303	Sequence 303, App	373	7	0.9	1390	14	US-10-137-418A-2	Sequence 2, Appl
301	7	0.9	902	14	US-10-184-634-303	Sequence 303, App	374	7	0.9	1419	14	US-10-123-155-517	Sequence 517, App
302	7	0.9	902	14	US-10-063-685-93	Sequence 93, Appl	375	7	0.9	1419	14	US-10-146-731-517	Sequence 517, App
303	7	0.9	933	13	US-10-087-192-1980	Sequence 1980, Ap	376	7	0.9	1419	14	US-10-140-472-517	Sequence 517, App

377	7	0.9	1419	14	US-10-141-761-517	Sequence 517, App	450	7	0.9	1665	14	US-10-184-644-285	Sequence 285, App
378	7	0.9	1419	14	US-10-142-885-517	Sequence 517, App	451	7	0.9	1665	14	US-10-184-634-285	Sequence 285, App
379	7	0.9	1419	14	US-10-158-790-517	Sequence 517, App	452	7	0.9	1665	14	US-10-063-685-85	Sequence 85, App
380	7	0.9	1419	15	US-10-137-871-517	Sequence 517, App	453	7	0.9	1686	13	US-10-092-219-2	Sequence 2, Appli
381	7	0.9	1419	15	US-10-140-923-517	Sequence 517, App	454	7	0.9	1730	14	US-10-123-155-7	Sequence 7, Appli
382	7	0.9	1419	15	US-10-141-756-517	Sequence 517, App	455	7	0.9	1730	14	US-10-146-731-7	Sequence 7, Appli
383	7	0.9	1419	15	US-10-141-756-517	Sequence 517, App	456	7	0.9	1730	14	US-10-140-472-7	Sequence 7, Appli
384	7	0.9	1419	15	US-10-140-805-517	Sequence 517, App	457	7	0.9	1730	14	US-10-141-761-7	Sequence 7, Appli
385	7	0.9	1419	15	US-10-140-864-517	Sequence 517, App	458	7	0.9	1730	14	US-10-142-885-7	Sequence 7, Appli
386	7	0.9	1419	15	US-10-092-900A-82	Sequence 82, Appl	459	7	0.9	1730	14	US-10-158-790-7	Sequence 7, Appli
387	7	0.9	1419	15	US-10-142-426-517	Sequence 517, App	460	7	0.9	1730	15	US-10-137-871-7	Sequence 7, Appli
388	7	0.9	1423	15	US-10-092-900A-86	Sequence 86, Appl	461	7	0.9	1730	15	US-10-140-923-7	Sequence 7, Appli
389	7	0.9	1434	8	US-08-954-701A-10	Sequence 10, Appl	462	7	0.9	1730	15	US-10-141-756-7	Sequence 7, Appli
390	7	0.9	1434	10	US-09-754-032-10	Sequence 10, Appl	463	7	0.9	1730	15	US-10-141-759-7	Sequence 7, Appli
391	7	0.9	1434	14	US-10-421-446-10	Sequence 10, Appl	464	7	0.9	1730	15	US-10-140-805-7	Sequence 7, Appli
392	7	0.9	1439	16	US-10-220-481-73	Sequence 73, Appl	465	7	0.9	1730	15	US-10-140-864-7	Sequence 7, Appli
393	7	0.9	1447	8	US-08-954-701A-19	Sequence 19, Appl	466	7	0.9	1730	15	US-10-142-426-7	Sequence 7, Appli
394	7	0.9	1447	9	US-09-898-533-5	Sequence 5, Appli	467	7	0.9	1771	14	US-10-184-644-17	Sequence 17, Appl
395	7	0.9	1447	10	US-09-754-032-19	Sequence 19, Appl	468	7	0.9	1771	14	US-10-184-634-17	Sequence 17, Appl
396	7	0.9	1447	14	US-10-421-446-19	Sequence 19, Appl	469	7	0.9	1775	15	US-10-335-977-5267	Sequence 5267, Ap
397	7	0.9	1449	15	US-10-282-122A-65711	Sequence 65711, A	470	7	0.9	1808	14	US-10-123-155-47	Sequence 47, Appl
398	7	0.9	1454	16	US-10-742-345-2	Sequence 2, Appli	471	7	0.9	1808	14	US-10-146-731-47	Sequence 47, Appl
399	7	0.9	1457	16	US-10-220-481-71	Sequence 71, Appl	472	7	0.9	1808	14	US-10-140-472-47	Sequence 47, Appl
400	7	0.9	1457	16	US-10-742-345-4	Sequence 4, Appli	473	7	0.9	1808	14	US-10-141-761-47	Sequence 47, Appl
401	7	0.9	1458	13	US-10-054-691-2	Sequence 2, Appli	474	7	0.9	1808	14	US-10-142-885-47	Sequence 47, Appl
402	7	0.9	1458	16	US-10-478-245-1	Sequence 1, Appli	475	7	0.9	1808	14	US-10-158-790-47	Sequence 47, Appl
403	7	0.9	1468	15	US-10-282-122A-65027	Sequence 65027, A	476	7	0.9	1808	15	US-10-137-871-47	Sequence 47, Appl
404	7	0.9	1471	14	US-10-123-155-281	Sequence 281, App	477	7	0.9	1808	15	US-10-140-923-47	Sequence 47, Appl
405	7	0.9	1471	14	US-10-146-731-281	Sequence 281, App	478	7	0.9	1808	15	US-10-141-756-47	Sequence 47, Appl
406	7	0.9	1471	14	US-10-140-472-281	Sequence 281, App	479	7	0.9	1808	15	US-10-141-759-47	Sequence 47, Appl
407	7	0.9	1471	14	US-10-141-761-281	Sequence 281, App	480	7	0.9	1808	15	US-10-140-805-47	Sequence 47, Appl
408	7	0.9	1471	14	US-10-142-885-281	Sequence 281, App	481	7	0.9	1808	15	US-10-140-864-47	Sequence 47, Appl
409	7	0.9	1471	14	US-10-158-790-281	Sequence 281, App	482	7	0.9	1808	15	US-10-142-426-47	Sequence 47, Appl
410	7	0.9	1471	15	US-10-137-871-281	Sequence 281, App	483	7	0.9	1849	14	US-10-184-644-133	Sequence 133, App
411	7	0.9	1471	15	US-10-140-923-281	Sequence 281, App	484	7	0.9	1849	14	US-10-184-634-133	Sequence 133, App
412	7	0.9	1471	15	US-10-141-756-281	Sequence 281, App	485	7	0.9	1849	14	US-10-063-685-21	Sequence 21, Appl
413	7	0.9	1471	15	US-10-141-759-281	Sequence 281, App	486	7	0.9	1883	14	US-10-123-155-501	Sequence 501, App
414	7	0.9	1471	15	US-10-140-805-281	Sequence 281, App	487	7	0.9	1883	14	US-10-146-731-501	Sequence 501, App
415	7	0.9	1471	15	US-10-140-864-281	Sequence 281, App	488	7	0.9	1883	14	US-10-140-472-501	Sequence 501, App
416	7	0.9	1471	15	US-10-142-426-281	Sequence 281, App	489	7	0.9	1883	14	US-10-141-761-501	Sequence 501, App
417	7	0.9	1484	14	US-10-123-155-447	Sequence 447, App	490	7	0.9	1883	14	US-10-142-885-501	Sequence 501, App
418	7	0.9	1484	14	US-10-146-731-447	Sequence 447, App	491	7	0.9	1883	14	US-10-158-790-501	Sequence 501, App
419	7	0.9	1484	14	US-10-140-472-447	Sequence 447, App	492	7	0.9	1883	15	US-10-137-871-501	Sequence 501, App
420	7	0.9	1484	14	US-10-141-761-447	Sequence 447, App	493	7	0.9	1883	15	US-10-140-923-501	Sequence 501, App
421	7	0.9	1484	14	US-10-142-885-447	Sequence 447, App	494	7	0.9	1883	15	US-10-141-756-501	Sequence 501, App
422	7	0.9	1484	14	US-10-158-790-447	Sequence 447, App	495	7	0.9	1883	15	US-10-141-759-501	Sequence 501, App
423	7	0.9	1484	15	US-10-137-871-447	Sequence 447, App	496	7	0.9	1883	15	US-10-140-805-501	Sequence 501, App
424	7	0.9	1484	15	US-10-140-923-447	Sequence 447, App	497	7	0.9	1883	15	US-10-140-864-501	Sequence 501, App
425	7	0.9	1484	15	US-10-141-759-447	Sequence 447, App	498	7	0.9	1883	15	US-10-142-426-501	Sequence 501, App
426	7	0.9	1484	15	US-10-140-864-447	Sequence 447, App	499	7	0.9	1912	15	US-10-188-186-48	Sequence 48, Appl
427	7	0.9	1484	15	US-10-140-805-447	Sequence 447, App	500	7	0.9	1943	15	US-10-282-122A-58750	Sequence 58750, A
428	7	0.9	1484	15	US-10-140-864-447	Sequence 447, App	501	7	0.9	1974	9	US-09-895-913A-12	Sequence 12, Appl
429	7	0.9	1484	15	US-10-142-426-447	Sequence 447, App	502	7	0.9	1975	14	US-10-123-155-105	Sequence 105, App
430	7	0.9	1515	14	US-10-184-644-399	Sequence 399, App	503	7	0.9	1975	14	US-10-146-731-105	Sequence 105, App
431	7	0.9	1515	14	US-10-184-634-399	Sequence 399, App	504	7	0.9	1975	14	US-10-140-472-105	Sequence 105, App
432	7	0.9	1515	14	US-10-063-685-157	Sequence 157, App	505	7	0.9	1975	14	US-10-141-761-105	Sequence 105, App
433	7	0.9	1536	14	US-10-184-644-461	Sequence 461, App	506	7	0.9	1975	14	US-10-142-885-105	Sequence 105, App
434	7	0.9	1536	14	US-10-184-634-461	Sequence 461, App	507	7	0.9	1975	14	US-10-158-790-105	Sequence 105, App
435	7	0.9	1576	15	US-10-335-977-5266	Sequence 5266, Ap	508	7	0.9	1975	15	US-10-137-871-105	Sequence 105, App
436	7	0.9	1584	17	US-10-732-923-12885	Sequence 12885, A	509	7	0.9	1975	15	US-10-140-923-105	Sequence 105, App
437	7	0.9	1624	14	US-10-123-155-181	Sequence 181, App	510	7	0.9	1975	15	US-10-141-756-105	Sequence 105, App
438	7	0.9	1624	14	US-10-146-731-181	Sequence 181, App	511	7	0.9	1975	15	US-10-140-805-105	Sequence 105, App
439	7	0.9	1624	14	US-10-140-472-181	Sequence 181, App	512	7	0.9	1975	15	US-10-141-759-105	Sequence 105, App
440	7	0.9	1624	14	US-10-141-761-181	Sequence 181, App	513	7	0.9	1975	15	US-10-140-864-105	Sequence 105, App
441	7	0.9	1624	14	US-10-142-885-181	Sequence 181, App	514	7	0.9	1975	15	US-10-142-426-105	Sequence 105, App
442	7	0.9	1624	14	US-10-158-790-181	Sequence 181, App	515	7	0.9	2037	14	US-10-184-644-591	Sequence 591, App
443	7	0.9	1624	15	US-10-137-871-181	Sequence 181, App	516	7	0.9	2037	14	US-10-184-634-591	Sequence 591, App
444	7	0.9	1624	15	US-10-140-923-181	Sequence 181, App	517	7	0.9	2055	17	US-10-481-582-3	Sequence 3, Appli
445	7	0.9	1624	15	US-10-141-756-181	Sequence 181, App	518	7	0.9	2103	14	US-10-184-644-319	Sequence 319, App
446	7	0.9	1624	15	US-10-141-759-181	Sequence 181, App	519	7	0.9	2103	14	US-10-184-634-319	Sequence 319, App
447	7	0.9	1624	15	US-10-140-805-181	Sequence 181, App	520	7	0.9	2103	14	US-10-063-685-105	Sequence 105, App
448	7	0.9	1624	15	US-10-140-864-181	Sequence 181, App	521	7	0.9	2134	14	US-10-123-155-179	Sequence 179, App
449	7	0.9	1624	15	US-10-142-426-181	Sequence 181, App	522	7	0.9	2134	14	US-10-146-731-179	Sequence 179, App

523	7	0.9	2134	14	US-10-140-472-179	Sequence 179, App	596	7	0.9	2615	14	US-10-184-644-523	Sequence 523, App
524	7	0.9	2134	14	US-10-141-761-179	Sequence 179, App	597	7	0.9	2615	14	US-10-184-634-523	Sequence 523, App
525	7	0.9	2134	14	US-10-142-885-179	Sequence 179, App	598	7	0.9	2732	14	US-10-238-075-1119	Sequence 1119, App
526	7	0.9	2134	14	US-10-158-790-179	Sequence 179, App	599	7	0.9	2819	14	US-10-184-644-109	Sequence 109, App
527	7	0.9	2134	15	US-10-137-871-179	Sequence 179, App	600	7	0.9	2819	14	US-10-184-634-109	Sequence 109, App
528	7	0.9	2134	15	US-10-140-923-179	Sequence 179, App	601	7	0.9	2834	14	US-10-085-959-252	Sequence 252, App
529	7	0.9	2134	15	US-10-141-756-179	Sequence 179, App	602	7	0.9	2834	14	US-10-123-155-69	Sequence 69, App
530	7	0.9	2134	15	US-10-141-759-179	Sequence 179, App	603	7	0.9	2916	14	US-10-146-731-69	Sequence 69, App
531	7	0.9	2134	15	US-10-140-805-179	Sequence 179, App	604	7	0.9	2916	14	US-10-140-472-69	Sequence 69, App
532	7	0.9	2134	15	US-10-140-805-179	Sequence 179, App	605	7	0.9	2916	14	US-10-141-761-69	Sequence 69, App
533	7	0.9	2134	15	US-10-142-426-179	Sequence 179, App	606	7	0.9	2916	14	US-10-140-472-69	Sequence 69, App
534	7	0.9	2237	14	US-10-123-155-45	Sequence 45, App	607	7	0.9	2916	14	US-10-142-885-69	Sequence 69, App
535	7	0.9	2237	14	US-10-146-731-45	Sequence 45, App	608	7	0.9	2916	15	US-10-158-790-69	Sequence 69, App
536	7	0.9	2237	14	US-10-140-472-45	Sequence 45, App	609	7	0.9	2916	15	US-10-137-871-69	Sequence 69, App
537	7	0.9	2237	14	US-10-141-761-45	Sequence 45, App	610	7	0.9	2916	15	US-10-140-923-69	Sequence 69, App
538	7	0.9	2237	14	US-10-142-885-45	Sequence 45, App	611	7	0.9	2916	15	US-10-141-756-69	Sequence 69, App
539	7	0.9	2237	14	US-10-158-790-45	Sequence 45, App	612	7	0.9	2916	15	US-10-141-759-69	Sequence 69, App
540	7	0.9	2237	15	US-10-137-871-45	Sequence 45, App	613	7	0.9	2916	15	US-10-140-805-69	Sequence 69, App
541	7	0.9	2237	15	US-10-140-923-45	Sequence 45, App	614	7	0.9	2916	15	US-10-140-864-69	Sequence 69, App
542	7	0.9	2237	15	US-10-141-756-45	Sequence 45, App	615	7	0.9	2956	14	US-10-142-426-69	Sequence 69, App
543	7	0.9	2237	15	US-10-141-756-45	Sequence 45, App	616	7	0.9	2956	14	US-10-184-644-73	Sequence 73, App
544	7	0.9	2237	15	US-10-140-805-45	Sequence 45, App	617	7	0.9	3033	14	US-10-184-634-73	Sequence 73, App
545	7	0.9	2237	15	US-10-140-805-45	Sequence 45, App	618	7	0.9	3033	14	US-10-184-644-1	Sequence 1, App
546	7	0.9	2237	15	US-10-142-426-45	Sequence 45, App	619	7	0.9	3033	14	US-10-184-634-1	Sequence 1, App
547	7	0.9	2274	15	US-10-267-502-373	Sequence 373, App	620	7	0.9	3038	14	US-10-184-644-261	Sequence 261, App
548	7	0.9	2274	17	US-10-805-684-140	Sequence 140, App	621	7	0.9	3038	14	US-10-184-634-261	Sequence 261, App
549	7	0.9	2275	14	US-10-184-644-401	Sequence 401, App	622	7	0.9	3089	14	US-10-184-644-61	Sequence 61, App
550	7	0.9	2275	14	US-10-184-634-401	Sequence 401, App	623	7	0.9	3089	14	US-10-184-634-61	Sequence 61, App
551	7	0.9	2303	15	US-10-267-502-371	Sequence 371, App	624	7	0.9	3122	14	US-10-200-562-201	Sequence 201, App
552	7	0.9	2303	17	US-10-852-335A-109	Sequence 109, App	625	7	0.9	3122	14	US-10-237-551-201	Sequence 201, App
553	7	0.9	2338	14	US-10-029-386-31982	Sequence 31982, A	626	7	0.9	3122	18	US-10-237-551-250	Sequence 250, App
554	7	0.9	2387	14	US-10-123-155-527	Sequence 527, App	627	7	0.9	3122	18	US-10-945-050-201	Sequence 201, App
555	7	0.9	2387	14	US-10-146-731-527	Sequence 527, App	628	7	0.9	3150	14	US-10-945-050-250	Sequence 250, App
556	7	0.9	2387	14	US-10-140-472-527	Sequence 527, App	629	7	0.9	3150	14	US-10-184-644-81	Sequence 81, App
557	7	0.9	2387	14	US-10-141-761-527	Sequence 527, App	630	7	0.9	3152	14	US-10-184-634-81	Sequence 81, App
558	7	0.9	2387	14	US-10-142-885-527	Sequence 527, App	631	7	0.9	3192	14	US-10-123-155-75	Sequence 75, App
559	7	0.9	2387	14	US-10-158-790-527	Sequence 527, App	632	7	0.9	3192	14	US-10-146-731-75	Sequence 75, App
560	7	0.9	2387	15	US-10-137-871-527	Sequence 527, App	633	7	0.9	3192	14	US-10-140-472-75	Sequence 75, App
561	7	0.9	2387	15	US-10-140-923-527	Sequence 527, App	634	7	0.9	3192	14	US-10-141-761-75	Sequence 75, App
562	7	0.9	2387	15	US-10-141-756-527	Sequence 527, App	635	7	0.9	3192	14	US-10-142-885-75	Sequence 75, App
563	7	0.9	2387	15	US-10-141-759-527	Sequence 527, App	636	7	0.9	3192	15	US-10-158-790-75	Sequence 75, App
564	7	0.9	2387	15	US-10-140-805-527	Sequence 527, App	637	7	0.9	3192	15	US-10-137-871-75	Sequence 75, App
565	7	0.9	2387	15	US-10-140-864-527	Sequence 527, App	638	7	0.9	3192	15	US-10-140-923-75	Sequence 75, App
566	7	0.9	2387	15	US-10-142-426-527	Sequence 527, App	639	7	0.9	3192	15	US-10-141-756-75	Sequence 75, App
567	7	0.9	2397	14	US-10-184-644-29	Sequence 29, App	640	7	0.9	3192	15	US-10-141-759-75	Sequence 75, App
568	7	0.9	2397	14	US-10-184-644-323	Sequence 323, App	641	7	0.9	3192	15	US-10-140-805-75	Sequence 75, App
569	7	0.9	2397	14	US-10-184-634-29	Sequence 29, App	642	7	0.9	3192	15	US-10-140-864-75	Sequence 75, App
570	7	0.9	2397	14	US-10-184-634-323	Sequence 323, App	643	7	0.9	3192	15	US-10-142-426-75	Sequence 75, App
571	7	0.9	2397	14	US-10-063-685-107	Sequence 107, App	644	7	0.9	3194	15	US-10-282-122A-59046	Sequence 59046, A
572	7	0.9	2431	9	US-09-901-106-2	Sequence 2, App	645	7	0.9	3233	14	US-10-123-155-81	Sequence 81, App
573	7	0.9	2457	14	US-10-184-644-569	Sequence 569, App	646	7	0.9	3233	14	US-10-146-731-81	Sequence 81, App
574	7	0.9	2457	14	US-10-184-634-569	Sequence 569, App	647	7	0.9	3233	14	US-10-140-472-81	Sequence 81, App
575	7	0.9	2478	14	US-10-184-644-107	Sequence 107, App	648	7	0.9	3233	14	US-10-141-761-81	Sequence 81, App
576	7	0.9	2478	14	US-10-184-634-107	Sequence 107, App	649	7	0.9	3233	14	US-10-142-885-81	Sequence 81, App
577	7	0.9	2497	17	US-10-181-582-4	Sequence 4, App	650	7	0.9	3233	14	US-10-158-790-81	Sequence 81, App
578	7	0.9	2558	14	US-10-184-644-103	Sequence 103, App	651	7	0.9	3233	15	US-10-137-871-81	Sequence 81, App
579	7	0.9	2558	14	US-10-184-634-103	Sequence 103, App	652	7	0.9	3233	15	US-10-140-923-81	Sequence 81, App
580	7	0.9	2594	14	US-10-123-155-245	Sequence 245, App	653	7	0.9	3233	15	US-10-141-756-81	Sequence 81, App
581	7	0.9	2594	14	US-10-146-731-245	Sequence 245, App	654	7	0.9	3233	15	US-10-141-759-81	Sequence 81, App
582	7	0.9	2594	14	US-10-140-472-245	Sequence 245, App	655	7	0.9	3233	15	US-10-140-805-81	Sequence 81, App
583	7	0.9	2594	14	US-10-141-761-245	Sequence 245, App	656	7	0.9	3233	15	US-10-140-864-81	Sequence 81, App
584	7	0.9	2594	14	US-10-142-885-245	Sequence 245, App	657	7	0.9	3240	14	US-10-142-426-81	Sequence 81, App
585	7	0.9	2594	14	US-10-158-790-245	Sequence 245, App	658	7	0.9	3240	14	US-10-184-644-415	Sequence 415, App
586	7	0.9	2594	15	US-10-137-871-245	Sequence 245, App	659	7	0.9	3240	14	US-10-184-634-415	Sequence 415, App
587	7	0.9	2594	15	US-10-140-923-245	Sequence 245, App	660	7	0.9	3233	14	US-10-123-155-167	Sequence 167, App
588	7	0.9	2594	15	US-10-141-756-245	Sequence 245, App	661	7	0.9	3233	14	US-10-146-731-167	Sequence 167, App
589	7	0.9	2594	15	US-10-141-759-245	Sequence 245, App	662	7	0.9	3233	14	US-10-140-472-167	Sequence 167, App
590	7	0.9	2594	15	US-10-140-805-245	Sequence 245, App	663	7	0.9	3233	14	US-10-141-761-167	Sequence 167, App
591	7	0.9	2594	15	US-10-140-864-245	Sequence 245, App	664	7	0.9	3233	14	US-10-142-885-167	Sequence 167, App
592	7	0.9	2594	15	US-10-142-426-245	Sequence 245, App	665	7	0.9	3233	14	US-10-158-790-167	Sequence 167, App
593	7	0.9	2598	14	US-10-063-685-151	Sequence 151, App	666	7	0.9	3233	15	US-10-137-871-167	Sequence 167, App
594	7	0.9	2609	14	US-10-184-644-407	Sequence 407, App	667	7	0.9	3233	15	US-10-140-923-167	Sequence 167, App
595	7	0.9	2609	14	US-10-184-634-407	Sequence 407, App	668	7	0.9	3233	15	US-10-141-756-167	Sequence 167, App

669	7	0.9	3323	15	US-10-140-805-167	Sequence 167, App	742	6	0.8	13	15	US-10-411-869A-53	Sequence 53, Appl
670	7	0.9	3323	15	US-10-140-864-167	Sequence 167, App	743	6	0.8	14	14	US-10-312-691-6	Sequence 6, Appl
671	7	0.9	3323	15	US-10-142-426-167	Sequence 167, App	744	6	0.8	14	16	US-10-813-638-1304	Sequence 1304, Ap
672	7	0.9	3401	14	US-10-184-644-411	Sequence 411, App	745	6	0.8	15	10	US-09-880-748-2970	Sequence 2970, Ap
673	7	0.9	3401	14	US-10-184-634-411	Sequence 411, App	746	6	0.8	15	15	US-10-293-418-2970	Sequence 2970, Ap
674	7	0.9	3552	14	US-10-123-155-339	Sequence 339, App	747	6	0.8	15	16	US-10-412-964-68	Sequence 68, Appl
675	7	0.9	3552	14	US-10-146-731-339	Sequence 339, App	748	6	0.8	18	15	US-10-187-496A-20	Sequence 20, Appl
676	7	0.9	3552	14	US-10-140-472-339	Sequence 339, App	749	6	0.8	19	9	US-09-932-923-1	Sequence 1, Appl
677	7	0.9	3552	14	US-10-141-761-339	Sequence 339, App	750	6	0.8	16	16	US-10-297-969-6	Sequence 6, Appl
678	7	0.9	3552	14	US-10-142-885-339	Sequence 339, App	751	6	0.8	21	15	US-10-449-735-3	Sequence 3, Appl
679	7	0.9	3552	14	US-10-158-790-339	Sequence 339, App	752	6	0.8	23	14	US-10-097-065-356	Sequence 356, App
680	7	0.9	3552	15	US-10-137-871-339	Sequence 339, App	753	6	0.8	23	15	US-10-372-876-356	Sequence 356, App
681	7	0.9	3552	15	US-10-140-923-339	Sequence 339, App	754	6	0.8	24	10	US-09-843-221A-129	Sequence 129, App
682	7	0.9	3552	15	US-10-141-756-339	Sequence 339, App	755	6	0.8	24	10	US-09-843-221A-130	Sequence 130, App
683	7	0.9	3552	15	US-10-141-759-339	Sequence 339, App	756	6	0.8	24	12	US-09-999-608-129	Sequence 129, App
684	7	0.9	3552	15	US-10-140-805-339	Sequence 339, App	757	6	0.8	24	12	US-09-999-608-130	Sequence 130, App
685	7	0.9	3552	15	US-10-140-864-339	Sequence 339, App	758	6	0.8	24	16	US-10-425-115-338692	Sequence 338692,
686	7	0.9	3552	15	US-10-142-426-339	Sequence 339, App	759	6	0.8	24	16	US-10-839-037-129	Sequence 129, App
687	7	0.9	3871	14	US-10-184-644-347	Sequence 347, App	760	6	0.8	24	16	US-10-839-037-130	Sequence 130, App
688	7	0.9	3871	14	US-10-184-634-347	Sequence 347, App	761	6	0.8	25	9	US-09-911-888-35	Sequence 35, Appl
689	7	0.9	4040	14	US-10-123-155-425	Sequence 425, App	762	6	0.8	25	9	US-09-911-927-35	Sequence 35, Appl
690	7	0.9	4040	14	US-10-146-731-425	Sequence 425, App	763	6	0.8	26	15	US-10-243-355-472	Sequence 472, App
691	7	0.9	4040	14	US-10-140-472-425	Sequence 425, App	764	6	0.8	28	10	US-09-843-221A-53	Sequence 93, Appl
692	7	0.9	4040	14	US-10-141-761-425	Sequence 425, App	765	6	0.8	28	10	US-09-843-221A-94	Sequence 94, Appl
693	7	0.9	4040	14	US-10-142-885-425	Sequence 425, App	766	6	0.8	28	12	US-09-999-608-93	Sequence 93, Appl
694	7	0.9	4040	14	US-10-158-790-425	Sequence 425, App	767	6	0.8	28	12	US-09-999-608-94	Sequence 94, Appl
695	7	0.9	4040	15	US-10-137-871-425	Sequence 425, App	768	6	0.8	28	14	US-10-261-208-4	Sequence 4, Appl
696	7	0.9	4040	15	US-10-140-923-425	Sequence 425, App	769	6	0.8	28	15	US-10-424-599-156146	Sequence 156146,
697	7	0.9	4040	15	US-10-141-756-425	Sequence 425, App	770	6	0.8	28	16	US-10-839-037-93	Sequence 93, Appl
698	7	0.9	4040	15	US-10-141-759-425	Sequence 425, App	771	6	0.8	28	16	US-10-839-037-94	Sequence 94, Appl
699	7	0.9	4060	14	US-10-141-761-197	Sequence 197, App	772	6	0.8	28	17	US-10-926-683-1203	Sequence 1203, Ap
700	7	0.9	4060	15	US-10-140-805-425	Sequence 425, App	773	6	0.8	30	10	US-09-843-221A-124	Sequence 124, App
701	7	0.9	4060	14	US-10-140-864-425	Sequence 425, App	774	6	0.8	30	10	US-09-843-221A-125	Sequence 125, App
702	7	0.9	4060	14	US-10-142-426-425	Sequence 425, App	775	6	0.8	30	10	US-09-843-221A-125	Sequence 125, App
703	7	0.9	4060	14	US-10-123-155-197	Sequence 197, App	776	6	0.8	30	12	US-09-999-608-124	Sequence 124, App
704	7	0.9	4060	14	US-10-146-731-197	Sequence 197, App	777	6	0.8	30	12	US-09-999-608-125	Sequence 125, App
705	7	0.9	4060	14	US-10-140-472-197	Sequence 197, App	778	6	0.8	30	12	US-09-999-608-158	Sequence 158, App
706	7	0.9	4060	14	US-10-142-885-197	Sequence 197, App	779	6	0.8	30	16	US-10-437-963-138633	Sequence 138633,
707	7	0.9	4060	14	US-10-158-790-197	Sequence 197, App	780	6	0.8	30	16	US-10-839-037-124	Sequence 124, App
708	7	0.9	4060	15	US-10-137-871-197	Sequence 197, App	781	6	0.8	30	16	US-10-839-037-125	Sequence 125, App
709	7	0.9	4060	15	US-10-140-923-197	Sequence 197, App	782	6	0.8	30	16	US-10-839-037-125	Sequence 125, App
710	7	0.9	4060	15	US-10-141-756-197	Sequence 197, App	783	6	0.8	31	13	US-10-097-079-50	Sequence 50, Appl
711	7	0.9	4060	15	US-10-141-759-197	Sequence 197, App	784	6	0.8	33	9	US-09-864-761-35842	Sequence 35842, A
712	7	0.9	4060	15	US-10-140-805-197	Sequence 197, App	785	6	0.8	33	14	US-10-000-256A-175	Sequence 175, App
713	7	0.9	4060	15	US-10-140-864-197	Sequence 197, App	786	6	0.8	33	14	US-10-029-386-33592	Sequence 33592, A
714	7	0.9	4060	15	US-10-142-426-197	Sequence 197, App	787	6	0.8	33	15	US-10-424-599-205494	Sequence 205494,
715	7	0.9	4106	11	US-09-980-217-23	Sequence 23, Appl	788	6	0.8	34	10	US-09-843-221A-88	Sequence 88, Appl
716	7	0.9	4106	17	US-10-732-923-20549	Sequence 20549, A	789	6	0.8	34	10	US-09-843-221A-89	Sequence 89, Appl
717	7	0.9	4640	14	US-10-184-644-75	Sequence 75, Appl	790	6	0.8	34	10	US-09-843-221A-122	Sequence 122, App
718	7	0.9	4640	14	US-10-184-634-75	Sequence 75, Appl	791	6	0.8	34	10	US-09-935-384-755	Sequence 755, App
719	7	0.9	4679	9	US-09-804-898-2	Sequence 2, Appl	792	6	0.8	34	10	US-09-935-384-756	Sequence 756, App
720	7	0.9	4999	9	US-09-976-059-14	Sequence 14, Appl	793	6	0.8	34	12	US-09-999-608-88	Sequence 88, Appl
721	7	0.9	8026	14	US-10-132-134-12	Sequence 12, Appl	794	6	0.8	34	12	US-09-999-608-89	Sequence 89, Appl
722	7	0.9	18636	14	US-10-073-912-17	Sequence 17, Appl	795	6	0.8	34	12	US-09-999-608-122	Sequence 122, App
723	7	0.9	35346	17	US-10-874-049-2	Sequence 2, Appl	796	6	0.8	34	15	US-10-282-122A-70169	Sequence 70169, A
724	7	0.9	35823	17	US-10-874-049-1	Sequence 1, Appl	797	6	0.8	34	16	US-10-425-115-265306	Sequence 265306,
725	7	0.9	36946	18	US-10-840-512-155	Sequence 155, App	798	6	0.8	34	16	US-10-839-037-88	Sequence 88, Appl
726	6	0.8	9	10	US-09-935-384-116	Sequence 116, App	799	6	0.8	34	16	US-10-839-037-89	Sequence 89, Appl
727	6	0.8	9	10	US-09-935-384-219	Sequence 219, App	800	6	0.8	34	16	US-10-839-037-122	Sequence 122, App
728	6	0.8	9	10	US-09-935-384-447	Sequence 447, App	801	6	0.8	35	16	US-10-425-115-356970	Sequence 356970,
729	6	0.8	9	10	US-09-935-384-613	Sequence 613, App	802	6	0.8	35	16	US-09-864-761-35450	Sequence 35450, A
730	6	0.8	10	10	US-09-572-404B-512	Sequence 512, App	803	6	0.8	36	16	US-10-437-963-134795	Sequence 134795,
731	6	0.8	10	10	US-09-935-384-158	Sequence 158, App	804	6	0.8	36	16	US-10-437-963-195293	Sequence 195293,
732	6	0.8	10	10	US-09-935-384-266	Sequence 266, App	805	6	0.8	36	16	US-10-425-115-227274	Sequence 227274,
733	6	0.8	10	10	US-09-935-384-268	Sequence 268, App	806	6	0.8	36	16	US-10-425-115-263124	Sequence 263124,
734	6	0.8	10	10	US-09-935-384-473	Sequence 473, App	807	6	0.8	38	9	US-09-864-761-33780	Sequence 33780, A
735	6	0.8	10	10	US-09-935-384-573	Sequence 573, App	808	6	0.8	39	14	US-10-029-386-30437	Sequence 30437, A
736	6	0.8	10	14	US-10-319-340-4	Sequence 4, Appl	809	6	0.8	39	16	US-10-425-115-367446	Sequence 367446,
737	6	0.8	10	14	US-10-319-340-5	Sequence 5, Appl	810	6	0.8	40	15	US-10-424-599-158157	Sequence 158157,
738	6	0.8	10	14	US-10-319-340-6	Sequence 6, Appl	811	6	0.8	41	15	US-10-424-599-159947	Sequence 159947,
739	6	0.8	10	14	US-10-319-340-19	Sequence 19, Appl	812	6	0.8	41	15	US-10-424-599-170123	Sequence 170123,
740	6	0.8	10	16	US-10-297-969-2	Sequence 2, Appl	813	6	0.8	41	15	US-10-424-599-238198	Sequence 238198,
741	6	0.8	12	16	US-10-700-330-137	Sequence 137, App	814	6	0.8	42	15	US-10-424-599-269505	Sequence 269505,

815	6	0.8	42	15	US-10-424-599-270459	Sequence 270459	888	6	0.8	58	16	US-10-425-115-316296	Sequence 316296
816	6	0.8	42	16	US-10-425-115-273437	Sequence 273437	889	6	0.8	59	9	US-09-864-761-42686	Sequence 42686, A
817	6	0.8	43	15	US-10-424-599-254844	Sequence 254844	890	6	0.8	59	15	US-10-424-599-187445	Sequence 187445
818	6	0.8	43	16	US-10-424-599-254844	Sequence 254844, A	891	6	0.8	59	16	US-10-437-963-196161	Sequence 196161
819	6	0.8	43	16	US-10-425-115-284961	Sequence 284961	892	6	0.8	59	16	US-10-767-701-33262	Sequence 33262, A
820	6	0.8	44	9	US-09-925-299-1094	Sequence 1094, Ap	893	6	0.8	59	16	US-10-425-115-198279	Sequence 198279
821	6	0.8	44	10	US-09-925-299-1094	Sequence 1094, Ap	894	6	0.8	59	16	US-10-425-115-230151	Sequence 230151
822	6	0.8	44	14	US-10-083-357-858	Sequence 858, App	895	6	0.8	59	16	US-10-425-115-268417	Sequence 268417
823	6	0.8	44	14	US-10-097-111-462	Sequence 462, App	896	6	0.8	59	16	US-10-425-115-36057	Sequence 36057
824	6	0.8	44	15	US-10-424-599-181073	Sequence 181073	897	6	0.8	60	9	US-09-864-761-36505	Sequence 36505, A
825	6	0.8	44	15	US-10-424-599-208117	Sequence 208117	898	6	0.8	60	10	US-09-935-384-773	Sequence 773, App
826	6	0.8	44	15	US-10-424-599-222849	Sequence 222849	899	6	0.8	60	10	US-09-935-384-774	Sequence 774, App
827	6	0.8	45	15	US-10-424-599-200405	Sequence 200405	900	6	0.8	60	14	US-10-106-698-5326	Sequence 5326, Ap
828	6	0.8	45	16	US-10-424-599-215060	Sequence 215060	901	6	0.8	60	15	US-10-424-599-217289	Sequence 217289
829	6	0.8	46	15	US-10-424-599-193929	Sequence 193929	902	6	0.8	60	15	US-10-424-599-255017	Sequence 255017
830	6	0.8	46	15	US-10-424-599-250018	Sequence 250018	903	6	0.8	60	15	US-10-424-599-275730	Sequence 275730
831	6	0.8	46	15	US-10-424-599-284367	Sequence 284367	904	6	0.8	60	15	US-10-424-599-278739	Sequence 278739
832	6	0.8	47	15	US-10-424-599-164462	Sequence 164462	905	6	0.8	60	15	US-10-424-599-278739	Sequence 278739
833	6	0.8	47	15	US-10-424-599-175289	Sequence 175289	906	6	0.8	60	15	US-10-466-205-33	Sequence 33, Appl
834	6	0.8	49	15	US-10-424-599-214676	Sequence 214676	907	6	0.8	60	15	US-10-240-801A-15	Sequence 15, Appl
835	6	0.8	49	15	US-10-424-599-247006	Sequence 247006	908	6	0.8	60	16	US-10-437-963-145637	Sequence 145637
836	6	0.8	49	16	US-10-425-115-201029	Sequence 201029	909	6	0.8	60	16	US-10-437-963-145637	Sequence 1, Appl
837	6	0.8	49	16	US-10-425-115-212882	Sequence 212882	910	6	0.8	60	16	US-10-425-115-249337	Sequence 249337
838	6	0.8	49	16	US-10-425-115-343792	Sequence 343792	911	6	0.8	60	16	US-10-425-115-258455	Sequence 258455
839	6	0.8	50	15	US-10-424-599-142892	Sequence 142892	912	6	0.8	60	16	US-10-425-115-282677	Sequence 282677
840	6	0.8	50	16	US-10-437-963-143258	Sequence 143258	913	6	0.8	60	16	US-10-425-115-288275	Sequence 288275
841	6	0.8	50	16	US-10-437-963-144934	Sequence 144934	914	6	0.8	60	16	US-10-425-115-340928	Sequence 340928
842	6	0.8	50	16	US-10-425-115-246059	Sequence 246059	915	6	0.8	61	15	US-10-424-599-216350	Sequence 216350
843	6	0.8	50	16	US-10-425-115-258548	Sequence 258548	916	6	0.8	61	16	US-10-425-115-225088	Sequence 225088
844	6	0.8	50	16	US-10-425-115-289140	Sequence 289140	917	6	0.8	61	16	US-10-425-115-273735	Sequence 273735
845	6	0.8	50	16	US-10-425-115-345542	Sequence 345542	918	6	0.8	62	16	US-10-425-115-351161	Sequence 351161
846	6	0.8	51	9	US-09-864-761-41434	Sequence 41434, A	919	6	0.8	62	15	US-10-424-599-178215	Sequence 178215
847	6	0.8	51	9	US-09-864-761-43533	Sequence 43533, A	920	6	0.8	62	15	US-10-424-599-244018	Sequence 244018
848	6	0.8	51	9	US-09-738-626-4205	Sequence 4205, Ap	921	6	0.8	62	16	US-10-424-599-246325	Sequence 246325
849	6	0.8	51	15	US-10-424-599-188733	Sequence 188733	922	6	0.8	62	16	US-10-425-115-226730	Sequence 226730
850	6	0.8	51	15	US-10-424-599-192988	Sequence 192988	923	6	0.8	62	16	US-10-425-115-251725	Sequence 251725
851	6	0.8	51	16	US-10-425-115-229574	Sequence 229574	924	6	0.8	62	16	US-10-425-115-280551	Sequence 280551
852	6	0.8	51	16	US-10-425-115-281091	Sequence 281091	925	6	0.8	63	9	US-09-864-761-48451	Sequence 48451, A
853	6	0.8	52	9	US-09-764-847-804	Sequence 804, App	926	6	0.8	63	9	US-09-764-860-354	Sequence 354, App
854	6	0.8	52	14	US-10-092-154-804	Sequence 32686, A	927	6	0.8	63	9	US-09-738-626-5130	Sequence 5130, App
855	6	0.8	52	14	US-10-029-386-32686	Sequence 32686, A	928	6	0.8	63	14	US-10-074-095-354	Sequence 354, App
856	6	0.8	52	15	US-10-424-599-210870	Sequence 210870	929	6	0.8	63	15	US-10-212-872-354	Sequence 354, App
857	6	0.8	52	15	US-10-424-599-241749	Sequence 241749	930	6	0.8	63	15	US-10-424-599-198003	Sequence 198003
858	6	0.8	52	16	US-10-437-963-135363	Sequence 135363	931	6	0.8	63	15	US-10-424-599-213260	Sequence 213260
859	6	0.8	52	16	US-10-437-963-183149	Sequence 183149	932	6	0.8	63	15	US-10-424-599-239634	Sequence 239634
860	6	0.8	52	16	US-10-437-963-183149	Sequence 183149	933	6	0.8	63	16	US-10-425-115-185582	Sequence 185582
861	6	0.8	53	15	US-10-424-599-233874	Sequence 233874	934	6	0.8	63	16	US-10-425-115-207449	Sequence 207449
862	6	0.8	53	16	US-10-425-115-209875	Sequence 209875	935	6	0.8	63	16	US-10-425-115-265999	Sequence 265999
863	6	0.8	53	16	US-10-425-115-273163	Sequence 273163	936	6	0.8	64	15	US-10-425-115-293345	Sequence 293345
864	6	0.8	54	15	US-10-424-599-192315	Sequence 192315	937	6	0.8	64	15	US-10-349-607-130	Sequence 130, App
865	6	0.8	54	15	US-10-424-599-236359	Sequence 236359	938	6	0.8	64	15	US-10-424-599-154815	Sequence 154815
866	6	0.8	54	16	US-10-425-115-211925	Sequence 211925	939	6	0.8	64	16	US-10-425-115-234850	Sequence 234850
867	6	0.8	54	16	US-10-425-115-261837	Sequence 261837	940	6	0.8	64	16	US-10-425-115-255147	Sequence 255147
868	6	0.8	54	16	US-10-425-115-308996	Sequence 308996	941	6	0.8	64	16	US-10-425-115-312105	Sequence 312105
869	6	0.8	54	16	US-10-425-115-333948	Sequence 333948	942	6	0.8	65	9	US-09-864-761-39981	Sequence 39981, A
870	6	0.8	54	17	US-10-808-187-1904	Sequence 1904, Ap	943	6	0.8	65	13	US-10-001-870-119	Sequence 119, App
871	6	0.8	55	9	US-09-864-761-47472	Sequence 47472, A	944	6	0.8	65	14	US-10-097-111-388	Sequence 388, App
872	6	0.8	55	15	US-10-424-599-150228	Sequence 150228	945	6	0.8	65	16	US-10-425-115-279901	Sequence 279901
873	6	0.8	55	16	US-10-424-599-281675	Sequence 281675	946	6	0.8	65	16	US-10-856-499-604	Sequence 604, App
874	6	0.8	55	9	US-09-864-761-38992	Sequence 38992, A	947	6	0.8	66	15	US-10-424-599-193996	Sequence 193996
875	6	0.8	56	9	US-09-939-980-332	Sequence 332, App	948	6	0.8	66	15	US-10-424-599-198991	Sequence 198991
876	6	0.8	56	15	US-10-424-599-181170	Sequence 181170	949	6	0.8	66	15	US-10-424-599-223134	Sequence 223134
877	6	0.8	56	15	US-10-424-599-196379	Sequence 196379	950	6	0.8	66	16	US-10-425-115-336417	Sequence 336417
878	6	0.8	56	15	US-10-424-599-249260	Sequence 249260	951	6	0.8	67	14	US-10-156-761-8250	Sequence 8250, Ap
879	6	0.8	56	16	US-10-424-599-211496	Sequence 211496	952	6	0.8	67	15	US-10-424-599-160950	Sequence 160950
880	6	0.8	57	9	US-09-864-761-46468	Sequence 46468, A	953	6	0.8	67	15	US-10-424-599-261870	Sequence 261870
881	6	0.8	57	15	US-10-424-599-155487	Sequence 155487	954	6	0.8	67	15	US-10-424-599-266764	Sequence 266764
882	6	0.8	57	15	US-10-424-599-173228	Sequence 173228	955	6	0.8	67	16	US-10-424-599-313696	Sequence 313696
883	6	0.8	57	15	US-10-424-599-249260	Sequence 249260	956	6	0.8	68	15	US-10-424-599-205787	Sequence 205787
884	6	0.8	57	16	US-10-437-963-104783	Sequence 104783	957	6	0.8	68	16	US-10-425-115-189961	Sequence 189961
885	6	0.8	57	16	US-10-437-963-145277	Sequence 145277	958	6	0.8	68	16	US-10-425-115-213549	Sequence 213549
886	6	0.8	57	16	US-10-425-115-335915	Sequence 335915	959	6	0.8	68	16	US-10-425-115-215610	Sequence 215610
887	6	0.8	58	16	US-10-425-115-218982	Sequence 218982	960	6	0.8	69	14	US-10-029-386-29743	Sequence 29743, A
										69	15	US-10-424-599-153521	Sequence 153521


```
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-606-618-4

Query Match      100.0%; Score 797; DB 17; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSA 60

Qy 61 IIKSLYATGPDVVRVETADQQLLTWIERPTIGSNIITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGPDVVRVETADQQLLTWIERPTIGSNIITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQYFNQATLNOAVAGLEKEEYLRGKLNQITPKVTKLARNRVDITIDEGSKAKITDIE 180
Db 121 SQYFNQATLNOAVAGLEKEEYLRGKLNQITPKVTKLARNRVDITIDEGSKAKITDIE 180

Qy 181 PEGNQVSDRKLQMSLTEGGIITWLTLSNQFNEQKFAQDMKVTDFYQNNGYDFDPRIL 240
Db 181 PEGNQVSDRKLQMSLTEGGIITWLTLSNQFNEQKFAQDMKVTDFYQNNGYDFDPRIL 240

Qy 241 DTDIQTNEDEKTKQITIKITVHEGFRNGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300
Db 241 DTDIQTNEDEKTKQITIKITVHEGFRNGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300

Qy 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNK 360
Db 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNK 360

Qy 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNSL 420
Db 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNSL 420

Qy 421 RSTGSLDLSAGVQDGTGLVMSAGVQDNLFQGTGKSAALRASRKTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDLSAGVQDGTGLVMSAGVQDNLFQGTGKSAALRASRKTTLNGSLSFDPYFTA 480

Qy 481 DGVSGLGVDYVKGAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGVDYVKGAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

Qy 541 YNKAPHYADFIKKYKTDGTDGSGFKGWLKGTGWRNKTDTSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPHYADFIKKYKTDGTDGSGFKGWLKGTGWRNKTDTSALWPTRGYLTGVNAEIA 600

Qy 601 LPGSKLOYYSATHNQWTFPLSKTFTLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPLSKTFTLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVR 660

Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVDG 720

Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFPYVPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFPYVPLKK 780

Qy 781 KPEDEIQRFQGLGTTFF 797
Db 781 KPEDEIQRFQGLGTTFF 797
```

RESULT 3

```
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
```

```
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-3

Query Match      94.4%; Score 752; DB 14; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADPTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGPFDDVRVETAD 80
Db 21 ADPTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGPFDDVRVETAD 80

Qy 81 GQLLLTVIERPTIGSNIITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLEKEEY 140
Db 81 GQLLLTVIERPTIGSNIITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLEKEEY 140

Qy 141 LGRGKLNQITPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSRDKLMRQMSLTE 200
Db 141 LGRGKLNQITPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSRDKLMRQMSLTE 200

Qy 201 GGIWTLTRSNQFNEQKFAQDMKVTDFYQNNGYDFDRIILDTIDQNEDEKTKQITIKITVH 260
Db 201 GGIWTLTRSNQFNEQKFAQDMKVTDFYQNNGYDFDRIILDTIDQNEDEKTKQITIKITVH 260

Qy 261 ECGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQDMTAVLGEIQNRMSAGYAYS 320
Db 261 ECGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQDMTAVLGEIQNRMSAGYAYS 320

Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMSAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMSAPYDTS 380

Qy 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNSLTERSTGSLDLSAGWQDTGLVM 440

Qy 441 SAGVSQDNLFQGTGKSAALRASRKTTLNGSLSFDPYFTADGVSIGYDYVKGAFDPRKAS 500
Db 441 SAGVSQDNLFQGTGKSAALRASRKTTLNGSLSFDPYFTADGVSIGYDYVKGAFDPRKAS 500

Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKTDG 560

Qy 561 TDGSPFKGWLKGTGWRNKTDTSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSPFKGWLKGTGWRNKTDTSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620

Qy 621 LSKTFTLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVGIAGGYRTKEIPFFENFYGGGLGSVRGYESGTLGPKVYDEYGEKIS 680

Qy 681 YGNNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVDGKTYDDNSSATGGRVQNIYG 740
Db 681 YGNNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVDGKTYDDNSSATGGRVQNIYG 740

Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFP 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFP 772
```

RESULT 4

US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS

; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181.660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

Query Match 94.4%; Score 752; DB 14; Length 797;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	21	ADFTIQDIRVEGLQRTSPSTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Db	21	ADFTIQDIRVEGLQRTSPSTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Qy	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY	140
Db	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY	140
Qy	141	LGRGKLNIOITPKVTKLARNRVDIITIDEGSKAKITDIEFEGNOVYSRDKLMRQMSLTE	200
Db	141	LGRGKLNIOITPKVTKLARNRVDIITIDEGSKAKITDIEFEGNOVYSRDKLMRQMSLTE	200
Qy	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTQTIKITH	260
Db	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTQTIKITH	260
Qy	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Db	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Db	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Qy	381	KLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Db	381	KLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Qy	441	SAGVSQDNLFOTGKSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDYVYKAFDPRKAS	500
Db	441	SAGVSQDNLFOTGKSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDYVYKAFDPRKAS	500
Qy	501	TSIIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Db	501	TSIIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Qy	561	TGGSFPGWLYKGTVWGGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP	620
Db	561	TGGSFPGWLYKGTVWGGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP	620
Qy	621	LSKFTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPVKYDYEYGEKIS	680
Db	621	LSKFTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPVKYDYEYGEKIS	680
Qy	681	YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG	740
Db	681	YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG	740

Qy	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772
Db	741	AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772

RESULT 5

US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

Query Match 94.4%; Score 752; DB 15; Length 797;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	21	ADFTIQDIRVEGLQRTSPSTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Db	21	ADFTIQDIRVEGLQRTSPSTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Qy	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY	140
Db	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY	140
Qy	141	LGRGKLNIOITPKVTKLARNRVDIITIDEGSKAKITDIEFEGNOVYSRDKLMRQMSLTE	200
Db	141	LGRGKLNIOITPKVTKLARNRVDIITIDEGSKAKITDIEFEGNOVYSRDKLMRQMSLTE	200
Qy	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTQTIKITH	260
Db	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTQTIKITH	260
Qy	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Db	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Db	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Qy	381	KLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Db	381	KLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Qy	441	SAGVSQDNLFOTGKSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDYVYKAFDPRKAS	500
Db	441	SAGVSQDNLFOTGKSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDYVYKAFDPRKAS	500
Qy	501	TSIIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Db	501	TSIIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Qy	561	TGGSFPGWLYKGTVWGGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP	620
Db	561	TGGSFPGWLYKGTVWGGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP	620

```

QY 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
DB 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
QY 681 YGNNKANVSAELLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
DB 681 YGNNKANVSAELLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
QY 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
DB 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 6
US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-3

Query Match          94.4%; Score 752; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
DB 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
DB 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
QY 141 LGRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLQRMQSLTE 200
DB 141 LGRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLQRMQSLTE 200
QY 201 GGIWTLTRSNQFNEQKPAQDMKVTDYFQNNGYDFDRIILDTDIQTNEDEKTKQTIKTIHV 260
DB 201 GGIWTLTRSNQFNEQKPAQDMKVTDYFQNNGYDFDRIILDTDIQTNEDEKTKQTIKTIHV 260
QY 261 EGRFRWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMGSAGYAYS 320
DB 261 EGRFRWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMGSAGYAYS 320
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
DB 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
QY 381 KQRSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
DB 381 KQRSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
QY 441 SAGVQNLFGTGSAALRASRSTTLNGSLSFDPYFTADGSLGVYDVYKGAFPDRKAS 500
DB 441 SAGVQNLFGTGSAALRASRSTTLNGSLSFDPYFTADGSLGVYDVYKGAFPDRKAS 500
QY 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTGD 560
DB 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTGD 560

```

```

DB 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTGD 560
QY 561 TDGSPFGWLYKGTVWGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYISATHNQTWFFP 620
DB 561 TDGSPFGWLYKGTVWGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYISATHNQTWFFP 620
QY 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
DB 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
QY 681 YGNNKANVSAELLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
DB 681 YGNNKANVSAELLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
QY 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
DB 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 7
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-11

Query Match          94.4%; Score 752; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
DB 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
DB 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
QY 141 LGRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLQRMQSLTE 200
DB 141 LGRGKLNIOITPKVTKLARNRVDITIDEGKSAKITDIEFEGNOVYSDRKLQRMQSLTE 200
QY 201 GGIWTLTRSNQFNEQKPAQDMKVTDYFQNNGYDFDRIILDTDIQTNEDEKTKQTIKTIHV 260
DB 201 GGIWTLTRSNQFNEQKPAQDMKVTDYFQNNGYDFDRIILDTDIQTNEDEKTKQTIKTIHV 260
QY 261 EGRFRWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMGSAGYAYS 320
DB 261 EGRFRWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMGSAGYAYS 320
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
DB 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
QY 381 KQRSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
DB 381 KQRSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440

```


Qy	262	GGRFRWGKVSIEGDTNVEVPKAELEKLLTNKPKGWYEROQMTAVLGEIQNRMGSGAGYAYSE	321
Db	241	GGRFRWGKVSIEGDTNVEVPKAELEKLLTNKPKGWYEROQMTAVLGEIQNRMGSGAYAYSE	300
Qy	322	ISVQPLPNAETKTDVFLHIHBPGRKIYNEIHIITGNKNTRDVRVRELRQMESAPYDTSK	381
Db	301	ISVQPLPNAETKTDVFLHIHBPGRKIYNEIHIITGNKNTRDVRVRELRQMESAPYDTSK	360
Qy	382	LQRSKERVELLGYPDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDITGLVMS	441
Db	361	LQRSKERVELLGYPDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDITGLVMS	420
Qy	442	AGVSQDNLFGTKSAALRASRSKTTINGLSLSTDPYFTADGVSGLGYDVYVKAFDPRKAST	501
Db	421	AGVSQDNLFGTKSAALRASRSKTTINGLSLSTDPYFTADGVSGLGYDVYVKAFDPRKAST	480
Qy	502	SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTDGT	561
Db	481	SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTDGT	540
Qy	562	DGSPKGMWLYKGTGVGMRNKTDLSALMPTGGLYTGUNAEIALPGSKLOYYSATNQWTFPPL	621
Db	541	DGSPKGMWLYKGTGVGMRNKTDLSALMPTGGLYTGUNAEIALPGSKLOYYSATNQWTFPPL	600
Qy	622	SKTFTLMLGGEVGIAGGYGRKTEIPFPENFYGGGLGSRGYESGTLGPKVYDEYGEKLSY	681
Db	601	SKTFTLMLGGEVGIAGGYGRKTEIPFPENFYGGGLGSRGYESGTLGPKVYDEYGEKLSY	660
Qy	682	GGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYTDNNSSSATGGRVQNIYGA	741
Db	661	GGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYTDNNSSSATGGRVQNIYGA	720
Qy	742	GNTHKSTFTTNELRYRSAGAVTWLSPGLPMKF	772
Db	721	GNTHKSTFTTNELRYRSAGAVTWLSPGLPMKF	751

```

RESULT 10
US-10-181-600-5
; Sequence 5, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-5

Query Match          94.2%; Score 751; DB 16; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22  DFTIQDIRVEGLQRTBSTVFNYLPMVKVGDTYNDTHGSAIIKISLYATGFFDDVRVETADG 81
Db      1  DFTIQDIRVEGLQRTBSTVFNYLPMVKVGDTYNDTHGSAIIKISLYATGFFDDVRVETADG 60
Qy      82  QLLLTIVERTPTIGSLNTGAKWLQNDAIKNKLESFGLAQSOYFNQATLNQAVAGLKEEYL 141
Db      61  QLLLTIVERTPTIGSLNTGAKWLQNDAIKNKLESFGLAQSOYFNQATLNQAVAGLKEEYL 120
Qy      142 GRGKLNITQITPKVTKLARNRVDITITDEGSKAKITDIEFGNQVYSDRKLMRQMSLITEG 201

```

121	GRGKLNITQITPKVTKLARNRVDIIDITDEGSAKITDIEFGNQVYSRDKLMRQMSL	TEG	18
202	GIWTWLTFRSQNFQEKFAQDMKVTDFYQNNGYDFRILDTDDIQNEBKTKOTIKITVHE	261	
181	GIWTWLTFRSQNFQEKFAQDMKVTDFYQNNGYDFRILDTDDIQNEBKTKOTIKITVHE	240	
262	GGFRWGKVSIEGDTNEVPKAEKLLTMKPGKWERQOMTAVLGEIQNRMGSA	YAYSE	321
241	GGFRWGKVSIEGDTNEVPKAEKLLTMKPGKWERQOMTAVLGEIQNRMGSA	YAYSE	300
322	ISVQPLPNAETKTVDVFLHIEBPGRKIYNEIHTGNKNKTRDEVVRRELQOMESAPYDTSK	381	
301	ISVQPLPNAETKTVDVFLHIEBPGRKIYNEIHTGNKNKTRDEVVRRELQOMESAPYDTSK	360	
382	LQRSKERVLLGYFDNQVDFAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQD	TGLVMS	441
361	LQRSKERVLLGYFDNQVDFAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQD	TGLVMS	420
442	AGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSLGYDVYGKAFDPRKAST	501	
421	AGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSLGYDVYGKAFDPRKAST	480	
502	SIKOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTKDGT	561	
481	SIKOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTKDGT	540	
562	DGSPKGLYKGTVCWGRNKTTDSALMPTRGYLTGVNAETALPGSKLOYYSATHNQTFPPL	621	
541	DGSPKGLYKGTVCWGRNKTTDSALMPTRGYLTGVNAETALPGSKLOYYSATHNQTFPPL	600	
622	SKFTFTMLGSEVGIAGGYGRTEKIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKISY	681	
601	SKFTFTMLGSEVGIAGGYGRTEKIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKISY	660	
682	GGNKANVSARELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA	741	
661	GGNKANVSARELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA	720	
742	GNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	772	
721	GNTHKSTFTNELRYSAGGAVTWLSPLGPMKF	751	
RESULT 11			
US-10-181-600-13			
; Sequence 13, Application US/10181600			
; Publication No. US20040249125A1			
; GENERAL INFORMATION:			
; APPLICANT: CHIRON SpA			
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS			
; FILE REFERENCE: P023785WO			
; CURRENT APPLICATION NUMBER: US/10/181.600			
; CURRENT FILING DATE: 2002-07-17			
; PRIOR APPLICATION NUMBER: GB-0001067.8			
; PRIOR FILING DATE: 2000-01-17			
; PRIOR APPLICATION NUMBER: GB-0005699.4			
; PRIOR FILING DATE: 2000-03-09			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: SeqWin99, version 1.02			
; SEQ ID NO 13			
; LENGTH: 776			
; TYPE: PRT			
; ORGANISM: Neisseria meningitidis			
US-10-181-600-13			

TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS

```

; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-5

```

Query Match 94.2%; Score 751; DB 16; Length 776;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels

Qy	22	DFTI	QD	IR	VE	GL	Q	T	E	P	S	T	V	N	I	P	V	K	V	G	D	T	Y	N	D	T	H	G	S	A	I	I	K	S	I	Y	A	T	G	F	F	D	V	R	V	E	T	A	D	G	81						
Db	1	DFTI	QD	IR	VE	GL	Q	T	E	P	S	T	V	N	I	P	V	K	V	G	D	T	Y	N	D	T	H	G	S	A	I	I	K	S	I	Y	A	T	G	F	F	D	V	R	V	E	T	A	D	G	60						
Qy	82	Q	L	L	T	V	I	E	R	P	T	I	G	S	N	I	T	G	A	K	W	L	Q	N	D	A	I	K	Q	N	E	S	F	G	L	A	O	S	Q	Y	F	N	Q	A	T	L	N	Q	A	V	A	G	K	E	Y	L	141
Db	61	Q	L	L	T	V	I	E	R	P	T	I	G	S	N	I	T	G	A	K	W	L	Q	N	D	A	I	K	Q	N	E	S	F	G	L	A	O	S	Q	Y	F	N	Q	A	T	L	N	Q	A	V	A	G	K	E	Y	L	120
Qy	142	G	R	G	K	N	I	Q	I	T	P	K	V	T	K	L	A	R	N	V	D	I	T	I	D	E	G	S	A	K	I	T	I	E	F	E	G	N	O	V	Y	S	D	R	K	L	M	R	Q	S	I	T	E	G	201		

Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDD

82 Q11LTVIERPTIGSINITGAKWIONDAIKKONIESEGI.AOISOYENOATI.NOA

[illegible]

Db 61 QLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSYFNFQATLNQA

QY 142 GRGKLNQITPKVTKLARNRVDITIDECKSAKITDIEFEGNQVYSRKL

```
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQYFNAQATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQYFNAQATLNQAVAGLKEEYL 120
Qy 142 GRGKLNITQIPKVTKLARNVDIDITIDEKSAKITDIEPEGNOVYSDRKLQMSLTEG 201
Db 121 GRGKLNITQIPKVTKLARNVDIDITIDEKSAKITDIEPEGNOVYSDRKLQMSLTEG 180
Qy 202 GIWTLTRSNQFNQKFAQMEKVTDYFQNNGYDFRILDTDIOTNEDKTKQIKITVHE 261
Db 181 GIWTLTRSNQFNQKFAQMEKVTDYFQNNGYDFRILDTDIOTNEDKTKQIKITVHE 240
Qy 262 GGRFRWKVSIEGDNEVPKAELEKLTMRPKWYERQOMTAVLGEIQNRMSGAGYAYSE 321
Db 241 GGRFRWKVSIEGDNEVPKAELEKLTMRPKWYERQOMTAVLGEIQNRMSGAGYAYSE 300
Qy 322 ISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKKTREDEVVRRRELQWESAPYDTSK 381
Db 301 ISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKKTREDEVVRRRELQWESAPYDTSK 360
Qy 382 LQRSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWVDOTGLVMS 441
Db 361 LQRSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWVDOTGLVMS 420
Qy 442 AGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSLGYDYVYGKAFDPRKAST 501
Db 421 AGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSLGYDYVYGKAFDPRKAST 480
Qy 502 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYGTDTGT 561
Db 481 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYGTDTGT 540
Qy 562 DGSFKGWLKXGTGVGGRNKTDLSLWPRGYLTGVNAEIALPGSKLOYYSATHNQTWPFPL 621
Db 541 DGSFKGWLKXGTGVGGRNKTDLSLWPRGYLTGVNAEIALPGSKLOYYSATHNQTWPFPL 600
Qy 622 SKFTTLMGGEVGIAGGYRTEKEIPFFENFYGGSLGSRVYEGSTLGPKYVDEYGEKISY 681
Db 601 SKFTTLMGGEVGIAGGYRTEKEIPFFENFYGGSLGSRVYEGSTLGPKYVDEYGEKISY 660
Qy 682 GGNKANVSAELLFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYGA 741
Db 661 GGNKANVSAELLFPMGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYISAGGAVTWLSPLGPMKF 772
Db 721 GNTHKSTFTNELRYISAGGAVTWLSPLGPMKF 751

RESULT 12
US-10-181-660-7
; Sequence 7, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-7

Query Match 26.3%; Score 210; DB 14; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SQYFNAQATLNQAVAGLKEEYLGRGKLNITQIPKVTKLARNVDIDITIDEKSAKITDIE 180
Db 121 SQYFNAQATLNQAVAGLKEEYLGRGKLNITQIPKVTKLARNVDIDITIDEKSAKITDIE 180
Qy 181 FEGNOVYSDRKLQMSLTEGGIWTWLTTRS 210
Db 181 FEGNOVYSDRKLQMSLTEGGIWTWLTTRS 210

RESULT 13
US-10-181-600-7
; Sequence 7, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-7

Query Match 26.3%; Score 210; DB 16; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SQYFNAQATLNQAVAGLKEEYLGRGKLNITQIPKVTKLARNVDIDITIDEKSAKITDIE 180
Db 121 SQYFNAQATLNQAVAGLKEEYLGRGKLNITQIPKVTKLARNVDIDITIDEKSAKITDIE 180
Qy 181 FEGNOVYSDRKLQMSLTEGGIWTWLTTRS 210
Db 181 FEGNOVYSDRKLQMSLTEGGIWTWLTTRS 210

RESULT 14
US-10-181-660-9
; Sequence 9, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
```

```
Query Match 26.3%; Score 210; DB 14; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
```


; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-9

Query Match 23.7%; Score 189; DB 14; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.5e-178;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTIVERTIGSLNITGAKMLQNDAIKKNLSEFGLAQSYFNQATLNQAVAGLKEEYL 141
Db 61 QLLLTIVERTIGSLNITGAKMLQNDAIKKNLSEFGLAQSYFNQATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNVDIITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 201
Db 121 GRGKLNIIQITPKVTKLARNVDIITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 180
Qy 202 GIWTLTRS 210
Db 181 GIWTLTRS 189

RESULT 15
US-10-181-600-9
; Sequence 9, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-9

Query Match 23.7%; Score 189; DB 16; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.5e-178;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTIVERTIGSLNITGAKMLQNDAIKKNLSEFGLAQSYFNQATLNQAVAGLKEEYL 141
Db 61 QLLLTIVERTIGSLNITGAKMLQNDAIKKNLSEFGLAQSYFNQATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNVDIITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 201
Db 121 GRGKLNIIQITPKVTKLARNVDIITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 180
Qy 202 GIWTLTRS 210
Db 181 GIWTLTRS 189

Search completed: July 6, 2005, 16:02:16
Job time : 177 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:18:21 ; Search time 49.968 Seconds
(without alignments)
1374.310 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178

Perfect score: 885

Sequence: 1 MKLKQIASALMMLGISPLAF.....RNRVDITIDECKSAK178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pcp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	792	14	US-10-181-660-7
2	885	100.0	792	16	US-10-181-660-7
3	885	100.0	797	9	US-09-994-192-4
4	885	100.0	797	17	US-10-606-618-4
5	879	99.3	797	14	US-10-181-660-3
6	879	99.3	797	15	US-10-320-800-6
7	879	99.3	797	16	US-10-181-660-3
8	875	98.9	797	14	US-10-181-660-11
9	875	98.9	797	16	US-10-181-660-11
10	863	97.5	792	9	US-09-994-192-2
11	863	97.5	792	16	US-10-467-534-92

12	863	97.5	792	17	US-10-606-618-2	Sequence 2, Appli
13	788	89.0	771	14	US-10-181-660-9	Sequence 9, Appli
14	788	89.0	771	16	US-10-181-660-9	Sequence 9, Appli
15	788	89.0	776	14	US-10-181-660-5	Sequence 5, Appli
16	788	89.0	776	14	US-10-181-660-13	Sequence 13, Appli
17	788	89.0	776	16	US-10-181-660-5	Sequence 5, Appli
18	788	89.0	776	16	US-10-181-660-13	Sequence 13, Appli
19	286	32.3	813	16	US-10-896-725-2	Sequence 2, Appli
20	286	32.3	813	16	US-10-896-725-4	Sequence 4, Appli
21	193	21.8	252	16	US-10-437-963-114029	Sequence 114029,
22	151	17.1	896	14	US-10-210-296-5	Sequence 5, Appli
23	151	17.1	896	15	US-10-449-462-5	Sequence 5, Appli
24	100	11.3	792	16	US-10-467-534-25	Sequence 25, Appli
25	98	11.1	792	17	US-10-498-327-55	Sequence 55, Appli
26	97	11.0	21	14	US-10-181-660-8	Sequence 8, Appli
27	97	11.0	21	16	US-10-181-660-8	Sequence 8, Appli
28	95	10.7	614	15	US-10-335-977-4918	Sequence 4918, Ap
29	95	10.7	847	10	US-09-988-0678-8	Sequence 8, Appli
30	95	10.7	925	15	US-10-335-977-4919	Sequence 4919, Ap
31	94.5	10.7	665	16	US-10-437-963-126949	Sequence 126949,
32	94	10.6	299	15	US-10-335-977-4917	Sequence 4917, Ap
33	93.5	10.6	795	15	US-10-289-762-314	Sequence 314, App
34	92	10.4	865	14	US-10-287-274-354	Sequence 354, App
35	92	10.4	865	15	US-10-282-122A-42646	Sequence 42646, A
36	91.5	10.3	790	15	US-10-312-273-147	Sequence 147, App
37	91	10.3	21	14	US-10-181-660-4	Sequence 4, Appli
38	91	10.3	21	16	US-10-181-660-4	Sequence 4, Appli
39	90.5	10.2	541	15	US-10-282-122A-48825	Sequence 48825, A
40	89.5	10.1	2412	16	US-10-408-765A-214	Sequence 214, App
41	88.5	10.0	731	15	US-10-282-122A-52576	Sequence 52576, A
42	87	9.8	21	14	US-10-181-660-12	Sequence 12, Appli
43	87	9.8	21	16	US-10-181-660-12	Sequence 12, Appli
44	87	9.8	638	15	US-10-282-122A-48112	Sequence 48112, A
45	87	9.8	1427	15	US-10-282-122A-48514	Sequence 48514, A

ALIGNMENTS

RESULT 1
US-10-181-660-7
; Sequence 7, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-7

Query Match 100.0%; Score 885; DB 14; Length 792;
Best Local Similarity 100.0%; Pred. No. 3.4e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLKQIASALMMLGISPLAFDFTQDIRVEGLQRTPESTVFNYPVKVGDVTYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFDFTQDIRVEGLQRTPESTVFNYPVKVGDVTYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120

```
QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 2
US-10-181-600-7
; Sequence 7, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-7

Query Match 100.0%; Score 885; DB 16; Length 792;
Best Local Similarity 100.0%; Pred. No. 3.4e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 3
US-09-994-192-4
; Sequence 4, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match 100.0%; Score 885; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 3.4e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
```

```
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 4
US-10-606-618-4
; Sequence 4, Application US/10606618
; Publication No. US20050074458A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/10/606,618
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-606-618-4

Query Match 100.0%; Score 885; DB 17; Length 797;
Best Local Similarity 100.0%; Pred. No. 3.4e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 5
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-3
```

```
Query Match          99.3%; Score 879; DB 14; Length 797;
Best Local Similarity -99.4%; Pred. No. 1.5e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178

RESULT 6
US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

Query Match          99.3%; Score 879; DB 15; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178

RESULT 7
US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P0237850
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001667.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
US-10-181-600-3
```

```
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-3

Query Match          99.3%; Score 879; DB 16; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178

RESULT 8
US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P0237850
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

Query Match          98.9%; Score 875; DB 14; Length 797;
Best Local Similarity 98.9%; Pred. No. 4e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDITIDTGKSAKITD 178

RESULT 9
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P0237850
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; SOFTWARE: Seqwin99, version 1.02
US-10-181-600-11
```

```
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-11

Query Match          98.9%; Score 875; DB 16; Length 797;
Best Local Similarity 98.9%; Pred. No. 4e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 10
US-09-994-192-2
; Sequence 2, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2

Query Match          97.5%; Score 863; DB 9; Length 792;
Best Local Similarity 98.3%; Pred. No. 7.5e-83;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIVCPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 11
US-10-467-534-92
; Sequence 92, Application US/10467534
; Publication No. US20040131625A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
```

```
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/10/467,534
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-534-92

Query Match          97.5%; Score 863; DB 16; Length 792;
Best Local Similarity 98.3%; Pred. No. 7.5e-83;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIVCPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 12
US-10-606-618-2
; Sequence 2, Application US/10606618
; Publication No. US20050074458A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/10/606,618
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-606-618-2

Query Match          97.5%; Score 863; DB 17; Length 792;
Best Local Similarity 98.3%; Pred. No. 7.5e-83;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIVCPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
```

```
Db 121 SQYFNQATLNQAVAGLKEEYVGRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
|||||
RESULT 13
US-10-181-660-9
; Sequence 9, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-9

Query Match 89.0%; Score 788; DB 14; Length 771;
Best Local Similarity 100.0%; Pred. No. 7.4e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60

QY 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 120

QY 142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db 121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157

RESULT 14
US-10-181-600-9
; Sequence 9, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-9

Query Match 89.0%; Score 788; DB 16; Length 771;
Best Local Similarity 100.0%; Pred. No. 7.4e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60

QY 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 120

QY 142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db 121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157

RESULT 15
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match 89.0%; Score 788; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. No. 7.5e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60

QY 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 120

QY 142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db 121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157

Search completed: July 6, 2005, 15:42:20
Job time : 50.968 secs
```

```
QY 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 120

QY 142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db 121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157

RESULT 15
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match 89.0%; Score 788; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. No. 7.5e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60

QY 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNQATLNQAVAGLKEEYL 120

QY 142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db 121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157

Search completed: July 6, 2005, 15:42:20
Job time : 50.968 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:57:40 ; Search time 11.5584 Seconds

(without alignments)
1481.738 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178

Perfect score: 885

Sequence: 1 MKLKQIASALMMLGSLAP.....RNRVDITIDECKSAK178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: piri:*

2: piri:*

3: piri:*

4: piri:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	879	99.3	797	2	G81228
2	875	98.9	797	2	D82000
3	346	39.1	784	2	E82731
4	305.5	34.5	803	2	AB0530
5	304.5	34.4	795	2	AC0129
6	295.5	33.4	797	2	H83190
7	295.5	33.4	810	2	A64742
8	295.5	33.4	810	2	C90651
9	295.5	33.4	810	2	C85502
10	292.5	33.1	803	2	B82099
11	239	27.0	768	2	D71726
12	236.5	26.7	797	2	JC4078
13	236.5	26.7	808	2	F64102
14	233	26.3	768	2	B97725
15	221	25.0	769	2	F87486
16	191.5	21.6	774	2	D97527
17	191.5	21.6	774	2	AE2746
18	182.5	20.6	617	2	H84957
19	160	18.1	781	2	AH3355
20	154	17.4	739	2	A81430
21	108.5	12.3	846	2	F75525
22	100	11.3	792	2	B71539
23	96.5	10.9	853	2	A71339
24	96	10.8	792	2	H81693
25	95.5	10.8	861	2	F77409
26	95	10.7	906	2	F71910
27	95	10.7	916	2	G64501
28	92	10.4	865	1	C64737
29	91.5	10.3	790	2	D86528

30	91.5	10.3	790	2	D72094
31	89	10.1	821	2	B70199
32	88	9.9	778	2	C70412
33	87.5	9.9	866	2	G90646
34	85.5	9.7	832	2	G85497
35	85.5	9.7	863	2	AE0525
36	84.5	9.5	507	2	B69316
37	84.5	9.5	639	2	A71008
38	84	9.5	236	2	D84961
39	83.5	9.4	447	2	E69061
40	83.5	9.4	676	2	AE2417
41	83.5	9.4	811	2	S67315
42	82.5	9.3	408	2	AI3296
43	82	9.3	728	2	F97262
44	81.5	9.2	452	2	AE1710
45	81.5	9.2	452	2	AG1339

ALIGNMENTS

RESULT 1

G81228

outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58 ser: C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: G81228

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: AB1000; MUID:20175755; PMID:10710307

A;Accession: G81228

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-797 <TET>

A;Cross-references: UNIPROT:Q9K1H0; GB:AE002375; GB:AE002098; MID:g7225394; PIDN:AAF4063;

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB0182

C;Superfamily: protective surface antigen D-15

Query Match 99.3%; Score 879; DB 2; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.3e-67;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKLKQIASALMMLGSLAPAFDTIODIRVEGLQRTPESTVENYLPVKVGDYNDTHGSA 60

Db 1 MKLKQIASALMMLGSLAPALADFTIODIRVEGLQRTPESTVENYLPVKVGDYNDTHGSA 60

OY 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120

Db 61 IIKSLVATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120

OY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDECKSAKITD 178

Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDECKSAKITD 178

RESULT 2

D82000

outer membrane protein Omp85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491 ser: C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: D82000

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: AB1775; MUID:20222556; PMID:10761919

A;Accession: D82000

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <PAR>
A;Cross-references: UNIPROT:Q9UX31; GB:AL162752; GB:AL157959; NID:97378778; PIDN:CAB834d
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: omp85; NMA0085
C;Superfamily: protective surface antigen D-15

Query Match 98.9%; Score 875; DB 2; Length 797;
Best Local Similarity 98.9%; Pred. No. 2.9e-67;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQYFNOATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKITD 178
Db 121 SQYFNOATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKITD 178

RESULT 3
E82731

outer membrane antigen XF1046 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82731
A;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-784 <STM>
A;Cross-references: UNIPROT:Q9PEI2; GB:AE003941; GB:AE003849; NID:99105978; PIDN:AAF8385
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrato, D.M.; Carter, H
as-Neto, E.; Docena, C.; El-Dorriy, H.; Pacincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1046
C;Superfamily: protective surface antigen D-15

Query Match 39.1%; Score 346; DB 2; Length 784;
Best Local Similarity 43.2%; Pred. No. 8.8e-22;
Matches 73; Conservative 30; Mismatches 56; Indels 0; Gaps 0;

Qy 8 SALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYA 67
Db 15 AANFSLPVLQAASFFVANDIRVDGLQRIASGTFYLPVNRGDTVDKAVDAIRALYR 74

Qy 68 TGFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNOA 127
Db 75 TGFENVRIDRQGNILVVKVKRPAINKLTITGNKDIKSELLKGLSEIGLSGGTDFDL 134

Qy 128 TLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKI 176
Db 135 SLDRVTOELKQYNNRGNVQMTTTPLDNRNRVDVTAIKEGAKI 183

RESULT 4
AB0530

outer membrane protein precursor yaeT [imported] - Salmonella enterica subsp. enterica ser
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0530
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-803 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08682.1; PID:g16501505; GSPDB:GN00176
C;Genetics:
A;Gene: yaeT
C;Superfamily: protective surface antigen D-15

Query Match 34.5%; Score 305.5; DB 2; Length 803;
Best Local Similarity 38.4%; Pred. No. 2.7e-18;
Matches 68; Conservative 36; Mismatches 72; Indels 1; Gaps 1;

Qy 1 MKLKQIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGS 59
Db 1 MAMKLLIASLLFSSATVVGAGFVVKDHFEGQLRVAVGAALLSNPVTGDTVNDSDS 60

Qy 60 AIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLA 119
Db 61 NTIRALFATGNFEDVRVLRDGNLTLLVQVKRPITIASITFSGNKSVDKMLKQNLASGVR 120

Qy 120 SQYFNOATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKI 176
Db 121 VGESLDRTTLSIDIEKGLDFYSGVKSASVAVVTPLRNRVDLKLVPQEGVSAXI 177

RESULT 5
AC0129

probable surface antigen YPO1052 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0129
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-795 <KUR>
A;Cross-references: UNIPROT:Q8ZH58; GB:AL590842; PIDN:CAC89894.1; PID:g15979119; GSPDB:GN
C;Genetics:
A;Gene: YPO1052
C;Superfamily: protective surface antigen D-15

Query Match 34.4%; Score 304.5; DB 2; Length 795;
Best Local Similarity 37.9%; Pred. No. 3.3e-18;
Matches 67; Conservative 36; Mismatches 73; Indels 1; Gaps 1;

Qy 1 MKLKQIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGS 59
Db 1 MAMKLLIASLLFSGSATVVGADGVVNDHFEGQLRVAVGAALLNMPVGVGDTVSDDDIG 60

Db 1 MAMKLLIASLFFSSATVYGAEFGVVKDHFHFEGLQVAVGAALLSMPVRTGDTVNDEIS 60
 Qy 60 AIKSLYATGFPDDVRVETADGQLLTIVERTTIGSLNITGAKMLQNDIAKKNLESFGLA 119
 Db 61 NTRALFATGTFEDVRVLRDGDTLLVQVKERTIASITFTSGNKSVDKDDMLKNLEASGVR 120
 Qy 120 QSOYFNQATLNOQAVAGLKEEYLGRGKLNITQITPKVTKLARNRVDIDITIDEGSAKI 176
 Db 121 VGESLDRITTIADIEKGLEDFYYSVGKYSASVAVVTPPLPRNRVDLKLVFQEGVSAEI 177

RESULT 8
 C90651
 hypothetical protein ECs0179 [imported] - Escherichia coli (strain O157:H7, substrain RIN
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C:Accession: C90651
 R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
 DNA Res. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
 A:Reference number: A99629; MUID:21156231; PMID:11258796
 A:Accession: C90651
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-810 <HAY>
 A:Cross-references: UNIPROT:P39170; GB:BA000007; PIDN:BA333602.1; PID:gl3359635; GSPDB:G
 A:Experimental source: strain O157:H7, substrain RIMD 0509952
 C:Genetics:
 A:Gene: ECs0179
 C:Superfamily: protective surface antigen D-15

Query Match 33.4%; Score 295.5; DB 2; Length 810;
 Best Local Similarity 37.3%; Pred. No. 2e-17; Mismatches 37; Indels 1; Gaps 1;
 Matches 66; Conservative 37; Mismatches 37; Indels 1; Gaps 1;

Qy 1 MKLKGATASALMMLGISPLAFAD-FTIQDIRVEGLQRTPEPTVFNTPLPVKVGDTYNDTHGS 59
 Db 1 MAMKLLIASLFFSSATVYGAEFGVVKDHFHFEGLQVAVGAALLSMPVRTGDTVNDEIS 60
 Qy 60 AIKSLYATGFPDDVRVETADGQLLTIVERTTIGSLNITGAKMLQNDIAKKNLESFGLA 119
 Db 61 NTRALFATGTFEDVRVLRDGDTLLVQVKERTIASITFTSGNKSVDKDDMLKNLEASGVR 120
 Qy 120 QSOYFNQATLNOQAVAGLKEEYLGRGKLNITQITPKVTKLARNRVDIDITIDEGSAKI 176
 Db 121 VGESLDRITTIADIEKGLEDFYYSVGKYSASVAVVTPPLPRNRVDLKLVFQEGVSAEI 177

RESULT 9
 C85502
 hypothetical protein yaeT [imported] - Escherichia coli (strain O157:H7, substrain EDL93;
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C85502
 R.Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C85502
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-810 <STO>
 A:Cross-references: UNIPROT:P39170; GB:AE005174; NID:gl2152902; PIDN:AAG54479.1; GSPDB:G
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: yaeT
 C:Superfamily: protective surface antigen D-15

Query Match 33.4%; Score 295.5; DB 2; Length 810;
 Best Local Similarity 37.3%; Pred. No. 2e-17;

C;Superfamily: protective surface antigen D-15

Query Match 27.0%; Score 239; DB 2; Length 768;
Best Local Similarity 32.8%; Pred. No. 1.4e-12;
Matches 60; Conservative 35; Mismatches 72; Indels 16; Gaps 4;

QY 1 MKLKQTASALMMLGISPLAFADFTIQDIRVGLQRTPESTVENYLPAVKVGDTYNDTHGSA 60
Db :
4 ISISKULTILLTIPYYHISFADYVIRKTIIBGNHRVERSTIESYLKLNVGETYNNSKEDE 63

QY 61 IIKSLVATGFDDVRVE-TADGQLLTIVIERPTTGSLNITGAQMKLONDAIKKNLESFGLA 119
Db :
64 AIKRLYATSLFRNNIMTYINDGNLIIVNTETPIFISSVFSG-----NSKITNI-----LA 114

QY 120 QSQV-----FNQATLNQAAGLKEEYLGRGKLNIIQTPKVTKLARNRVDIIDITIDEGKS 173
Db :
115 KEIYTMSGESLSQAKIELDVKKILEIYKSRGFSFKVPKIKSLENNRVKVIPIFDIAEGPK 174

QY 174 AKI 176
Db |
175 TVI 177

RESULT 12
JC4078
protective surface antigen D-15 precursor - Haemophilus influenzae (type b)
C;Species: Haemophilus influenzae
A;Variety: type b
C;Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004
C;Accession: JC4078
R;Flack, F.S.; Loomore, S.; Chong, P.; Thomas, W.R.
Gene 156, 97-99, 1995
A;Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influenzae
A;Reference number: JC4078; MUID:95255676; PMID:7737523
A;Accession: JC4078
A;Molecule type: DNA
A;Residues: 1-797 <FLA>
A;Cross-references: UNIPROT:P46024; GB:U13961; NID:G537447; PIDN:AAA85645.1; PID:G537448
A;Experimental source: type b
C;Superfamily: protective surface antigen D-15
C;Keywords: surface antigen
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-797/Product: protective surface antigen D-15 #status predicted <MAT>

Query Match 26.7%; Score 236.5; DB 2; Length 797;
Best Local Similarity 30.3%; Pred. No. 2.3e-12;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;

QY 3 LKQTASALMMLGISPLAF-ADFTIQDIRVGLQRTPESTVENYLPAVKVGDTYNDTHGSAI 61
Db 1 MKLLIASLLFGITTTTFAPPFVAKDINVGVGGDLQQIRASLPVRAGORVTNDVNANI 60

QY 62 IKSLVATGFDDVRVE-TADGQLLTIVIERPTTGSLNITGAQMKLONDAIKKNLESFGLAQ 121
Db :
61 VRSLEVSRGDFDDVKAHQEGDVLVSVVAKSIISDVKIRGNSVIPTEALKQNLDANGFKVG 120

QY 122 QYFNQATLNQAAGLKEEYLGRGKLNIIQTPKVTKLARNRVDIIDITIDEGSKAKI 176
Db :
121 DVLIRESKLNFEPAKSVKEHYASVGRYNATVEPIVNTLPNNRAELIQINEDDKAKL 175

RESULT 13
F64102
protective surface antigen D-15 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998
C;Accession: F64102
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.J.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: F64102
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-808 <TIGR>
A;Cross-references: GB:L42023; TIGR:HI0917
C;Superfamily: protective surface antigen D-15
C;Keywords: surface antigen

Query Match 26.7%; Score 236.5; DB 2; Length 808;
Best Local Similarity 30.3%; Pred. No. 2.4e-12;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;
QY 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAI 61
DB 14 MKLLIASLFGITTTVAAPFVAKDIRDVGQDLEQQIRASLPVRAGQRTDNDVANI 73
QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
DB 74 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIGNSIIPTEALKQNLDANGFKVG 133
QY 122 QYFNQATLNOAVAGLKEEYGRGKLNITQITPKVTKLARNRVDIDITIDEKSAKI 176
DB 134 DVLIREKLNEFAKSVKSHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKL 188

RESULT 14
B97725
outer membrane protein omp1 [imported] - Rickettsia conorii (strain Malish 7)
C;Species: Rickettsia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: B97725
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, P.; R
Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
A;Reference number: A97700; MUID:21442074; PMID:11557893
A;Accession: B97725
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-768 <KUR>
A;Cross-references: UNIPROT:Q92J67; GB:AE006914; PIDN:AAL02740.1; PID:g15619252; GSPDB:G
C;Genetics:
A;Gene: omp1
C;Superfamily: protective surface antigen D-15

Query Match 26.3%; Score 233; DB 2; Length 768;
Best Local Similarity 33.1%; Pred. No. 4.4e-12;
Matches 60; Conservative 32; Mismatches 73; Indels 16; Gaps 4;
QY 3 LKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAI 62
DB 6 ISKLTILLITIFYHHISLADSVIRKITEGHNHRVERSTIESYKLVKVGETYNNKSEDEVI 65
QY 63 KSLYATGFFDDVRVE-TADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
DB 66 KRLYATSLFRNNHITNDGNLIVNVTPTFISWFSF-----NSKIKTNM-----LAKE 116
QY 122 QY-----FNOATLNOAVAGLKEEYGRGKLNITQITPKVTKLARNRVDIDITIDEKSAK 175
DB 117 IYTWSGESLSQAKIELDVKKILEYKSGRFAITVTPKLENLNNRVKVFIDIAEGPKTG 176
QY 176 I 176
DB 177 I 177

RESULT 15
F87486
outer membrane protein CC1915 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87486
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-769 <STO>
A;Cross-references: UNIPROT:Q9A711; GB:AE005673; MID:g13423368; PIDN:AAK23890.1; GSPDB:G
C;Genetics:
A;Gene: CC1915
C;Superfamily: protective surface antigen D-15

Query Match 25.0%; Score 221; DB 2; Length 769;
Best Local Similarity 30.9%; Pred. No. 4.8e-11;
Matches 54; Conservative 36; Mismatches 73; Indels 12; Gaps 3;
QY 11 MMLGISPL-----AFADF---TIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAI 61
DB 3 LLGGSTALVAPQQAFAAQAQTGVVQRIIVQGNRIEQGTVLSYLPQPQGVDSQRLDLA 62
QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
DB 63 LKTLARTDLFADVKIEMLGGLVVKVVENPIINQVVFEGNSSLKEDKLDKDEVQ---IRPR 119
QY 122 QYFNQATLNOAVAGLKEEYGRGKLNITQITPKVTKLARNRVDIDITIDEKSAKI 176
DB 120 GIFTRAKVQADVQRIIETELVRRSGRISATVTPKVVELPQKRVDLVFEINEGAKGV 174

Search completed: July 6, 2005, 15:19:13
Job time : 12.5584 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:53:24 ; Search time 7.68831 Seconds
(without alignments)
1307.930 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745

Perfect score: 140
Sequence: 1 GKTYDDNSSSATGGRVQNIYAGNTH 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Genesecp16Dec04:*
2: Genesecp1980s:*
3: Genesecp1950s:*
4: Genesecp2000s:*
5: Genesecp2001s:*
6: Genesecp2002s:*
7: Genesecp2003as:*
8: Genesecp2003bs:*
9: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	797	3	AAY84947 Amino aci
2	140	100.0	797	4	AUU03959 Neisseria
3	140	100.0	797	4	AUU03957 Neisseria
4	140	100.0	797	4	AUU04451 Neisseria
5	140	100.0	797	4	AAB23788 Neisseria
6	140	100.0	797	4	AAB23784 Neisseria
7	140	100.0	797	4	AAB84746 Amino aci
8	140	100.0	797	4	AAB84744 Amino aci
9	140	100.0	797	5	ABF79802 Neisseria
10	94	67.1	25	4	AUU04412 Neisseria
11	55	39.3	351	5	ABG79591 Candida g
12	55	39.3	1504	8	ADN19818 Bacterial
13	53	37.9	10	4	AUU03975 Neisseria
14	53	37.9	1652	8	ADN20570 Bacterial
15	51.5	36.8	172	4	ABG18158 Novel hum
16	51	36.4	366	5	ABG79585 Candida f
17	51	36.4	366	5	ABG79580 Candida f
18	51	36.4	367	5	ABG79587 Candida g
19	51	36.4	367	5	ABG79561 Candida g
20	51	36.4	368	5	ABG79570 Candida m
21	51	36.4	368	5	ABG79582 Candida g
22	51	36.4	385	5	ABG79572 Candida i
23	51	36.4	385	5	ABG79590 Candida g
24	51	36.4	1266	7	ADB70308 C. neofo
25	50	35.7	31	5	ABG80440 Anti-huma

26	50	35.7	358	5	ABG79568	Abg79568	Candida p
27	50	35.7	359	5	ABG79580	Abg79580	Candida p
28	50	35.7	360	5	ABG79585	Abg79585	Candida i
29	50	35.7	360	5	ABG79576	Abg79576	Candida g
30	50	35.7	361	5	ABG79577	Abg79577	Yeast typ
31	50	35.7	361	5	ABG79566	Abg79566	Candida r
32	50	35.7	361	5	ABG79579	Abg79579	Candida g
33	50	35.7	365	5	ABG79567	Abg79567	Candida u
34	50	35.7	365	5	ABG79589	Abg79589	Candida g
35	50	35.7	366	5	ABG79578	Abg79578	Candida g
36	50	35.7	366	5	ABG79573	Abg79573	Candida k
37	50	35.7	367	5	ABG79574	Abg79574	Candida g
38	50	35.7	367	5	ABG79569	Abg79569	Candida f
39	50	35.7	368	5	ABG79583	Abg79583	Candida g
40	50	35.7	368	5	ABG79583	Abg79583	Candida a
41	50	35.7	369	5	ABG79562	Abg79562	Candida t
42	50	35.7	369	5	ABG79584	Abg79584	Candida g
43	50	35.7	386	8	ADJ71673	Adj71673	Human NOV
44	50	35.7	581	7	ADB37538	Adb37538	Neural th
45	50	35.7	1428	6	ABR53041	Abr53041	Protein s

ALIGNMENTS

RESULT 1	
AAY84947	
ID	AAY84947 standard; protein; 797 AA.
XX	
AC	AAY84947;
XX	
DT	21-AUG-2000 (first entry)
XX	
DE	Amino acid sequence of outer membrane protein (omp) 85.
XX	
KW	Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
KW	meningococcal infection; protective immune response; vaccine.
XX	
OS	Neisseria meningitidis.
XX	
PN	WO200023595-A1.
XX	
PD	27-APR-2000.
XX	
PF	22-OCT-1998; 98WO-US022352.
XX	
PR	22-OCT-1998; 98WO-US022352.
XX	
PA	(UYMO-) UNIV MONTANA.
XX	
PI	Judd RC, Manning SD;
XX	
DR	WPI; 2000-339694/29.
DR	N-PSDB; AAA15156.
XX	
PT	New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
PT	meningitidis useful for vaccine, therapeutic and diagnostic compositions
PT	for gonococcal or meningococcal infections.
XX	
PS	Claim 41; Page 89-92; 98pp; English.
XX	
CC	The present sequence represents an outer membrane protein (omp) 85 of
CC	Neisseria meningitidis. The omp polypeptides and polynucleotides are
CC	useful in compositions for use in the prevention, treatment and diagnosis
CC	of non-symptomatic gonococcal infection or meningococcal infection and
CC	symptomatic disease. They are also useful for the detection of
CC	hybridisation complexes. Antigens and antibodies specific omp proteins
CC	also provide diagnostic, therapeutic and prophylactic compositions for
CC	the treatment or prevention of the infections described above. The
CC	antibodies are useful for inducing a protective immune response in humans
CC	or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC	species. The proteins, antibodies and polynucleotide sequences of the
CC	present invention may also be used in the screening and development of

CC chemical compounds such as drugs or vaccines

XX Sequence 797 AA;

Query Match 100.0%; Score 140; DB 3; Length 797;

Best Local Similarity 100.0%; Pred. No. 4.3e-11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVQNIYGAGNTH 26

DB 720 GKYDDNSSATGGRVQNIYGAGNTH 745

RESULT 2

AAU03957

ID AAU03957 standard; protein; 797 AA.

AC AAU03957;

XX 23-OCT-2001 (first entry)

XX Neisseria gonorrhoeae antigenic protein.

XX Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;

KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.

XX Neisseria gonorrhoeae.

XX Key Location/Qualifiers

FT Peptide 1..21

FT /note= "Signal peptide"

FT Protein 22..797

FT /note= "Mature N. gonorrhoeae antigen"

XX WO200138350-A2.

XX 31-MAY-2001.

XX 28-NOV-2000; 2000WO-IB001851.

XX 29-NOV-1999; 99GB-00028197.

XX 09-MAR-2000; 2000GB-00005698.

XX (CHIR-) CHIRON SPA.

XX (STAT-) STATENS INST FOLKEHELSE.

XX Giuliani MM, Pizza M, Rappuoli R, Holst J;

XX WPI; 2001-381289/40.

XX N-PSDB; AAS07279.

XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria

gonorrhoeae, useful in the manufacture of a medicament for treating and

preventing Neisserial bacteria infection.

XX Claim 1; Page 37-39; 92pp; English.

XX The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.

XX N. gonorrhoeae is closely related to N. meningitidis, which colonises the

pharynx, causing meningitis and, occasionally, septicaemia in the absence

of meningitis. This antigenic protein is useful in the manufacture of a

medicament for treating or preventing infection due to Neisseria

bacteria, such as meningitis and septicaemia. It is also useful as a

diagnostic reagent for detecting the presence of Neisseria bacteria or

antibodies raised against Neisseria, and as a reagent for raising the

antibodies. The Neisserial nucleotide sequences can be expressed in a

variety of different expression systems, for example, mammalian cells,

CC baculoviruses, plants, bacteria and yeast

XX Sequence 797 AA;

SQ

Query Match 100.0%; Score 140; DB 4; Length 797;

Best Local Similarity 100.0%; Pred. No. 4.3e-11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVQNIYGAGNTH 26

DB 720 GKYDDNSSATGGRVQNIYGAGNTH 745

RESULT 3

AAU03957

ID AAU03957 standard; protein; 797 AA.

XX AAU03957;

XX 23-OCT-2001 (first entry)

XX Neisseria meningitidis serogroup B antigenic protein.

XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;

KW bacterial infection; baculovirus; yeast.

XX Neisseria meningitidis.

XX Key Location/Qualifiers

FT Peptide 1..21

FT /note= "Signal peptide"

FT Protein 22..797

FT /note= "Mature N. meningitidis serogroup B antigen"

FT Binding-site 715..722

FT /note= "ATP/GTP-binding site motif A (P-loop)"

XX WO200138350-A2.

XX 31-MAY-2001.

XX 28-NOV-2000; 2000WO-IB001851.

XX 29-NOV-1999; 99GB-00028197.

XX 09-MAR-2000; 2000GB-00005698.

XX (CHIR-) CHIRON SPA.

XX (STAT-) STATENS INST FOLKEHELSE.

XX Giuliani MM, Pizza M, Rappuoli R, Holst J;

XX WPI; 2001-381289/40.

XX N-PSDB; AAS07277.

XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria

gonorrhoeae, useful in the manufacture of a medicament for treating and

preventing Neisserial bacteria infection.

XX Claim 1; Fig 1; 92pp; English.

XX The sequence represents a Neisseria meningitidis serogroup B 85 kDa

antigenic protein. Neisseria meningitidis colonises the pharynx, causing

meningitis and, occasionally, septicaemia in the absence of meningitis.

XX This antigenic protein is useful in the manufacture of a medicament for

treating or preventing infection due to Neisseria bacteria, such as

meningitis and septicaemia. It is also useful as a diagnostic reagent for

detecting the presence of Neisseria bacteria or antibodies raised against

Neisseria, and as a reagent for raising the antibodies. The Neisserial

nucleotide sequences can be expressed in a variety of different

expression systems, for example, mammalian cells, baculoviruses, plants,

bacteria and yeast

XX Sequence 797 AA;

SQ

Query Match 100.0%; Score 140; DB 4; Length 797;

Best Local Similarity 100.0%; Pred. No. 4.3e-11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVQNIYGAGNTH 26

DB 720 GKYDDNSSATGGRVQNIYGAGNTH 745

Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 4
AAU04451
ID AAU04451 standard; protein; 797 AA.
XX
AC AAU04451;
XX
XX 23-OCT-2001 (first entry)
XX
XX Neisseria meningitidis serogroup A antigenic protein #2.
XX
XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.
KW
XX Neisseria meningitidis.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /note= "Signal peptide"
FT Protein 22..797
FT /note= "Mature N. meningitidis serogroup A antigen"
XX
XX WO200138350-A2.
PN
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WO-IB001851.
PF
XX 29-NOV-1999; 99GB-00028197.
PR
XX 09-MAR-2000; 2000GB-00005698.
XX
XX (CHIR-) CHIRON SPA.
PA
XX (STAT-) STATENS INST FOLKEHELSE.
XX
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX WPI; 2001-381289/40.
XX
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX
XX Claim 1; Page 39-40; 92pp; English.
XX
XX The sequence represents a Neisseria meningitidis serogroup A 85 kDa
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicaemia in the absence of meningitis.
CC This antigenic protein is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast. Note: There are two versions of this sequence
CC displayed in the specification (see AAU03958)
XX
XX Sequence 797 AA;
XX
Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
|||||
Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 5
AAB23788
ID AAB23788 standard; protein; 797 AA.

XX AAB23788;
AC
XX 12-JAN-2001 (first entry)
DT
XX
DE Neisseria meningitidis serogroup A amino acid sequence.
XX
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX
XX Neisseria meningitidis.
OS
XX
XX WO2000050075-A2.
PN
XX
XX 31-AUG-2000.
XX
XX 09-FEB-2000; 2000WO-IB000176.
PF
XX 26-FEB-1999; 99US-0121792P.
PR
XX (CHIR-) CHIRON SPA.
PA
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
PI WPI; 2001-015529/02.
XX
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
XX Claim 22; Page 33; 39pp; English.
XX
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (i) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup A amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention
XX
XX Sequence 797 AA;
XX
Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
|||||
Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 6
AAB23784
ID AAB23784 standard; protein; 797 AA.
XX
AC AAB23784;
XX
XX 12-JAN-2001 (first entry)
DT
XX
XX Neisseria meningitidis serogroup B amino acid sequence.
DE
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW

KW immune response.
XX Neisseria meningitidis.
XX WO200050075-A2.
XX 31-AUG-2000.
XX 09-FEB-2000; 2000WO-IB000176.
XX 26-FEB-1999; 99US-0121792P.
XX (CHIR-) CHIRON SPA.
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX WPI; 2001-015529/02.
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX Claim 22; Page 32; 39pp; English.
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup B amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention
XX
SQ Sequence 797 AA;

Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db |||||
720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 7
AAB84746
ID AAB84746 standard; protein; 797 AA.
XX
AC AAB84746;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a Neisseria serogroup A protein.
XX
KW Serogroup A protein; outer membrane protein; Neisserial infection;
KW vaccine.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "mature protein"
XX
PN WO200152885-A1.
XX

PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-IB000166.
XX
XX 17-JAN-2000; 2000GB-00001067.
PR 09-MAR-2000; 2000GB-00005699.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Pizza M, Rappuoli R, Giuliani M;
XX WPI; 2001-451895/48.
DR N-PSDB; AAH42130.
XX
XX Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisserial bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX
XX Disclosure; Page 71-74; 83pp; English.
XX
XX The present sequence represents a Neisseria serogroup A protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO95/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO95/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisserial
CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX
SQ Sequence 797 AA;

Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db |||||
720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 8
AAB84744
ID AAB84744 standard; protein; 797 AA.
XX
AC AAB84744;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a Neisseria serogroup B protein.
XX
KW Serogroup B protein; outer membrane protein; Neisserial infection;
KW vaccine.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "mature protein"
XX
PN WO200152885-A1.
XX
XX 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-IB000166.
XX

PR 17-JAN-2000; 2000GB-00001067.
 .PR 09-MAR-2000; 2000GB-00005699.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Pizza M, Rappuoli R, Giuliani M;
 XX WPI; 2001-451895/48.
 DR N-PSDB; AAH42128.
 XX
 XX Composition for treating or preventing infection to, detecting, or for
 PT raising antibodies against Neisserial bacteria, comprises an N.
 PT meningitidis serogroup B outer membrane preparation and an immunogenic
 PT component.
 XX
 XX Disclosure; Page 59-61; 83pp; English.
 XX
 CC The present sequence represents a Neisseria serogroup B protein. The
 CC protein is used to produce the compositions of the invention. The
 CC specification describes a composition, comprising a Neisseria
 CC meningitidis serogroup B outer membrane preparation and an immunogenic
 CC component. The immunogenic component is protein disclosed in WO99/57280,
 CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
 CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
 CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
 CC medicament for treating or preventing infection due to Neisserial
 CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
 CC bacteria or of antibodies raised against Neisserial bacteria; and/or a
 CC reagent which can raise antibodies against Neisserial bacteria. It may
 CC also be used as a vaccine
 XX
 XX Sequence 797 AA;
 SQ
 Query Match 100.0%; Score 140; DB 4; Length 797;
 Best Local Similarity 100.0%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GKYDDNSSATGGRVQNIYAGNTH 26
 Db |||||
 720 GKYDDNSSATGGRVQNIYAGNTH 745
 RESULT 9
 ABB79802
 ID ABB79802 standard; protein; 797 AA.
 XX
 AC ABB79802;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Neisseria meningitidis outer membrane protein Omp85.
 XX
 KW Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
 KW antibacterial.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= signal_peptide
 FT Protein 22..797
 FT /label= Mature_protein
 XX
 XX US2002086028-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 26-NOV-2001; 2001US-00994192.
 XX
 PR 22-OCT-1998; 98US-00177039.
 XX
 PA (JUDD/) JUDD R C.
 PA (MANN/) MANNING D S.

XX Judd RC, Manning DS;
 XX WPI; 2002-642234/69.
 XX
 PT Novel immunogenic composition for vaccinating against meningococcal or
 PT gonococcal infection, comprises Omp85 protein of Neisseria meningitidis
 PT or Neisseria gonorrhoeae, or nucleic acid encoding the protein.
 XX
 PS Claim 13; Fig 5; 30pp; English.
 XX
 CC The present sequence is that of the Neisseria meningitidis strain HH
 CC outer membrane protein 85 (Omp85), as predicted from a gene that was
 CC obtained from a genomic DNA by PCR amplification using primers based on
 CC the gonococcal omp85 gene. The meningococcal Omp85 protein is 95%
 CC identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed
 CC immunogenic compositions comprise N. meningitidis Omp85, its fragments,
 CC fusion proteins including the Omp85, or nucleic acids encoding them,
 CC which induce a protective immune response in a subject. The immunogenic
 CC compositions may also include an antigen from a heterologous or
 CC homologous pathogen, or a nucleic acid encoding it. They are used in a
 CC claimed method of vaccinating a human or animal against non-symptomatic
 CC meningococcal infection or symptomatic disease. A kit for diagnosing
 CC infection with N. meningitidis comprising labelled Omp85 is also claimed.
 CC The Omp85 polypeptides and polynucleotides are also useful in drug
 CC screening and development
 XX
 SQ Sequence 797 AA;
 Query Match 100.0%; Score 140; DB 5; Length 797;
 Best Local Similarity 100.0%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GKYDDNSSATGGRVQNIYAGNTH 26
 Db |||||
 720 GKYDDNSSATGGRVQNIYAGNTH 745
 RESULT 10
 AAU04412
 ID AAU04412 standard; peptide; 25 AA.
 XX
 AC AAU04412;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Neisseria meningitidis serogroup B antigenic oligopeptide #34.
 XX
 KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX
 OS Neisseria meningitidis.
 XX
 XX WO200138350-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 28-NOV-2000; 2000WO-IB001851.
 XX
 PR 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (STAT-) STATENS INST FOLKEHELSE.
 XX
 PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.
 DR
 XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX

PS Claim 1; Page 85; 92pp; English.

XX The sequence represents a *Neisseria meningitidis* serogroup B antigenic oligopeptide. *Neisseria meningitidis* colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic peptide is useful in the manufacture of a medicament for treating or preventing infection due to *Neisseria* bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of *Neisseria* bacteria or antibodies raised against *Neisseria*, and as a reagent for raising the antibodies. The *Neisseria* nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants, bacteria and yeast.

XX Sequence 25 AA;

Query Match 67.1%; Score 94; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKTYYDDNSSSATGGRVQN 18
|||||
DB 8 GKTYYDDNSSSATGGRVQN 25
|||||

RESULT 11

ABG79591

ID ABG79591 standard; protein; 351 AA.

AC ABG79591;

XX

XX 15-NOV-2002 (first entry)

XX

XX Candida genus type II topoisomerase-associated protein #18.

XX

XX Yeast; type II topoisomerase; Candida detection; medicine; epidemiology; veterinary science; food; enzyme.

XX Unidentified.

OS

XX JP2002153276-A.

PN

XX 28-MAY-2002.

PD

XX

XX 17-NOV-2000; 2000JP-00351684.

PF

XX 17-NOV-2000; 2000JP-00351684.

PR

XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.

PA

XX WPI; 2002-602741/65.

DR

XX

XX Identification and detection of a *Candida* genus yeast by using type II topoisomerase gene as the index, a kit for the identification and detection.

PT

XX

XX Example 2; Fig 7; 39pp; Japanese.

PS

XX The invention relates to a method for the identification of a *Candida* genus yeast. The method includes the following steps: (1) preparing an oligonucleotide which can anneal species-specifically to a DNA encoding type II topoisomerase of a *Candida* genus yeast; (2) preparing a solution containing the oligonucleotide prepared by (1) and a sample from which detection of the *Candida* genus yeast is presumed; (3) repeatedly heating and cooling the solution prepared by (2) under a condition a PCR (polymerase chain reaction) can occur; (4) detecting the *Candida* genus yeast by the presence of a PCR product. The method can be used in the fields of medical science, epidemiology, veterinary science and foods. ABG79542-ABG79591 represent *Candida* type II topoisomerase amino acid sequences and associated peptides of the invention

XX

SQ Sequence 351 AA;

Query Match 39.3%; Score 55; DB 5; Length 351;
Best Local Similarity 63.2%; Pred. No. 23;
Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDDNSSSATGGRVQNIYGA 22
|||||
DB 62 YDDNQKKVTGGR--NGYGA 78
|||||

RESULT 12

ADN19818

ID ADN19818 standard; protein; 1504 AA.

XX

XX ADN19818;

XX

XX 02-DEC-2004 (first entry)

XX

XX Bacterial polypeptide #2471.

DE

XX

XX Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

KW

XX Bacteria.

OS

XX US2003233675-A1.

PN

XX 18-DEC-2003.

PD

XX

XX 20-FEB-2003; 2003US-00369493.

PF

XX

XX 21-FEB-2002; 2002US-0360039P.

PR

XX (CAOY/) CAO Y.

PA

PA (HINK/) HINKLE G J.

PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

XX

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

PI

XX WPI; 2004-061375/06.

DR

XX

XX New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

PT

XX

XX Claim 1; SEQ ID NO 2471; 122pp; English.

PS

XX The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan

CC

CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1504 AA;
 Query Match 39.3%; Score 55; DB 8; Length 1504;
 Best Local Similarity 63.2%; Pred. No. 1.2e+02;
 Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDSSSSATGRVQNIYGA 22
 ||||| ||||| |||||
 Db 215 YDNNQKKVTGR--NGVGA 231

RESULT 13
 AAU03975
 ID AAU03975 standard; peptide; 10 AA.
 XX AC AAU03975;

XX DT 23-OCT-2001 (first entry)
 XX DE Neisseria meningitidis serogroup B antigenic protein AMPHI region #16.
 XX KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast; AMPHI region.
 XX OS Neisseria meningitidis.

XX PN WO200138350-A2.
 XX PD 31-MAY-2001.
 XX PF 28-NOV-2000; 2000WO-IB001851.
 XX PR 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.

XX (CHIR-) CHIRON SPA.
 XX (STAT-) STATENS INST FOLKEHELSE.
 XX PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.

XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX Claim 1; Page 79; 92pp; English.

XX The sequence represents a Neisseria meningitidis serogroup B antigenic
 CC oligopeptide. Neisseria meningitidis colonises the pharynx, causing
 CC meningitis and, occasionally, septicaemia in the absence of meningitis.
 CC This antigenic peptide is useful in the manufacture of a medicament for
 CC treating or preventing infection due to Neisseria bacteria, such as
 CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
 CC detecting the presence of Neisseria bacteria or antibodies raised against
 CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
 CC nucleotide sequences can be expressed in a variety of different
 CC expression systems, for example, mammalian cells, baculoviruses, plants,
 CC bacteria and yeast.

XX SQ Sequence 10 AA;
 Query Match 37.9%; Score 53; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.84;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GRVQNIYGAG 23
 ||||| ||||| |||||

Db RESULT 14
 ID ADN20570
 XX ADN20570 standard; protein; 1652 AA.

XX AC ADN20570;
 XX DT 02-DEC-2004 (first entry)
 XX DE Bacterial polypeptide #3223.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.

XX OS Bacteria.
 XX PN US2003233675-A1.
 XX PD 18-DEC-2003.
 XX PF 20-FEB-2003; 2003US-00369493.
 XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX WPI; 2004-061375/06.

XX New recombinant DNA construct comprising a promoter positioned to provide
 PT for expression of a polynucleotide encoding a polypeptide from a
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 3223; 122pp; English.

XX The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the
 CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1652 AA;

Query Match 37.9%; Score 53; DB 8; Length 1652;
 Best Local Similarity 46.2%; Pred. No. 2.5e+02;
 Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Best Local Similarity 52.4%; Pred. No. 33;
 Matches 11; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 1 GKTYYDSSSSATGGRVQNIYAGNTH 26
 DB 184 GSNFDDNEKTVGGR--NGYGAKLTN 207

QY 6 DNSSSATGGRVQNIYAGNTH 26
 DB 3 DNPSGTDGGR-NRAFGAGNIH 22

Search completed: July 6, 2005, 15:13:15
 Job time : 8.68831 secs

RESULT 15
 ABG18158
 ID ABG18158 standard; protein; 172 AA.
 XX AC ABG18158;
 XX 18-FEB-2002 (first entry)
 XX DE Novel human diagnostic protein #18149.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX OS Homo sapiens.
 XX WO200175067-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US008631.
 XX 31-MAR-2000; 2000US-00540217.
 XX 23-AUG-2000; 2000US-00649167.
 XX (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 XX N-PSDB; AAS82345.

New isolated polynucleotide and encoded polypeptides, useful in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits and to assess
 biodiversity.

Claim 20; SEQ ID NO 48517; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II)
 sequences. (I) is useful as hybridisation probes, polymerase chain
 reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 and in recombinant production of (II). The polynucleotides are also used
 in diagnostics as expressed sequence tags for identifying expressed
 genes. (I) is useful in gene therapy techniques to restore normal
 activity of (II) or to treat disease states involving (II). (II) is
 useful for generating antibodies against it, detecting or quantitating a
 polypeptide in tissue, as molecular weight markers and as a food
 supplement. (II) and its binding partners are useful in medical imaging
 of sites expressing (II). (I) and (II) are useful for treating disorders
 involving aberrant protein expression or biological activities. The
 polypeptide and polynucleotide sequences have application in
 diagnostics, forensics, gene mapping, identification of mutations
 responsible for genetic disorders or other traits to assess biodiversity
 and to produce other types of data and products dependent on DNA and
 amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 amino acid sequences of the invention. Note: The sequence data for this
 patent did not appear in the printed specification, but was obtained in
 electronic format directly from WIPO at
 ftp.wipo.int/pub/published_pct_sequences

Sequence 172 AA;

Query Match 36.8%; Score 51.5; DB 4; Length 172;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:05:39 : Search time 2 Seconds
(without alignments)
970,438 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745
Perfect score: 140
Sequence: 1 GKYDDNSSATGGRVQNIYGAGNTH 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	797	4	US-09-994-192-4
2	50	35.7	1531	4	US-09-976-594-203
3	49	35.0	550	4	US-09-107-532A-5564
4	47	33.6	172	4	US-09-252-991A-22814
5	47	33.6	354	4	US-09-198-452A-504
6	47	33.6	354	4	US-09-438-185A-471
7	47	33.6	409	4	US-09-949-016-11141
8	47	33.6	428	3	US-08-301-162-18
9	47	33.6	428	3	US-09-461-240-18
10	47	33.6	428	4	US-09-968-927-18
11	47	33.6	437	3	US-08-961-083-70
12	47	33.6	437	4	US-09-536-784-70
13	47	33.6	627	4	US-09-583-110-5137
14	47	33.6	637	4	US-09-107-433-4391
15	47	33.6	667	3	US-09-303-064-55
16	47	33.6	667	3	US-09-086-503-55
17	46	32.9	350	4	US-09-489-039A-13959
18	46	32.9	457	4	US-09-248-796A-19185
19	45.5	32.5	501	4	US-09-107-433-2872
20	45.5	32.5	2213	1	US-08-727-034-3
21	45	32.1	94	4	US-09-489-039A-8163
22	45	32.1	1070	2	US-08-633-770A-2
23	45	32.1	1070	4	US-09-280-197-6
24	44.5	31.8	543	4	US-09-583-110-4669
25	44.5	31.8	825	4	US-09-328-352-5974
26	44.5	31.8	1216	4	US-09-134-000C-5130
27	44	31.4	79	4	US-09-489-039A-14024

```

28 44. 31.4 91 1 US-08-480-604A-8 Sequence 8, Appli
29 44 31.4 91 2 US-08-405-496A-8 Sequence 8, Appli
30 44 31.4 91 3 US-08-915-136-8 Sequence 8, Appli
31 44 31.4 91 3 US-08-957-310-8 Sequence 8, Appli
32 44 31.4 91 4 US-10-011-366-8 Sequence 8, Appli
33 44 31.4 91 4 US-09-084-517-8 Sequence 37, Appli
34 44 31.4 353 2 US-08-687-702-37 Sequence 16634, A
35 44 31.4 518 4 US-09-248-796A-16634 Sequence 15457, A
36 44 31.4 581 4 US-09-248-796A-15457 Sequence 7, Appli
37 44 31.4 811 1 US-08-480-604A-7 Sequence 7, Appli
38 44 31.4 811 2 US-08-405-496A-7 Sequence 7, Appli
39 44 31.4 811 3 US-08-915-136-7 Sequence 7, Appli
40 44 31.4 811 3 US-08-957-310-7 Sequence 7, Appli
41 44 31.4 811 4 US-10-011-366-7 Sequence 7, Appli
42 44 31.4 811 4 US-09-084-517-7 Sequence 29, Appli
43 44 31.4 812 1 US-08-480-604A-29 Sequence 29, Appli
44 44 31.4 812 3 US-08-915-136-29 Sequence 29, Appli
45 44 31.4 812 4 US-09-084-517-29

```

ALIGNMENTS

```

RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UNSC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

```

```

Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.5e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 GKYDDNSSATGGRVQNIYGAGNTH 26
DB 720 GKYDDNSSATGGRVQNIYGAGNTH 745

```

```

RESULT 2
US-09-976-594-203
; Sequence 203, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 203
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens

```

```
;
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1867417CD1
US-09-976-594-203

Query Match          35.7%; Score 50; DB 4; Length 1531;
Best Local Similarity 57.9%; Pred. No. 1.3e+02;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY      4 YDDNSSSATGGRVQNIYGA 22
      |||: |||| |||| ||||
Db      151 YDDEKKVTGGR--NGYGA 167

RESULT 3
US-09-107-532A-5564
; Sequence 5564, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5564:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 550 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...550
; SEQUENCE DESCRIPTION: SEQ ID NO: 5564:
US-09-107-532A-5564

Query Match          35.0%; Score 49; DB 4; Length 550;
Best Local Similarity 47.6%; Pred. No. 55;
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY      4 YDDNSSSATGGRVQNIYAGN 24
      |||: |||| |||| ||||
Db      360 YEGNSSVTYKGRLSGGGAPN 380
```

```
RESULT 4
US-09-252-991A-22814
; Sequence 22814, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22814
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22814

Query Match          33.6%; Score 47; DB 4; Length 172;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      13 GGRVQNIYAGNTH 26
      |||: |||| |||| ||||
Db      135 GGRQRLHGAGGVH 148

RESULT 5
US-09-198-452A-504
; Sequence 504, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 504
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-504

Query Match          33.6%; Score 47; DB 4; Length 354;
Best Local Similarity 40.0%; Pred. No. 65;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY      1 GKTYDDNSSSATGGRVQNIYAGNT 25
      |||: |||| |||| ||||
Db      86 GPTAFINNSATSGGALINLSGIGST 110

RESULT 6
US-09-438-185A-471
; Sequence 471, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
```



```
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 354
; TYPE: PR1
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0469
US-09-438-185A-471

Query Match          33.6%; Score 47; DB 4; Length 354;
Best Local Similarity 40.0%; Pred. No. 65;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 GKTYDDNSSSATGGRVONIYGAGNT 25
Db 86 GPTAFINNSATGGALINLSGIGT 110

RESULT 7
US-09-949-016-11141
; Sequence 11141, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11141
; LENGTH: 409
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-11141

Query Match          33.6%; Score 47; DB 4; Length 409;
Best Local Similarity 38.1%; Pred. No. 77;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 3 TYDDNSSSATGGRVONIYGAG 23
Db 333 TMDLTTALEGNRVREFFSG 353

RESULT 8
US-08-301-162-18
; Sequence 18, Application US/08301162
; Patent No. 6022546
; GENERAL INFORMATION:
; APPLICANT: Knapp, Stefan
; APPLICANT: Ziegelmaier, Robert
; APPLICANT: Kupper, Hans
; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
; Preparation Thereof and the Use Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/461,240
; FILING DATE: 16-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,162
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,128
; FILING DATE:
; APPLICATION NUMBER: US 07/623,086
; FILING DATE: 06-DEC-1990
; APPLICATION NUMBER: DE P3940598.2
; FILING DATE: 08-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleschner, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 02481.1005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-301-162-18

Query Match          33.6%; Score 47; DB 3; Length 428;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 ATGGRVONIYGAGNT 25
Db 386 AAGGRVDAFGAGLT 400

RESULT 9
US-09-461-240-18
; Sequence 18, Application US/09461240
; Patent No. 6326008
; GENERAL INFORMATION:
; APPLICANT: Knapp, Stefan
; APPLICANT: Ziegelmaier, Robert
; APPLICANT: Kupper, Hans
; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
; Preparation Thereof and the Use Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,240
; FILING DATE: 16-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/301,162
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/167,128
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/623,086
; FILING DATE: 06-DEC-1990
; APPLICATION NUMBER: DE P3940598.2
; FILING DATE: 08-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Flechner, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 02481.1005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-461-240-18

Query Match 33.6%; Score 47; DB 3; Length 428;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 ATGGRVQNIYGAGNT 25
Db 386 AAGRVDAFGAGLT 400

RESULT 10
US-09-968-927-18
; Sequence 18, Application US/09968927
; Patent No. 6419525
; GENERAL INFORMATION:
; APPLICANT: Knapp, Stefan
; Ziegelmaier, Robert
; Kupper, Hans
; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
; Preparation Thereof and the Use Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,927
; FILING DATE: 03-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,162
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/167,128
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/623,086
; FILING DATE: 06-DEC-1990
; APPLICATION NUMBER: DE P3940598.2
; FILING DATE: 08-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Flechner, Raz E.
; REGISTRATION NUMBER: 34,331
```

```
; REFERENCE/DOCKET NUMBER: 02481.1005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-968-927-18

Query Match 33.6%; Score 47; DB 4; Length 428;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 ATGGRVQNIYGAGNT 25
Db 386 AAGRVDAFGAGLT 400

RESULT 11
US-08-961-083-70
; Sequence 70, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-083-70

Query Match 33.6%; Score 47; DB 3; Length 437;
Best Local Similarity 33.3%; Pred. No. 83;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KYTDNSSSA-----TGGRVQNIYGA 22
Db 182 KIWDNNSLSIVKVKNGKKIYLGGLDNVHGA 214
```

RESULT 12
US-09-536-784-70
; Sequence 70, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-536-784-70

Query Match 33.6%; Score 47; DB 4; Length 437;
Best Local Similarity 33.3%; Pred. No. 83;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KTYDDNSSA-----TGGRVQNIYGA 22
| : : : : :
Db 182 KIWDNSNSLSIVKVGKIKYILGGDLNVHGA 214
| : : : : :

RESULT 13
US-09-583-110-5137
; Sequence 5137, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5137

; LENGTH: 627
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5137

Query Match 33.6%; Score 47; DB 4; Length 627;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KTYDDNSSA-----TGGRVQNIYGA 22
| : : : : :
Db 203 KIWDNSNSLSIVKVGKIKYILGGDLNVHGA 235
| : : : : :

RESULT 14
US-09-107-433-4391
; Sequence 4391, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 893-5007
; TELEFAX: (781) 893-8277
; INFORMATION FOR SEQ ID NO: 4391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 637 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...637
; SEQUENCE DESCRIPTION: SEQ ID NO: 4391:
US-09-107-433-4391

Query Match 33.6%; Score 47; DB 4; Length 637;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KTYDDNSSA-----TGGRVQNIYGA 22
| : : : : :
Db 213 KIWDNSNSLSIVKVGKIKYILGGDLNVHGA 245
| : : : : :

RESULT 15
US-09-303-064-55
; Sequence 55, Application US/09303064
; Patent No. 6221619
; GENERAL INFORMATION:
; APPLICANT: MAINE, Gregory T.
; APPLICANT: HUNT, Jeffery C.
; APPLICANT: BROJANAC, Susan
; APPLICANT: JYH-TSING SHEU, Michael
; APPLICANT: CHOVAN, Linda E.
; APPLICANT: TYNER, Joan D.
; APPLICANT: HOWARD, Lawrence V.
; APPLICANT: PARMLEY, Stephen F.
; APPLICANT: REMINGTON, Jack S.
; APPLICANT: ARAUJO, Fausto
; APPLICANT: SUZUKI, Yashuhiro
; APPLICANT: LI, Shuli
; TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOF
; FILE REFERENCE: 6361.US.P1
; CURRENT APPLICATION NUMBER: US/09/303,064
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 09/086,503
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-303-064-55

Query Match 33.6% Score 47; DB 3; Length 667;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 11 ATGGRVQNIYCGAGNT 25
| | | | | : | | | |
Db 533 AAGGRVDAFGAGLT 547

Search completed: July 6, 2005, 15:20:41
Job time : 3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:57:40 ; Search time 1.68831 Seconds

(without alignments)

1481.738 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745

Perfect score: 140

Sequence: 1 GKTYYDNNSSSATGGRVQNIYGAGNTH 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	797	2 D82000	outer membrane pro
2	140	100.0	797	2 G81228	outer membrane pro
3	60	42.9	588	2 T51154	probable transmemb
4	55	39.3	1485	1 ISZPT2	DNA topoisomerase
5	54	38.6	1462	2 T06819	DNA topoisomerase
6	54	38.6	1473	2 S53599	DNA topoisomerase
7	50	35.7	260	2 T08463	carbonate dehydrat
8	50	35.7	314	1 JCA066	ADPGlyceromanno-he
9	50	35.7	1428	1 ISBYT2	DNA topoisomerase
10	50	35.7	1526	2 JN0598	DNA topoisomerase
11	50	35.7	1526	2 A4406	DNA topoisomerase
12	50	35.7	1528	2 JS0703	DNA topoisomerase
13	50	35.7	1530	2 A40493	DNA topoisomerase
14	50	35.7	1612	2 S59969	DNA topoisomerase
15	50	35.7	1626	2 A39242	DNA topoisomerase
16	48.5	34.6	147	1 S24310	flavodoxin - Desul
17	48	34.3	763	2 D86326	hypothetical prote
18	47	33.6	243	2 T28802	hypothetical prote
19	47	33.6	347	2 A86549	polymorphic outer
20	47	33.6	367	2 T24058	hypothetical prote
21	47	33.6	396	1 A58938	surface protein th
22	47	33.6	493	2 A55092	catalase [EC 1.11.
23	47	33.6	572	2 T34273	hypothetical prote
24	47	33.6	627	2 E95107	choline binding pr
25	47	33.6	627	2 G97975	hypothetical prote
26	46.5	33.2	432	2 S51474	hypothetical prote
27	46	32.9	544	2 AB1178	transport protein
28	46	32.9	1083	1 S53048	alpha-mannosidase
29	46	32.9	1103	2 T13590	distal tail fiber

30	-46	32.9	1230	2 T17187	CL3AB protein - ra
31	46	32.9	1231	2 T18390	latrophilin-3, spl
32	46	32.9	1240	2 T18393	latrophilin-3, spl
33	46	32.9	1273	2 T17188	CL3AC protein - ra
34	46	32.9	1274	2 T18391	latrophilin-3, spl
35	46	32.9	1283	2 T18394	latrophilin-3, spl
36	46	32.9	1298	2 T17199	CL3BB protein - ra
37	46	32.9	1299	2 T18398	latrophilin-3, spl
38	46	32.9	1308	2 T18408	latrophilin-3, spl
39	46	32.9	1341	2 T17200	CL3BC protein - ra
40	46	32.9	1342	2 T18405	latrophilin-3, spl
41	46	32.9	1351	2 T18409	latrophilin-3, spl
42	46	32.9	1459	2 T17186	CL3AA protein - ra
43	46	32.9	1503	2 T18389	latrophilin-3, spl
44	46	32.9	1512	2 T18392	latrophilin-3, spl
45	46	32.9	1527	2 T17198	CL3BA protein - ra

ALIGNMENTS

RESULT 1

D82000
outer membrane protein OMP85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491 se
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: D82000
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: D82000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-797 <PAR>
A:Cross-references: UNIPROT:Q9JX31; GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CA883401
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: omp85; NMA0085
C:Superfamily: protective surface antigen D-15

Query Match 100.0%; Score 140; DB 2; Length 797;

Best Local Similarity 100.0%; Pred. No. 3e-12; Mismatches 0; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKTYYDNNSSSATGGRVQNIYGAGNTH 26

|||||

Db 720 GKTYYDNNSSSATGGRVQNIYGAGNTH 745

RESULT 2

G81228
outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58 se
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: G81228
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: G81228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-797 <TET>
A:Cross-references: UNIPROT:Q9K1H0; GB:AE002375; GB:AE002098; NID:g7225394; PIDN:AAF4063;
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0182
C:Superfamily: protective surface antigen D-15

Query Match 100.0%; Score 140; DB 2; Length 797;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGGRVQNIYGANTH 26
 |||||
 Db 720 GKYDDNSSSATGGRVQNIYGANTH 745

RESULT 3
 T51154
 probable transmembrane protein G5p [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
 R:Comella, P.; Wu, H.J.; Laudie, M.; Berger, C.; Cooke, R.; Delseny, M.; Grellet, F.
 Plant Mol. Biol. 41, 687-700, 1999
 A:Title: Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1 locus on
 A:Reference number: Z24835; MUID:20108326; PMID:10645728
 A:Accession: T51154
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-588 <COM>
 A:Cross-references: UNIPROT:Q96328; EMBL:AF049236; PIDN:AAC14410.1
 R:Grellet, F.; Gaubier, P.; Wu, H.J.; Laudie, M.; Berger, C.; Delseny, M.
 submitted to the EMBL Data Library, September 1996
 A:Description: Structure of the Arabidopsis thaliana Em1 locus.
 A:Reference number: Z25319
 A:Accession: T51164
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-588 <GRE>
 A:Cross-references: EMBL:U72504; PIDN:AA818128.1
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Gene: AtG5
 A:Map position: 3
 A:Introns: 51/1; 76/1; 118/3; 149/2; 168/3; 187/3; 199/1; 226/1; 261/3; 290/3; 316/3; 336/3

Query Match 42.9%; Score 60; DB 2; Length 588;
 Best Local Similarity 50.0%; Pred. No. 0.94;
 Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KTYDDNSSSATGGRVQNIYGANT 25
 |||||
 Db 47 KPIDENASSGSPFRVSTIYGVGCT 70

RESULT 4
 IS2PT2
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: DNA-lyase; type II DNA topoisomerase
 C:Species: Schizosaccharomyces pombe
 C:Date: 30-Sep-1992 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: T39851; A24897
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volkart, G.
 submitted to the EMBL Data Library, July 1998
 A:Reference number: Z21885
 A:Accession: T39851
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1485 <WOO>
 A:Cross-references: UNIPROT:P08096; EMBL:AL031174; PIDN:CAA20107.1; GSPDB:GN00067
 R:Uemura, T.; Morikawa, K.; Yanagida, M.
 EMO J. 5, 2355-2361, 1986
 A:Title: The nucleotide sequence of the fission yeast DNA topoisomerase II gene: structure
 A:Reference number: A24897; MUID:87053875; PMID:3023070
 A:Accession: A24897
 A:Molecule type: DNA
 A:Residues: 55-993; 'I', 995-1485 <UEM>
 A:Cross-references: GB:X04326; NID:G5120; PIDN:CAA27857.1; PID:G5121

C:Comment: Type II DNA topoisomerase catalyzes the ATP-dependent transient breakage, pass
 C:Genetics:
 A:Gene: top2
 A:Map position: 2
 A:Introns: 28/3
 C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd;
 C:Keywords: ATP; DNA binding; DNA replication; heterotetramer; isomerase

Query Match 39.3%; Score 55; DB 1; Length 1485;
 Best Local Similarity 63.2%; Pred. No. 14;
 Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDDNSSSATGGRVQNIYGA 22
 |||||
 Db 196 YDDNQKKTGGR--NGYGA 212

RESULT 5
 T06819
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - garden pea
 C:Species: Pisum sativum (garden pea)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06819
 R:Reddy, M.K.; Nair, S.; Tewari, K.K.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z15832
 A:Accession: T06819
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1462 <RED>
 A:Cross-references: UNIPROT:O24308; EMBL:Y14559; PIDN:CAA74891.1
 C:Genetics:
 A:Note: TOP11
 C:Function:
 A:Description: involved in DNA replication and chromosome condensation
 C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd;
 C:Keywords: ATP; DNA binding; isomerase

Query Match 38.6%; Score 54; DB 2; Length 1462;
 Best Local Similarity 56.5%; Pred. No. 19;
 Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDDNSSSATGGRVQNIYGANTH 26
 |||||
 Db 139 YDDNVKKTGGR--NGYGAKLTN 159

RESULT 6
 S53599
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - Arabidopsis thaliana
 N:Alternate names: DNA-lyase; type II DNA topoisomerase
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 15-Jul-1995 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C:Accession: S53598; S53599; S53600
 R:Xie, S.; Lam, E.
 Nucleic Acids Res. 22, 5729-5736, 1994
 A:Title: Abundance of nuclear DNA topoisomerase II is correlated with proliferation in A
 A:Reference number: S53598; MUID:95140639; PMID:7838729
 A:Accession: S53598
 A:Molecule type: mRNA
 A:Residues: 1-1473 <XIE>
 A:Cross-references: UNIPROT:P30182; EMBL:L21015; NID:G474889; PIDN:AAA65448.1; PID:G47489
 A:Experimental source: ecotype Columbia
 A:Accession: S53599
 A:Molecule type: DNA
 A:Residues: 1202-1304 <XI>
 A:Cross-references: EMBL:U12284; NID:G520557; PIDN:AAC48999.1; PID:G520558
 A:Experimental source: ecotype Columbia
 A:Accession: S53600
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1202-1212, 'N', 1214-1244, 'G', 1246-1298, 'G', 1300-1304 <XIF>
 A:Cross-references: EMBL:U12285; NID:G520559; PIDN:AAC49000.1; PID:G520560

A;Experimental source: ecotype Kashmir
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Gene: TOP11
A;Introns: 1234/1; 1269/1; 1293/3
A;Note: list of introns is incomplete
C;Function:
A;Description: involved in DNA replication and chromosome condensation
C;Superfamily: eukaryotic type II DNA topoisomerase (ATP-hydrolyzing)
C;Keywords: ATP; DNA binding; isomerase; nucleus
F;673-905/Domain: phage T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4>

Query Match 38.6%; Score 54; DB 2; Length 1473;
Best Local Similarity 56.5%; Pred. No. 19;
Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDNNSSATGGRVONIYGAGNTH 26
||||| ||||| ||||| |||||
Db 151 YDNNVKTGGG--NGYGAKLTN 171

RESULT 7
T08463
carbonate dehydratase (EC 4.2.1.1) - zebra fish
C;Species: Brachydanio rerio (zebra fish)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08463
R;Peterson, R.E.; Tu, C.; Linseer, P.J.
J. Mol. Evol. 44, 432-439, 1997
A;Title: Isolation and characterization of a carbonic anhydrase homologue from the zebra fish
A;Reference number: Z16422; MUID: 97250269; PMID: 9089083
A;Accession: T08463
A;Status: preliminary; translated from GB/EMBL/DDBU
A;Molecule type: mRNA
A;Residues: 1-260 <PET>
A;Cross-references: UNIPROT:Q92051; EMBL:U55177; NID:92576334; PID:92576335
C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; zinc
F;5-259/Domain: carbonic anhydrase homology <CAH>

Query Match 35.7%; Score 50; DB 2; Length 260;
Best Local Similarity 45.5%; Pred. No. 11;
Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 5 DNSSSATGGRVONIYGAGNTH 26
||||| ||||| ||||| |||||
Db 73 DNSSSLAGGPIGTIVLRQFH 94

RESULT 8
JC4066
ADPglyceromanno-heptose 6-epimerase (EC 5.1.3.20) rfad VC0240 [similarity] - Vibrio cholerae
N;Alternate names: ADP-L-glycero-D-mannoheptose-6-epimerase; rfad protein
C;Species: Vibrio cholerae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC4066; S70952; G82345; S28467
R;Stroeher, U.H.; Karageorgios, L.E.; Morona, R.; Manning, P.A.
Gene 155, 67-72, 1995
A;Title: In Vibrio cholerae serogroup O1, rfad is closely linked to the rfb operon.
A;Reference number: JC4066; MUID:95212931; PMID:7698669
A;Contents: Inaba and Ogawa serotypes, 569B and O17
A;Accession: JC4066
A;Molecule type: DNA
A;Residues: 1-314 <STR>
A;Cross-references: UNIPROT:Q06963; EMBL:X59554; NID:948381; PIDN:CAA42133.1; PID:948382
R;Bik, E.M.; Bunschoten, A.E.; Willems, R.J.L.; Chang, A.C.Y.; Mooi, F.R.
Mol. Microbiol. 20, 799-811, 1996
A;Title: Genetic organization and functional analysis of the otn DNA essential for cell-division in Vibrio cholerae
A;Reference number: S70952; MUID:96386047; PMID:8793876
A;Accession: S70952
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-67, 'S', 69-314 <BK>

A;Cross-references: EMBL:X90547; NID:91469276; PIDN:CAA62134.1; PID:91107917
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: G82345
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-314 <HEI>
A;Cross-references: GB:AE004113; GB:AE003852; NID:99654648; PIDN:AAF93416.1; GSPDB:GN001;
A;Experimental source: serogroup O1; strain N6961; biotype El Tor
C;Comment: This enzyme is required for the biosynthesis of the lipopolysaccharide precursor
C;Genetics:
A;Gene: rfad; VC0240
A;Map position: 1
C;Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
C;Keywords: isomerase
F;7-12/Region: helix-turn-helix

Query Match 35.7%; Score 50; DB 1; Length 314;
Best Local Similarity 40.0%; Pred. No. 14;
Matches 10; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 KYDNNSSATGGRVONIYGAGNTH 26
||||| ||||| ||||| |||||
Db 158 KQHDETLSQLTGTFRVFNVPYGPREQH 182

RESULT 9
ISBYT2
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - yeast (Saccharomyces cerevisiae)
N;Alternate names: DNA gyrase; DNA topoisomerase II; protein N2244; protein YNL088w
C;Species: Saccharomyces cerevisiae
C;Date: 30-Sep-1992 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57534; A25630; S63027; S30866; S65093
R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57533
A;Accession: S57534
A;Molecule type: DNA
A;Residues: 1-1428 <SOL>
A;Cross-references: UNIPROT:P06786; EMBL:X89016; NID:9887621; PIDN:CAA61422.1; PID:988762;
R;Glaever, G.; Lynn, R.; Goto, T.; Wang, J.C.
J. Biol. Chem. 261, 12448-12454, 1986
A;Title: The complete nucleotide sequence of the structural gene TOP2 of yeast DNA topoisomerase II
A;Reference number: A25630; MUID:86304413; PMID:3017975
A;Accession: A25630
A;Molecule type: DNA
A;Residues: 1-74, 'N', 75-546, 'L', 548-836, 'R', 838-1428 <GIA>
A;Cross-references: GB:M13814; NID:9172997; PIDN:AAB36610.1; PID:9172998
R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63018
A;Accession: S63027
A;Molecule type: DNA
A;Residues: 1-1428 <SOW>
A;Cross-references: EMBL:271364; NID:91301988; PIDN:CAA95964.1; PID:91301989; GSPDB:GN000
R;Jannatipour, M.; Liu, Y.X.; Nitiss, J.L.
submitted to the EMBL Data Library, January 1993
A;Description: The top2-5 mutant of yeast topoisomerase II encodes an enzyme resistant to camptothecin
A;Reference number: S30866
A;Accession: S30866
A;Molecule type: DNA
A;Residues: 812-836, 'P', 838-882, 'P', 884, 'II', 887-977 <JAN>
A;Cross-references: EMBL:L08968; NID:9172999; PIDN:AAB59328.1; PID:9173000
R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
Yeast 12, 485-491, 1996
A;Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV (Chr. XIV)
A;Reference number: S65092; MUID:96310628; PMID:8740422

A;Accession: S65093
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1428 <SOF>
A;Cross-references: EMBL:X89016; NID:g887621; PIDN:CAA61422.1; PID:g887623
C;Comment: Type II DNA topoisomerase catalyzes the ATP-dependent transient breakage, pass
C;Genetics:
A;Gene: SGD:TOP2; TOR3; TRP3; TOP2-5; MIPS:YNL088W
A;Cross-references: SGD:S0005032; MIPS:YNL088W
A;Map position: 14L
C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; DNA replication; heterotetramer; isomerase; phosphoprotein

Query Match 35.7%; Score 50; DB 1; Length 1428;
Best Local Similarity 57.9%; Pred. No. 71;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
QY 4 YDNSSSSATGGRVQNIYGA 22
|||: ||||| |||||
Db 130 YDDDEKKTGGR--NGYGA 146

RESULT 10
JN0598
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - rat
N;Alternate names: DNA topoisomerase II
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C;Accession: JN0598; S32012
R;Park, S.H.; Yoon, J.H.; Kwon, Y.D.; Park, S.D.
Biochem. Biophys. Res. Commun. 193, 787-793, 1993
A;Title: Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase II.
A;Reference number: JN0598; MUID:93230677; PMID:8390253
A;Accession: JN0598
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1526 <PAR>
A;Cross-references: EMBL:Z19552; NID:g57963; PIDN:CAA79611.1; PID:g57964
A;Experimental source: testis
A;Note: the authors translated the codon GTG for residue 3 as Leu
C;Comment: This enzyme is required for the segregation of circular DNA molecules after r
C;Genetics:
A;Gene: rTOP2
C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA recombination; DNA repair; DNA replication; isomerase
F:689-916/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 35.7%; Score 50; DB 2; Length 1526;
Best Local Similarity 57.9%; Pred. No. 76;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
QY 4 YDNSSSSATGGRVQNIYGA 22
|||: ||||| |||||
Db 149 YDDDEKKTGGR--NGYGA 165

RESULT 11
A44406
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - Chinese hamster
N;Alternate names: DNA-gyrase; type II DNA topoisomerase
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A44406
R;Chan, V.T.; Ng, S.W.; Eder, J.P.; Schnipper, L.E.
J. Biol. Chem. 268, 2160-2165, 1993
A;Title: Molecular cloning and identification of a point mutation in the topoisomerase I
A;Reference number: A44406; MUID:93131977; PMID:8380592
A;Accession: A44406
A;Molecule type: nucleic acid
A;Residues: 1-1526 <CHA>
A;Cross-references: UNIPROT:P41515; GB:I04607; NID:g191217; PIDN:AAA37023.1; PID:g191218
A;Experimental source: ovary
A;Note: sequence extracted from NCBI backbone (NCBIP:123211)

C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; DNA replication; heterotetramer; isomerase

Query Match 35.7%; Score 50; DB 2; Length 1526;
Best Local Similarity 57.9%; Pred. No. 76;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
QY 4 YDNSSSSATGGRVQNIYGA 22
|||: ||||| |||||
Db 150 YDDDEKKTGGR--NGYGA 166

RESULT 12
JN0703
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: JS0703; S35483
R;Adachi, N.; Miyaike, M.; Ikeda, H.; Kikuchi, A.
Nucleic Acids Res. 20, 5297-5303, 1992
A;Title: Characterization of cDNA encoding the mouse DNA topoisomerase II that can comple
A;Reference number: S35483; MUID:93065194; PMID:1331984
A;Accession: JS0703
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-1528 <ADA>
A;Cross-references: UNIPROT:Q01320; DDBJ:D12513; NID:g220615; PIDN:BAA02076.1; PID:g22061
R;Adachi, N.; Miyaike, M.; Ikeda, H.; Kikuchi, A.
Nucleic Acids Res. 20, 5297-5303, 1992
A;Title: Characterization of cDNA encoding the mouse DNA topoisomerase II that can comple
A;Reference number: S35483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1528 <ADA2>
A;Cross-references: EMBL:D12513; NID:g220615; PIDN:BAA02076.1; PID:g220616
C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; isomerase; leucine zipper; nucleus
F:994-1015/Region: leucine zipper motif
F:804/Active site: Tyr #status predicted

Query Match 35.7%; Score 50; DB 2; Length 1528;
Best Local Similarity 57.9%; Pred. No. 76;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;
QY 4 YDNSSSSATGGRVQNIYGA 22
|||: ||||| |||||
Db 150 YDDDEKKTGGR--NGYGA 166

RESULT 13
A40493
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) alpha - human
C;Species: Homo sapiens (man)
C;Date: 07-Feb-1992 #sequence_revision 03-Apr-1992 #text_change 19-Dec-1998
C;Accession: A40493; A41278
R;Tsai-Pflugfelder, M.; Liu, L.F.; Liu, A.A.; Tewey, K.M.; Whang-Peng, J.; Knutsen, T.; F
proc. Natl. Acad. Sci. U.S.A. 85, 7177-7181, 1988
A;Title: Cloning and sequencing of cDNA encoding human DNA topoisomerase II and localizat
A;Reference number: A40493; MUID:89017161; PMID:2845399
A;Accession: A40493
A;Molecule type: mRNA
A;Residues: 1-1530 <TSA>
A;Cross-references: GB:J04088
R;Bugg, B.Y.; Danks, M.K.; Beck, W.T.; Suttle, D.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 7654-7658, 1991
A;Title: Expression of a mutant DNA topoisomerase II in CCRP-CEM human leukemic cells sel
A;Reference number: A41278; MUID:91352047; PMID:1652758
A;Accession: A41278
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 442-521 <BUG>
A;Note: a mutant with residue 449-Arg replaced by Gln was resistant to teniposide
C;Genetics:

A;Gene: GDB:TOP2A; TOP2
A;Cross-references: GDB:118884; OMIM:126430
A;Map position: 17q21-17q22
C;Superfamily: eukaryotic type II DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; isomerase; nucleus

Query Match 35.7%; Score 50; DB 2; Length 1530;
Best Local Similarity 57.9%; Pred. No. 76;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDNNSSATGGRVQNIYGA 22
|||: ||||| |||||
Db 150 YDDDEKVTGGR--NGYGA 166

RESULT 14
S59969
N;Alternate names: DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) isoform beta - Chinese hamster
N;Alternate names: DNA topoisomerase II isoform beta; DNA-gyrase
C;Species: Crictetus griseus (Chinese hamster)
C;Date: 15-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
C;Accession: S59969; S54154
R;Derreddre, S.; Frey, S.; Delaporte, C.; Jacquemin-Sablon, A.
Biochim. Biophys. Acta 1264, 178-182, 1995
A;Title: Cloning and characterization of full-length cDNAs coding for the DNA topoisom
A;Reference number: S59969; MUID:96085121; PMID:7495861
A;Accession: S59969
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-1612 <DB>
A;Cross-references: EMBL:X6455; NID:g790987; PIDN:CAA60173.1; PID:g790988
A;Experimental source: lung
C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
C;Keywords: ATP; DNA binding; DNA replication; isomerase; nucleus
F;697-927/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 35.7%; Score 50; DB 2; Length 1612;
Best Local Similarity 57.9%; Pred. No. 81;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDNNSSATGGRVQNIYGA 22
|||: ||||| |||||
Db 160 YDDDEKVTGGR--NGYGA 176

RESULT 15
A39242
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) beta, splice form 2 - human
N;Alternate names: DNA topoisomerase II isoform beta-2
N;Contains: DNA topoisomerase II isoform beta-1
C;Species: Homo sapiens (man)
C;Date: 04-Oct-1991 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
C;Accession: S26730; A39242; S10710; S33970; S30191; S41641; S30190
R;Jenkins, J.R.; Ayton, P.; Jones, T.; Davies, S.L.; Simmons, D.L.; Harris, A.L.; Sheer,
Nucleic Acids Res. 20, 5587-5592, 1992
A;Title: Isolation of cDNA clones encoding the beta isozyme of human DNA topoisomerase I
A;Reference number: S26730; MUID:93087165; PMID:1333583
A;Accession: S26730
A;Molecule type: mRNA
A;Residues: 1-23,29-1626 <JEN>
A;Cross-references: UNIPROT:Q02880; EMBL:X68060; NID:g37230; PIDN:CAA48197.1; PID:g37231
R;Chung, T.D.Y.; Drake, F.H.; Tan, K.B.; Per, S.R.; Crooke, S.T.; Mirabelli, C.K.
Proc. Natl. Acad. Sci. U.S.A. 86, 9431-9435, 1989
A;Title: Characterization and immunological identification of cDNA clones encoding two h
A;Reference number: A39242; MUID:90083281; PMID:2556712
A;Accession: A39242
A;Molecule type: mRNA
A;Residues: 149-1043 <CHU>
A;Cross-references: GB:M27504
R;Austin, C.A.; Fisher, L.M.
FEBS Lett. 266, 115-117, 1990
A;Title: Isolation and characterization of a human cDNA clone encoding a novel DNA topoi
A;Reference number: S10710; MUID:90306333; PMID:2163884

A;Accession: S10710
A;Molecule type: mRNA
A;Residues: 1043-1276 <AUS>
A;Cross-references: GB:X53662; GB:S56813; NID:g38324; PIDN:CAA37706.1; PID:g38325
R;Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M.
Biochim. Biophys. Acta 1172, 283-291, 1993
A;Title: Novel HeLa topoisomerase II is the II-beta isoform: complete coding sequence an
A;Reference number: S30190; MUID:93192319; PMID:8383537
A;Accession: S33970
A;Molecule type: mRNA
A;Residues: 1-23,29-1610,'A',1612-1626 <AU2>
A;Cross-references: EMBL:Z15111
R;Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M.
submitted to the EMBL Data Library, September 1992
A;Reference number: S30191
A;Accession: S30191
A;Molecule type: mRNA
A;Residues: 596-1430,'S',1432-1610,'A',1612-1626 <AU1>
A;Cross-references: EMBL:Z15115; NID:g288564; PIDN:CAA78821.1; PID:g288565
R;Davies, S.L.; Jenkins, J.R.; Hickson, I.D.
Nucleic Acids Res. 21, 3719-3723, 1993
A;Title: Human cells express two differentially spliced forms of topoisomerase II-beta m
A;Reference number: S41641; MUID:93376494; PMID:8396237
A;Accession: S41641
A;Molecule type: DNA
A;Residues: 24-80 <DAV>
A;Cross-references: EMBL:X71911; NID:g396540; PIDN:CAA50726.1; PID:g3980296
A;Note: this sequence represents a long minor splice form, designated beta-2
C;Genetics:
A;Gene: GDB:TOP2B
A;Cross-references: GDB:131575; OMIM:126431
A;Map position: 3p24-3p24
C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
C;Keywords: alternative splicing; ATP; dimer; isomerase; nucleus
F;1-1626/Product: DNA topoisomerase II beta-2 #status predicted <MINR>
F;1-23,29-1626/Product: DNA topoisomerase II beta-1 #status predicted <MAJR>
F;709-939/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 35.7%; Score 50; DB 2; Length 1626;
Best Local Similarity 57.9%; Pred. No. 82;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDNNSSATGGRVQNIYGA 22
|||: ||||| |||||
Db 172 YDDDEKVTGGR--NGYGA 188

Search completed: July 6, 2005, 15:19:14
Job time : 2.68831 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:18:21 ; Search time 7.2987 Seconds
(without alignments)
1374.310 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745
Perfect score: 140
Sequence: 1 GKYTDNSSSATGGRVQNIYGAGNTH 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pbp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pbp.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pbp.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pbp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pbp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pbp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pbp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pbp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pbp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pbp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pbp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pbp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pbp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pbp.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	776	14 US-10-181-660-5	Sequence 5, Appli
2	140	100.0	776	14 US-10-181-660-13	Sequence 13, Appl
3	140	100.0	776	16 US-10-181-600-5	Sequence 5, Appli
4	140	100.0	776	16 US-10-181-600-13	Sequence 13, Appl
5	140	100.0	797	9 US-09-994-192-4	Sequence 4, Appli
6	140	100.0	797	14 US-10-181-660-3	Sequence 3, Appli
7	140	100.0	797	14 US-10-181-660-11	Sequence 11, Appl
8	140	100.0	797	15 US-10-320-800-6	Sequence 6, Appli
9	140	100.0	797	16 US-10-181-600-3	Sequence 3, Appli
10	140	100.0	797	16 US-10-181-600-11	Sequence 11, Appl
11	140	100.0	797	17 US-10-606-618-4	Sequence 4, Appli

12	60	42.9	588	16	US-10-739-930-6705	Sequence 6705, Ap
13	59	42.1	315	14	US-10-156-761-10028	Sequence 10028, A
14	55	39.3	1504	15	US-10-369-493-2471	Sequence 2471, Ap
15	54	38.6	196	16	US-10-425-115-232640	Sequence 232640,
16	54	38.6	1487	16	US-10-437-963-161300	Sequence 161300,
17	53	37.9	1652	15	US-10-369-493-3223	Sequence 3223, Ap
18	51	36.4	193	16	US-10-425-115-288133	Sequence 288133,
19	51	36.4	219	15	US-10-425-114-64250	Sequence 64250, A
20	51	36.4	1666	15	US-10-320-797-3352	Sequence 3352, Ap
21	50.5	36.1	355	15	US-10-425-114-54797	Sequence 54797, A
22	50.5	36.1	589	15	US-10-424-599-164871	Sequence 164871,
23	50	35.7	260	17	US-10-732-923-19028	Sequence 19028, A
24	50	35.7	386	17	US-10-635-398-74	Sequence 74, Appl
25	50	35.7	581	14	US-10-198-070-20	Sequence 20, Appl
26	50	35.7	1428	15	US-10-369-493-1980	Sequence 1980, Ap
27	50	35.7	1429	15	US-10-448-871A-2	Sequence 2, Appli
28	50	35.7	1526	16	US-10-471-758-2	Sequence 347, App
29	50	35.7	1531	9	US-09-876-889-347	Sequence 2593, Ap
30	50	35.7	1531	9	US-09-998-598-2593	Sequence 222, App
31	50	35.7	1531	14	US-10-171-311-222	Sequence 211, App
32	50	35.7	1531	14	US-10-301-822-211	Sequence 46, Appl
33	50	35.7	1531	15	US-10-435-696-46	Sequence 2100, Ap
34	50	35.7	1531	16	US-10-723-860-2100	Sequence 42, Appl
35	50	35.7	1531	17	US-10-645-756-42	Sequence 1161, Ap
36	50	35.7	1621	15	US-10-296-115-1161	Sequence 3017, Ap
37	50	35.7	1626	16	US-10-408-765A-3017	Sequence 8754, Ap
38	49.5	35.4	1534	17	US-10-732-923-8754	Sequence 25453,
39	49	35.0	291	15	US-10-424-599-25453	Sequence 264378,
40	49	35.0	297	15	US-10-424-599-264378	Sequence 10695, A
41	49	35.0	692	9	US-09-815-242-10695	Sequence 57121, A
42	49	35.0	692	15	US-10-282-122A-57121	Sequence 43730, A
43	49	35.0	1953	15	US-10-282-122A-43730	Sequence 282071,
44	48.5	34.6	96	16	US-10-425-115-282071	Sequence 177136,
45	48	34.3	55	15	US-10-424-599-177136	

ALIGNMENTS

RESULT 1
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match 100.0%; Score 140; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. NO. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYTDNSSSATGGRVQNIYGAGNTH 26

Db 699 GKYTDNSSSATGGRVQNIYGAGNTH 724

RESULT 2
US-10-181-660-13
; Sequence 13, Application US/10181660

```
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-13

Query Match      100.0%; Score 140; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      699 GKYDDNSSSATGGRVQNIYGAGNTH 724

RESULT 3
US-10-181-600-5
; Sequence 5, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-5

Query Match      100.0%; Score 140; DB 16; Length 776;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      699 GKYDDNSSSATGGRVQNIYGAGNTH 724

RESULT 4
US-10-181-600-13
; Sequence 13, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
```

```
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-13

Query Match      100.0%; Score 140; DB 16; Length 776;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      699 GKYDDNSSSATGGRVQNIYGAGNTH 724

RESULT 5
US-09-994-192-4
; Sequence 4, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match      100.0%; Score 140; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 6
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-3

Query Match      100.0%; Score 140; DB 14; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 GKYDDNSSATGGRVONIYGAGNTH 26
Db 720 GKYDDNSSATGGRVONIYGAGNTH 745

RESULT 7

US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

Query Match 100.0%; Score 140; DB 14; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVONIYGAGNTH 26
Db 720 GKYDDNSSATGGRVONIYGAGNTH 745

RESULT 8

US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

Query Match 100.0%; Score 140; DB 15; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVONIYGAGNTH 26
Db 720 GKYDDNSSATGGRVONIYGAGNTH 745

RESULT 9

US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1

; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-3

Query Match 100.0%; Score 140; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVONIYGAGNTH 26
Db 720 GKYDDNSSATGGRVONIYGAGNTH 745

RESULT 10

US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-11

Query Match 100.0%; Score 140; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVONIYGAGNTH 26
Db 720 GKYDDNSSATGGRVONIYGAGNTH 745

RESULT 11

US-10-606-618-4
; Sequence 4, Application US/10606618
; Publication No. US20050074458A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSEC147AUSA
; CURRENT APPLICATION NUMBER: US/10/606,618
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039

```
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-606-618-4

Query Match      100.0%; Score 140; DB 17; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGRVQNIYGANTH 26
   |||||
Db 720 GKYDDNSSSATGRVQNIYGANTH 745
   |||||

RESULT 12
US-10-739-930-6705
; Sequence 6705, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 6705
; LENGTH: 588
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ARATH-23APR03-C7627_1.p
US-10-739-930-6705

Query Match      42.9%; Score 60; DB 16; Length 588;
Best Local Similarity 50.0%; Pred. No. 3.1;
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KTYDDNSSSATGRVQNIYGANT 25
   |||||
Db 47 KPLDENASSGSPTRVSTIYGVG 70
   |||||

RESULT 13
US-10-156-761-10028
; Sequence 10028, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10028
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10028

; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-606-618-4

Query Match      42.1%; Score 59; DB 14; Length 315;
Best Local Similarity 38.2%; Pred. No. 2.2;
Matches 13; Conservative 4; Mismatches 9; Indels 8; Gaps 1;

QY 1 GXYDDNSSSATG-----GRVQNIYGANTH 26
   |||||
Db 38 GRPYDDASGAHGVYGAHGVSGTTREAYGAGGTY 71
   |||||

RESULT 14
US-10-369-493-2471
; Sequence 2471, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2471
; LENGTH: 1504
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(1504)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-2471

Query Match      39.3%; Score 55; DB 15; Length 1504;
Best Local Similarity 63.2%; Pred. No. 52;
Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDDNSSSATGGRVQNIYGA 22
   |||||
Db 215 YDDNQKVTGGR--NGYGA 231
   |||||

RESULT 15
US-10-425-115-232640
; Sequence 232640, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 232640
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_143760C.1.p
US-10-425-115-232640

Query Match      38.6%; Score 54; DB 16; Length 196;
Best Local Similarity 63.2%; Pred. No. 7.1;
Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
```

Oy 4 YDDNSSSATGGRVONIYGA 22
| | | | |
Db 148 YDDNERKTTGGR--NGYGA 164

Search completed: July 6, 2005, 15:42:21
Job time : 8.2987 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:56:39 ; Search time 7.27273 Seconds
(without alignments)
1830.683 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745
Perfect score: 140
Sequence: 1 GKYTDNSSSATGGRVQNIYAGNTH 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	797	2	O30912
2	140	100.0	797	2	O9JX31
3	140	100.0	797	2	O9KH0
4	60	42.9	588	2	O96328
5	59	42.1	315	2	O82KB2
6	55	39.3	1077	2	O7NTE3
7	55	39.3	1427	2	O755V8
8	55	39.3	1485	1	TOP2_SCHPO
9	54	38.6	1482	1	TOP2_PEA
10	54	38.6	1473	1	TOP2_ARATH
11	54	38.6	1525	2	O6ZBD9
12	53	37.9	1127	2	O8EUA7
13	53	37.9	1923	2	O7S9W8
14	51	36.4	516	2	O8FPU1
15	51	36.4	782	2	O9HG4
16	51	36.4	782	2	O9HG4
17	51	36.4	782	2	O9HG6
18	51	36.4	1100	2	O8XU2
19	50.5	36.1	456	2	O8ECA8
20	50	35.7	68	2	O63BF2
21	50	35.7	260	1	CAHZ_BRARE
22	50	35.7	262	2	O81TW9
23	50	35.7	263	2	O6HM55
24	50	35.7	264	2	O9DFB6
25	50	35.7	295	2	O81AM9
26	50	35.7	303	2	O63T78
27	50	35.7	303	2	O733W0
28	50	35.7	303	2	O81YG1
29	50	35.7	303	2	O6HFR3
30	50	35.7	314	1	HLDD_VIBCH
31	50	35.7	345	2	O6PET9

32 50 35.7 363 2 Q82UQ3 Q82uq3 nitrosomona
33 50 35.7 386 1 BCAT_HUMAN P54687 homo sapien
34 50 35.7 507 2 Q8BRV5 Q8bry5 mus musculu
35 50 35.7 553 2 Q6BYE6 Q6bye6 debaryomyce
36 50 35.7 642 2 Q6LF16 Q6lfi6 plasmodium
37 50 35.7 772 2 Q9HGH0 Q9hgh0 kluyveromyc
38 50 35.7 777 2 Q9HGH8 Q9hgh8 kluyveromyc
39 50 35.7 782 2 Q9HGH1 Q9hgh1 pichia guil
40 50 35.7 804 2 Q9HGH7 Q9hgh7 issatchenki
41 50 35.7 1132 2 O7ZXS2 O7zxs2 xenopus lae
42 50 35.7 1406 1 TOP2_CANGA Q93794 candida gla
43 50 35.7 1428 1 TOP2_YEAST P06786 saccharomyc
44 50 35.7 1428 2 Q8TF86 Q8tf86 saccharomyc
45 50 35.7 1428 2 Q8TG43 Q8tg43 saccharomyc

ALIGNMENTS

RESULT 1
O30912 PRELIMINARY; PRT; 797 AA.
AC O30912
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;
QY 1 GKYTDNSSSATGGRVQNIYAGNTH 26
|||
Db 720 GKYTDNSSSATGGRVQNIYAGNTH 745
RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85".
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC175

```

RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagella K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whithead S., Spratt B.G., Barrett B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
DR EMBL: AL162752; CAB83401.1; -.
DR PIR: D82000; D82000.
DR InterPro: IPR000184; Bac_surfAg_D15.
DR InterPro: IPR010827; Surf Ag VNR.
DR Pfam: PF01103; Bac surface Ag; 1.
DR Pfam: PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88404 MW; 65DE47E0C9E1D1F CRC64;

Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVQNIYAGNTH 26
Db 720 GKYDDNSSATGGRVQNIYAGNTH 745
|||||
RESULT 3
Q9K1H0 PRELIMINARY; PRT; 797 AA.
ID Q9K1H0
AC Q9K1H0
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN OrderedLocuNames=NM0182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=MC58 / Serogroup B;
RC MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RX Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AR002375; AAF40639.1; -.
DR PIR: G81228; G81228.
DR TIGR: NMB0182; -.
DR InterPro: IPR000184; Bac_surfAg_D15.
DR InterPro: IPR010827; Surf Ag VNR.
DR Pfam: PF01103; Bac surface Ag; 1.
DR Pfam: PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88436 MW; B68BFC5A3D22BE8 CRC64;

Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVQNIYAGNTH 26
Db 720 GKYDDNSSATGGRVQNIYAGNTH 745
|||||
Db 720 GKYDDNSSATGGRVQNIYAGNTH 745
RESULT 4
Q96328 PRELIMINARY; PRT; 588 AA.
ID Q96328
AC Q96328;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transmembrane protein G5P (SAC domain protein 8).
DE Name=AtG5; Synonyms=At3G51830, SAC8;
GN Arabidopsis thaliana (Mouse-ear cress).
OS Arabidopsi thaliana (Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Spermatophyta; Brassicales; Brassicaceae; Arabidopsi.
OC eurosids II;
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Columbia;
RC Grelllet P., Gaubier P., Wu H.-J., Laudie M., Berger C., Delseny M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RP Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RP MEDLINE=20108326; PubMed=10645728; DOI=10.1023/A:1006395324818;
RX Comella P., Wu H.J., Laudie M., Berger C., Cooke R., Delseny M.,
RA Grelllet P.;
RT "Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1
RL locus on chromosome III."
RN Plant Mol. Biol. 41:687-700(1999).
RN [4]
SEQUENCE FROM N.A.
RP Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Huan V.W.,
RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wu H.C., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
SEQUENCE FROM N.A.
RP MEDLINE=22890165; PubMed=12805586; DOI=10.1104/pp.103.021444;
RX Zhong R., Ye Z.H.;
RT "The SAC domain-containing protein gene family in Arabidopsis."
RL Plant Physiol. 132:544-555(2003).
DR EMBL: U72504; AAB18128.1; -.
DR EMBL: AY080659; AAL86335.1; -.
DR EMBL: AF049236; AAC14410.1; -.
DR EMBL: AY133741; AAM91675.1; -.
DR EMBL: AY227251; AAP49841.1; -.
DR PIR: T51154; T51154.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR InterPro: IPR002013; Syja_N.
DR Pfam: PF02383; Syja_N; 1.
DR PROSITE: PS0275; SAC; 1.
KW Transmembrane.
SQ SEQUENCE 588 AA; 66463 MW; 6ADC187B7CC3753D CRC64;

Query Match 42.9%; Score 60; DB 2; Length 588;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;
```

RA	Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA	Atoufi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA	Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA	Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burty H.A.,
RA	Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA	Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA	Creczynski-Pasa T.B., Cunha-Junior N.C., Fgundes N., Falcao C.L.,
RA	Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA	Ferre M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA	Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA	Grattapaglia D., Griegard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA	Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA	Madeira H.M.F., Manlio G.P., Maranhao A.Q., Martins W.S.,
RA	di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA	Nascimento F.Z., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA	Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA	Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA	Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA	Santos E.B.P., Santos F.R., Schneider M.P.C., Seunaz H.N.,
RA	Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA	Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA	Ra Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA	Vettore A., Waesem R., Zaha A., Simpson A.J.G.
RT	The complete genome sequence of Chromobacterium violaceum reveals
RT	remarkable and exploitable bacterial adaptability."
RL	Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR	ENBL; AS016921; AAQ60782.2; -.
DR	InterPro: IPR008985; Cona like lec gl.
DR	InterPro: IPR008707; Neisseria_PilC.
DR	Pfam: PF05567; Neisseria_PilC; 1.
KW	Complete proteome.
SQ	SEQUENCE 1077 AA; 111476 MW; F2DB546DF27279DB CRC64;
Query Match	39.3%; Score 55; DB 2; Length 1077;
Best Local Similarity	50.0%; Pred. No. 45;
Matches 13; Conservative	4; Mismatches 7; Indels 2; Gaps
Qy	1 GKTYDDNSSATGGGRVQNI--YGAGN 24 : 179 GGYNDNTSSGPGAKPQNISLRGGS 204
Db	
RESULT 7	
Q755v8	PRELIMINARY; PRT; 1427 AA.
ID	Q755v8
AC	Q755v8
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	AER410wp.
GN	ORFNames=AER410w;
OS	Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX	NCBI_TaxID=33169;
ON	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 10895;
RC	Gates K., Dietrich F.S., Brachat S., Voegelé S.E., Lerch A.,
RA	Philippson P., Gaffney T.;
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC	-I- FUNCTION: Control of topological states of DNA by transient
CC	breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC	makes double-strand breaks (By similarity).
CC	-I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC	of double-stranded DNA.
CC	-I- SUBUNIT: Homodimer (By similarity).
CC	-I- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC	negative and positive supercoils, whereas prokaryotic enzymes
CC	relax only negative supercoils (By similarity).
CC	-I- SIMILARITY: Belongs to the type II topoisomerase family.
DR	ENBL; AS016818; RAS53089.1; -.
DR	AGD; AER410w; -.

SQ SEQUENCE 1485 AA; 167891 MW; 6D88F76243361B2F CRC64;
Query Match 39.3%; Score 55; DB 1; Length 1485;
Best Local Similarity 63.2%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
QY 4 YDNSSSATGGRVQNIYGA 22
|||||
Db 196 YDDNQKVTGGR--NGYGA 212
RESULT 9
TOP2_PEA STANDARD; PRT; 1462 AA.
AC O24308;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3) (PstOpII).
GN Name=TOP2; Synonyms=TOPII;
OS Pisum sativum (Garden pea);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=20023730; PubMed=10561074; DOI=10.1023/A:1006352820788;
RA Reddy M.K., Nair S., Tewari K.K., Mudgil Y., Yadav B.S., Sopory S.K.;
RT "Cloning and characterization of a cDNA encoding topoisomerase II in
RT pea and analysis of its expression in relation to cell
RT proliferation.";
RL Plant Mol. Biol. 41:125-137(1999).
CC -!- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- TISSUE SPECIFICITY: Abundant in proliferative tissues.
CC -!- INDUCTION: By light and growth factors.
CC -!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC ENBL; Y14559; CAA74891.1; --
CC FR; T06819; T06819.
CC HSSP; P06786; 1BJT.
CC InterPro; IPR003594; ATPbind ATPase.
CC InterPro; IPR003957; CBFA NFYB Topis.
CC InterPro; IPR001241; DNA_topoisomI.
CC InterPro; IPR002205; DNA_topoisomIV.
CC Pfam; PF00204; DNA_gyraseB; 1.
CC Pfam; PF00521; DNA_topoisomIV; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC PRINTS; PR00615; CCAATSUBUNTA.
CC PRINTS; PR00418; TPI2FAMILY.
CC ProDom; PD149633; DNA_gyrase_B; 1.
CC ProDom; PD000742; DNA_topoisomI; 1.
CC SMART; SM00387; HATPase_c; 1.
CC SMART; SM00433; TOP2c; 1.
CC SMART; SM00434; TOP4c; 1.
CC PROSITE; PS00177; TOPOISOMERASE_II; 1.

KW ATP-binding; DNA-binding; Isomerase; Topoisomerase.
FT NP_BIND 149 154 ATP (Potential).
FT ACT_SITE 761 761 DNA cleavage (By similarity).
SQ SEQUENCE 1462 AA; 164205 MW; D9212C54AE0F8B2E CRC64;
Query Match 38.6%; Score 54; DB 1; Length 1462;
Best Local Similarity 56.5%; Pred. No. 88;
Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;
QY 4 YDNSSSATGGRVQNIYGA 26
|||||
Db 139 YDDNVKKTGGR--NGYGAKLTN 159
RESULT 10
TOP2_ARATH STANDARD; PRT; 1473 AA.
AC P30182; Q38807;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 45, Last annotation update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3).
GN Name=TOP2; OrderedLocusNames=At3g23890; ORFNames=F14013.7;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=95148754; PubMed=7846176; DOI=10.1104/pp.106.4.1701;
RA Xie S., Lam E.;
RT "Characterization of a DNA Topoisomerase II cDNA from Arabidopsis
RT thaliana.";
RL Plant Physiol. 106:1701-1702(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia, and cv. Kas-1;
RX MEDLINE=95140639; PubMed=7838729;
RA Xie S., Lam E.;
RT "Abundance of nuclear DNA topoisomerase II is correlated with
RT proliferation in Arabidopsis thaliana.";
RL Nucleic Acids Res. 22:5729-5736(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
RT and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [4]
RP SEQUENCE OF 751-838 FROM N.A.
RA Gerhold D., Parsons A., Hadwiger L.A.;
RT "PCR-assisted cloning of a topoisomerase II gene from Arabidopsis.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks.
CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -!- SUBUNIT: Homodimer.
CC -!- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -!- SIMILARITY: Belongs to the type II topoisomerase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).

 DR EMBL; L21015; AAA65448.1; --
 DR EMBL; M84654; AAA32877.1; --
 DR EMBL; AP001297; BAB03006.1; --
 DR EMBL; U12284; AAC48999.1; --
 DR EMBL; U12285; AAC49000.1; --
 DR PIR; S53598; S53599.
 DR HSP; P06786; IBGW.
 DR GeneFarm; 2856; 246.

DR InterPro; IPR003594; ATPbind ATPase.
 DR InterPro; IPR003957; CBFA NFYB topis.
 DR InterPro; IPR001241; DNA_topoisomII.
 DR InterPro; IPR002205; DNA_topoisomI.
 DR Pfam; PF00204; DNA_gyraseB; 1.
 DR Pfam; PF00521; DNA_topoisomI; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR PRINTS; PR00615; CCAATSUBUNTA.
 DR PRINTS; PR00418; TPI2FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR ProDom; PD000742; DNA_topoisomI; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR SMART; SM00434; TOP4c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE II; 1.
 DR ATP-binding; DNA-binding; Isomerase; Polymorphism; Topoisomerase.
 FT NP_BIND 161 166 ATP (Potential).
 FT ACT_SITE 794 794 DNA cleavage (By similarity).
 FT VARIANT 1213 1213 K -> N (in cv. Kas-1).
 FT VARIANT 1245 1245 A -> G (in cv. Kas-1).
 FT VARIANT 1299 1299 E -> G (in cv. Kas-1).
 SQ SEQUENCE 1473 AA; 164106 MW; 00B6C4836E381403 CRC64;

Query Match 38.6%; Score 54; DB 1; Length 1473;
 Best Local Similarity 56.5%; Pred. No. 88;
 Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDSSSSATGGRVQNIYGAGNTH 26
 ||||| ||||| ||||| ||||| |||||
 Db 151 YDNNVKKTTGGR--NGYGAKLTN 171

RESULT 11
 Q6Z8D9 PRELIMINARY; PRT; 1525 AA.
 AC Q6Z8D9
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative DNA topoisomerase II.
 GN NameP0459B01.29;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Yamamoto K.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Control of topological states of DNA by transient
 CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
 CC makes double-strand breaks (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
 CC negative and positive supercoils, whereas prokaryotic enzymes
 CC relax only negative supercoils (By similarity).
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 DR EMBL; AP004778; BAD07880.1; --

DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
 DR GO; GO:0006265; P:DNA topological change; IEA.
 DR InterPro; IPR003594; ATPbind ATPase.
 DR InterPro; IPR003957; CBFA NFYB topis.
 DR InterPro; IPR001241; DNA_topoisomII.
 DR InterPro; IPR002205; DNA_topoisomI.
 DR Pfam; PF00204; DNA_gyraseB; 1.
 DR Pfam; PF00521; DNA_topoisomI; 1.
 DR Pfam; PF02518; HATPase_c; 1.
 DR PRINTS; PR00615; CCAATSUBUNTA.
 DR PRINTS; PR00418; TPI2FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR ProDom; PD000742; DNA_topoisomI; 1.
 DR SMART; SM00387; HATPase_c; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR SMART; SM00434; TOP4c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE II; 1.
 DR ATP-binding; DNA-binding; Isomerase; Topoisomerase.
 SQ SEQUENCE 1525 AA; 170334 MW; 564C712C68698C3B CRC64;

Query Match 38.6%; Score 54; DB 2; Length 1525;
 Best Local Similarity 56.5%; Pred. No. 92;
 Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDSSSSATGGRVQNIYGAGNTH 26
 ||||| ||||| ||||| ||||| |||||
 Db 148 YDNNVKKTTGGR--NGYGAKLTN 168

RESULT 12
 O8EUA7 PRELIMINARY; PRT; 1127 AA.
 ID Q8EUA7
 AC Q8EUA7
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Predicted protein-export membrane protein SecD.
 GN OrderedLocusNames=MYPE10240;
 OS Mycoplasma penetrans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=28227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HF-2;
 RA MEDLINE=22354719; PubMed=12466555; DOI=10.1093/nar/gkf667;
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
 RT "The complete genomic sequence of Mycoplasma penetrans, an
 RT intracellular bacterial pathogen in humans.";
 RL Nucleic Acids Res. 30:5293-5300(2002).
 DR EMBL; AP004174; BAC44809.1; --
 KW Complete proteome.
 SQ SEQUENCE 1127 AA; 124216 MW; 81DC036E4479A72E CRC64;

Query Match 37.9%; Score 53; DB 2; Length 1127;
 Best Local Similarity 52.0%; Pred. No. 92;
 Matches 13; Conservative 3; Mismatches 5; Indels 4; Gaps 2;

QY 4 YDNNSSSSATGGRVQ--NIYGAGN 24
 ||||| :|||: |||||
 Db 146 YDNNFNKNSSTGGYIEDPNIYGINN 170

RESULT 13
 Q7S9W8 PRELIMINARY; PRT; 1923 AA.
 ID Q7S9W8
 AC Q7S9W8
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.
GN Name=NCU06338.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
ON NCBI_TaxID=5141;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=OR74A;
RC Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnirre S.,
RA Kamal M., Kamyselis M., Maucelli E., Bieleke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Merzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbels D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa";
RL Nature 0:0-0(2003).
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils (By similarity).
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAX01000209; EAA33136.1; -;
DR HSPSP; P06786; 1BUT.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0005214; F:ATP binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR003957; CBFA_NFYB_topis.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomI.
DR InterPro: IPR002205; DNA_topoisomI.
DR Pfam: PF00204; DNA_gyraseB; 1.
DR Pfam: PF00521; DNA_topoisomI; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR PRINTS: PR00615; CCAATSUBUNITA.
DR PRINTS: PR00418; TPI2FAMILY.
DR ProDom: PD149633; DNA_gyrase_B; 1.
DR ProDom: PD000742; DNA_topoisomI; 1.
DR PROSITE: PS00177; TOPOISOMERASE_II; UNKNOWN_1.
KW ATP-binding; DNA-binding; Hypothetical protein; Isomerase;
KW Topoisomerase.
SQ SEQUENCE 1923 AA; 213143 MW; 10663EA61ED142E0 CRC64;
Query Match 37.9%; Score 53; DB 2; Length 1923;
Best Local Similarity 46.2%; Pred. No. 1.7e+02;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
QY 1 GKTYYDNNSSATGGRVONIVGAGNTH 26
DB 246 GSNFDDNEKXTVGGR--NGYGAKLTN 269
RESULT 14
Q8FPUI PRELIMINARY; PRT; 516 AA.
ID Q8FPUI

AC Q8FPUI;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative NADH dehydrogenase I chain M.
ON OrderedLocusNames=CEI1397;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriidae; Corynebacterium.
ON NCBI_TaxID=152794;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=YS-314;
RC MEDLINE=22723752; PubMed=12840036; DOI=10.1101/gr.1285603;
RX Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens";
RL Genome Res. 13:1572-1579(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL: AF005218; BAC18207.1; -;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO: GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR InterPro: IPR003916; NADH_oxred5.
DR InterPro: IPR001750; Oxidored_g1.
DR Pfam: PF00361; Oxidored_g1; 1.
DR PRINTS: PR01434; NADHGHNA5.
KW Complete proteome; Oxidoreductase; Transmembrane.
SQ SEQUENCE 516 AA; 54477 MW; 8B45EA8713F5ECF7 CRC64;
Query Match 36.4%; Score 51; DB 2; Length 516;
Best Local Similarity 58.8%; Pred. No. 77;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 GKTYYDNNSSATGGRVQ 17
DB 454 GSDADSASSATGGATQ 470
RESULT 15
Q8FGH4 PRELIMINARY; PRT; 782 AA.
ID Q8FGH4
AC Q8FGH4;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type II DNA topoisomerase (Fragment).
GN Name=top2;
OS Candida dubliniensis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetidae; mitosporic Saccharomycetales; Candida.
ON NCBI_TaxID=42374;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=16F;
RC MEDLINE=21363449; PubMed=11470534; DOI=10.1016/S0378-1119(01)00526-1;
RX Kato M., Ozeki M., Kikuchi A., Kanbe T.;
RT "Phylogenetic relationship and mode of evolution of yeast DNA
RT topoisomerase II gene in the pathogenic Candida species.";
RL Gene 272:275-281(2001).
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils (By similarity).
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

DR EMEL; AB049142; BAB13751.1; -.
DR HSP; P06786; IBJT.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO; GO:0006265; P:DNA topological change; IEA.
DR InterPro; IPR003594; ATPbind_ATPase.
DR InterPro; IPR003957; CBFA_NFYB_topis.
DR InterPro; IPR011558; DNA_gyrase_B.
DR InterPro; IPR001241; DNA_topoisomI.
DR InterPro; IPR002205; DNA_topoisomIV.
DR Pfam; PF00204; DNA_gyraseB; 1.
DR Pfam; PF00521; DNA_topoisomIV; 1.
DR Pfam; PF02518; HATPase_c; 1.
DR PRINTS; PR00615; CCAATSUBUNTA.
DR PRINTS; PR00418; TPI2FAMILY.
DR ProDom; PD149633; DNA_gyrase_B; 1.
DR ProDom; PD000742; DNA_topoisomIV; 1.
DR SMART; SM00387; HATPase_c; 1.
DR SMART; SM00433; TOP2c; 1.
DR SMART; SM00434; TOP4c; 1.
DR KW ATP-binding; DNA-binding; Isomerase; Topoisomerase.
FT NON_TER 1 1
FT NON_TER 782 782
SQ SEQUENCE 782 AA; 88384 MW; 3D3F6300B64669AB CRC64;

Query Match 36.4%; Score 51; DB 2; Length 782;
Best Local Similarity 57.9%; Pred.No. 1.2e+02;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 4 YDNNSSATGGRVQNIYGA 22
Db 85 YDDNEKKVTGGR--NGFGA 101

Search completed: July 6, 2005, 15:18:07
Job time : 9.27273 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:53:24 ; Search time 52.6354 Seconds
(without alignments)
1307.930 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178

Perfect score: 885

Sequence: 1 MKLKQIASALMWLGISPLAF.....RNRVDITIDEGSAK178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: Genesecp_16Dec04:*
2: Genesecp_1980s:*
3: Genesecp_1990s:*
4: Genesecp_2000s:*
5: Genesecp_2001s:*
6: Genesecp_2002s:*
7: Genesecp_2003as:*
8: Genesecp_2003bs:*
9: Genesecp_2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	792	4	Aau03958 Neisseria
2	885	100.0	792	4	Aab23786 Neisseria
3	885	100.0	792	4	Aab23786 Neisseria
4	885	100.0	792	6	Abp80499 N. gonorr
5	885	100.0	792	6	Abp79748 N. gonorr
6	885	100.0	797	3	Aay84947 Amino aci
7	885	100.0	797	5	Abb79802 Neisseria
8	879	99.3	797	4	Aau03957 Neisseria
9	879	99.3	797	4	Aab23784 Neisseria
10	879	99.3	797	4	Aab23784 Neisseria
11	875	98.9	797	4	Aau03959 Neisseria
12	875	98.9	797	4	Aau04451 Neisseria
13	875	98.9	797	4	Aab23788 Neisseria
14	875	98.9	797	4	Aab23788 Neisseria
15	863	97.5	792	3	Aay84946 Amino aci
16	863	97.5	792	5	Abb79801 Neisseria
17	863	97.5	792	5	Abb79801 Neisseria
18	297.5	33.6	798	6	Abm67563 Photorhab
19	296.5	33.5	827	7	Adf06140 Bacterial
20	295.5	33.4	821	7	Abp72267 Pseudomon
21	292	33.0	815	7	Abp72267 Pseudomon
22	289	32.7	813	8	Abp72267 Pseudomon
23	286	32.3	813	3	Aay44390 M. catarr
24	286	32.3	813	3	Aay44391 M. catarr
25	282	31.9	865	6	Ada36211 Acinetoba

26	276	31.2	825	7	ABO61952 Klebsiell
27	273	30.8	639	4	ABG17654 Novel hum
28	236.5	26.7	797	2	AAR53755 H. influe
29	236.5	26.7	797	2	AAR53754 H. influe
30	236.5	26.7	797	2	AAR53756 H. influe
31	234.5	26.5	792	2	AAR53757 H. influe
32	234.5	26.5	793	2	AAR53758 H. influe
33	201.5	22.8	792	8	ADH12911 Francisel
34	151	17.1	896	4	AG78603 Lawsonia
35	151	17.1	896	6	ABU92009 Omp100 po
36	151	17.1	896	7	ADJ33885 L. intrac
37	151	17.1	896	7	ADJ33885 L. intrac
38	151	17.1	896	8	ADJ33885 L. intrac
39	100	11.3	792	5	ABG91029 Chlamydia
40	100	11.3	792	7	AD43760 Chlamydia
41	97	11.0	21	4	AAB23787 Neisseria
42	96.5	10.9	837	2	AAY52774 Treponema
43	95.5	10.8	812	2	AAY52775 Treponema
44	95	10.7	497	5	ABU52025 Helicobac
45	95	10.7	518	5	ABU51207 Helicobac

ALIGNMENTS

RESULT 1
AAU03958
ID AAU03958 standard; protein; 792 AA.
XX AC AAU03958;
XX AC (first entry)
DT 23-OCT-2001 (first entry)
XX DE Neisseria meningitidis serogroup A antigenic protein #1.
XX KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.
XX OS Neisseria meningitidis.
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "Signal peptide"
FT /note= "Mature N. meningitidis serogroup A antigen"
XX PN WO200138350-A2.
XX PD 31-MAY-2001.
XX PF 28-NOV-2000; 2000WO-IB001851.
XX PR 29-NOV-1999; 99GB-00028197.
XX PR 09-MAR-2000; 2000GB-00005698.
XX (CHIR-) CHIRON SPA.
XX (STAT-) STATENS INST FOLKEHELSE.
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
WPI: 2001-381289/40.
XX N-PSDB; AAS07278.
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection.
XX Claim 1; Page 66-68; 92pp; English.
XX The sequence represents a Neisseria meningitidis serogroup A 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for

CC treating or preventing infection due to *Neisseria* bacteria, such as
CC meningitis and septicemia. It is also useful as a diagnostic reagent for
CC detecting the presence of *Neisseria* bacteria or antibodies raised against
CC *Neisseria*, and as a reagent for raising the antibodies. The *Neisseria*
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast. Note: There are two versions of this sequence
CC displayed in the specification (see AAU04451)

XX
SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGQRTPESTVFNYPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGQRTPESTVFNYPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
DB 121 SQYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 2

AAB23786
ID AAB23786 standard; protein; 792 AA.

XX
AC AAB23786;

XX
AC AAB23786;

DT 11-SEP-2003 (revised)

DT 12-JAN-2001 (first entry)

XX
DE *Neisseria* gonorrhoeae amino acid sequence.

XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW *Neisseria* antigen; *Neisseria* meningitidis; *Neisseria* gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.

XX
OS *Neisseria* gonorrhoeae.

XX
PN W0200050075-A2.

XX
PD 31-AUG-2000.

XX
PF 09-FEB-2000; 2000WO-IB000176.

XX
PR 26-FEB-1999; 99US-0121792P.

XX
PA (CHIR-) CHIRON SPA.

XX
PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;

XX
DR WPI; 2001-015529/02.

XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against *Neisseria* infection, comprises *Neisseria* antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.

XX
PS Claim 22; Page 32; 39pp; English.

XX The present invention describes an immunogenic composition (I) comprising
CC a *Neisseria* antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of

CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against *Neisseria* infection, preferably
CC *Neisseria* meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed *Neisseria* gonorrhoeae amino acid sequence
CC disclosed in GB-9928197.4, which is given in the present invention.
CC (Updated on 11-SEP-2003 to standardise OS field)

XX
SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGQRTPESTVFNYPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGQRTPESTVFNYPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
DB 121 SQYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 3

AAB84745
ID AAB84745 standard; protein; 792 AA.

XX
AC AAB84745;

XX
AC AAB84745;

DT 11-SEP-2003 (revised)

DT 17-SEP-2001 (first entry)

XX
DE Amino acid sequence of a *Neisseria* gonorrhoeae protein.

XX Serogroup B protein; outer membrane protein; *Neisseria* infection;
KW vaccine.

XX
OS *Neisseria* gonorrhoeae.

XX
FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "signal peptide"

FT Protein /note= "mature protein"

XX
PN W0200152885-A1.

XX
PD 26-JUL-2001.

XX
PF 17-JAN-2001; 2001WO-IB000166.

XX
PR 17-JAN-2000; 2000GB-00001067.

XX
PR 09-MAR-2000; 2000GB-00005699.

XX
PA (CHIR-) CHIRON SPA.

XX
PI Pizza M, Rappuoli R, Giuliani M;

XX
DR WPI; 2001-451895/48.

XX
DR N-PSDB; AAH42129.

XX Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against *Neisseria* bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.

XX
PS Disclosure; Page 65-67; 83pp; English.

XX
CC The present sequence represents a *Neisseria* gonorrhoeae protein. The

protein is used to produce the compositions of the invention. The specification describes a composition, comprising a *Neisseria meningitidis* serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in WO99/57280, WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413, WO99/31132, WO99/58683, WO99/55873, and/or *N. meningitidis* protein PorA, TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a medicament for treating or preventing infection due to *Neisseria* bacteria; a diagnostic reagent for detecting the presence of *Neisseria* bacteria or of antibodies raised against *Neisseria* bacteria; and/or a reagent which can raise antibodies against *Neisseria* bacteria. It may also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 792 AA;

Query Match 100.0%; Score 885; DB 4; Length 792;

Best Local Similarity 100.0%; Pred. No. 2.5e-85;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

DB 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQVFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITD 178

DB 121 SQVFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 4

ABP80499

ID ABP80499 standard; protein; 792 AA.

AC ABP80499;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae amino acid sequence SEQ ID 7528.

KW Antibacterial; infection; vaccine; gene therapy.

OS *Neisseria gonorrhoeae*.

XX WO200279243-A2.

XX 10-OCT-2002.

PF 12-FEB-2002; 2002WO-IB002069.

PR 12-FEB-2001; 2001GB-00003424.

PA (CHIR-) CHIRON SPA.

PI Fontana MR, Pizza M, Massignani V, Monaci E;

XX WPI; 2003-058415/05.

DR N-PSDB; ABZ41469.

PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection.

PS Disclosure; Page 736; 815pp; English.

CC The present invention relates to proteins from *Neisseria gonorrhoeae*.

CC Also disclosed are the nucleic acid molecules encoding the proteins and

CC antibodies that specifically bind to the proteins. The composition

CC comprising the protein, nucleic acid or antibody is useful for the

CC manufacture of a medicament for treating or preventing *N. gonorrhoeae*

CC infection, this may be in the form of a vaccine or gene therapy.

CC

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid

XX molecules of the invention

SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 6; Length 792;

Best Local Similarity 100.0%; Pred. No. 2.5e-85;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

DB 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQVFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITD 178

DB 121 SQVFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 5

ABP79748

ID ABP79748 standard; protein; 792 AA.

AC ABP79748;

DT 07-MAR-2003 (first entry)

DE N. gonorrhoeae amino acid sequence SEQ ID 6026.

KW Antibacterial; infection; vaccine; gene therapy.

OS *Neisseria gonorrhoeae*.

XX WO200279243-A2.

XX 10-OCT-2002.

PF 12-FEB-2002; 2002WO-IB002069.

PR 12-FEB-2001; 2001GB-00003424.

PA (CHIR-) CHIRON SPA.

PI Fontana MR, Pizza M, Massignani V, Monaci E;

XX WPI; 2003-058415/05.

DR N-PSDB; ABZ40718.

PT New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection.

PS Disclosure; Page 628; 815pp; English.

CC The present invention relates to proteins from *Neisseria gonorrhoeae*.

CC Also disclosed are the nucleic acid molecules encoding the proteins and

CC antibodies that specifically bind to the proteins. The composition

CC comprising the protein, nucleic acid or antibody is useful for the

CC manufacture of a medicament for treating or preventing *N. gonorrhoeae*

CC infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid

XX molecules of the invention

SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 6; Length 792;

Best Local Similarity 100.0%; Pred. No. 2.5e-85;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

DB 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQVFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITD 178

DB 121 SQVFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITD 178

Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITD 178

RESULT 6
AA84947
ID AAY84947 standard; protein; 797 AA.
XX
AC AAY84947;
XX
DT 21-AUG-2000 (first entry)
XX
DE Amino acid sequence of outer membrane protein (omp) 85.
XX
KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
KW meningococcal infection; protective immune response; vaccine.
XX
OS Neisseria meningitidis.
XX
PN WO200023595-A1.
XX
XX 27-APR-2000.
PD
XX 22-OCT-1998; 98WO-US022352.
PF
XX 22-OCT-1998; 98WO-US022352.
PR
XX (UYMO-) UNIV MONTANA.
PA
XX Judd RC, Manning SD;
PI
XX WPI; 2000-339694/29.
DR
DR N-PSDB; AAA15156.
XX
XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
PT meningitidis useful for vaccine, therapeutic and diagnostic compositions
PT for gonococcal or meningococcal infections.
XX
PS Claim 41; Page 89-92; 98pp; English.
XX
XX The present sequence represents an outer membrane protein (omp) 85 of
CC Neisseria meningitidis. The omp polypeptides and polynucleotides are
CC useful in compositions for use in the prevention, treatment and diagnosis
CC of non-symptomatic gonococcal infection or meningococcal infection and
CC symptomatic disease. They are also useful for the detection of
CC hybridisation complexes. Antigens and antibodies specific omp proteins
CC also provide diagnostic, therapeutic and prophylactic compositions for
CC the treatment or prevention of the infections described above. The
CC antibodies are useful for inducing a protective immune response in humans
CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC species. The proteins, antibodies and polynucleotide sequences of the
CC present invention may also be used in the screening and development of
CC chemical compounds such as drugs or vaccines
XX
SQ Sequence 797 AA;

Query Match 100.0%; Score 885; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 2.6e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVPVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGKSAKITD 178

RESULT 7
ABB79802
ID ABB79802 standard; protein; 797 AA.
XX
AC ABB79802;
XX
DT 15-NOV-2002 (first entry)
XX
DE Neisseria meningitidis outer membrane protein Omp85.
XX
KW Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
KW antibacterial.
XX
OS Neisseria meningitidis.
XX
XX Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= Signal_peptide
FT 22..797
FT /label= Mature_protein
XX
PN US2002086028-A1.
XX
XX 04-JUL-2002.
PD
XX 26-NOV-2001; 2001US-00994192.
PF
XX 22-OCT-1998; 98US-00177039.
PR
XX (JUDD/) JUDD R C.
PA (MANN/) MANNING D S.
XX
PI Judd RC, Manning DS;
XX
XX WPI; 2002-642234/69.
DR
XX Novel immunogenic composition for vaccinating against meningococcal or
PT gonococcal infection, comprises Omp85 protein of Neisseria meningitidis
PT or Neisseria gonorrhoeae, or nucleic acid encoding the protein.
XX
PS Claim 13; Fig 5; 30pp; English.
XX
XX The present sequence is that of the Neisseria meningitidis strain HH
CC outer membrane protein 85 (Omp85), as predicted from a gene that was
CC obtained from a genomic DNA by PCR amplification using primers based on
CC the gonococcal omp85 gene. The meningococcal Omp85 protein is 95%
CC identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed
CC immunogenic compositions comprise N. meningitidis Omp85, its fragments,
CC fusion proteins including the Omp85, or nucleic acids encoding them,
CC which induce a protective immune response in a subject. The immunogenic
CC compositions may also include an antigen from a heterologous or
CC homologous pathogen, or a nucleic acid encoding it. They are used in a
CC claimed method of vaccinating a human or animal against non-symptomatic
CC meningococcal infection or symptomatic disease. A kit for diagnosing
CC infection with N. meningitidis comprising labelled Omp85 is also claimed.
CC The Omp85 polypeptides and polynucleotides are also useful in drug
CC screening and development
XX
SQ Sequence 797 AA;

Query Match 100.0%; Score 885; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 2.6e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVPVKVGDYNDTHGSA 60

Db 1 MKLKQIASALMLGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKTD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKTD 178
RESULT 8
AAU03957
ID AAU03957 standard; protein; 797 AA.
XX
AC AAU03957;
XX
DT 23-OCT-2001 (first entry)
XX
DE Neisseria meningitidis serogroup B antigenic protein.
XX
KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "Signal peptide"
FT Binding-site 22..797
FT /note= "Mature N. meningitidis serogroup B antigen"
FT /note= "ATP/GTP-binding site motif A (P-loop)"
XX
PN WO200138350-A2.
XX
PD 31-MAY-2001.
XX
PF 28-NOV-2000; 2000WO-IB001851.
XX
PR 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX
PA (CHIR-) CHIRON SPA.
PA (STAT-) STATENS INST FOLKEHELSE.
XX
PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX
DR WPI; 2001-381289/40.
DR N-PSDB; AAS07277.
XX
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX
PS Claim 1; Fig 1; 92pp; English.
XX
CC The sequence represents a Neisseria meningitidis serogroup B 85 kDa
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicaemia in the absence of meningitis.
CC This antigenic protein is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast
XX
SQ Sequence 797 AA;
Query Match 99.3%; Score 879; DB 4; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.1e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKQIASALMLGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKTD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKTD 178
RESULT 9
AAB23784
ID AAB23784 standard; protein; 797 AA.
XX
AC AAB23784;
XX
DT 12-JAN-2001 (first entry)
XX
DE Neisseria meningitidis serogroup B amino acid sequence.
XX
KW CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX
OS Neisseria meningitidis.
XX
PN WO2000050075-A2.
XX
PD 31-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-IB000176.
XX
PR 26-FEB-1999; 99US-0121792P.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX
DR WPI; 2001-015529/02.
XX
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
PS Claim 22; Page 32; 39pp; English.
XX
CC The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup B amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention
XX
SQ Sequence 797 AA;
Query Match 99.3%; Score 879; DB 4; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.1e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLADFTIQDIRVEGLQRTPEPTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFDDVRVETAGQLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETAGQLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITD 178
RESULT 10
AAB84744
ID AAB84744 standard; protein; 797 AA.
XX
AC AAB84744;
XX
DT 17-SEP-2001 (first entry)
XX
DE Amino acid sequence of a Neisseria serogroup B protein.
XX
KW Serogroup B protein; outer membrane protein; Neisserial infection;
vaccine.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "mature protein"
XX
PN WO200152885-A1.
XX
PD 26-JUL-2001.
XX
PF 17-JAN-2001; 2001WO-IB000166.
XX
PR 17-JAN-2000; 2000GB-00001067.
PR 09-MAR-2000; 2000GB-00005699.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Pizza M, Rappuoli R, Giuliani M;
XX
DR WPI; 2001-451895/48.
DR N-PSDB; AAH42128.
XX
XX Composition for treating or preventing infection to, detecting, or for
raising antibodies against Neisserial bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX
PS Disclosure; Page 59-61; 83pp; English.
XX
CC The present sequence represents a Neisseria serogroup B protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisserial
CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria; or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX
SQ Sequence 797 AA;

Query Match 99.3%; Score 879; DB 4; Length 797;
Best Local Similarity 99.4%; Pred. NO. 1.1e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLADFTIQDIRVEGLQRTPEPTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFDDVRVETAGQLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETAGQLLTVIERPTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITD 178
RESULT 11
AAU03959
ID AAU03959 standard; protein; 797 AA.
XX
AC AAU03959;
XX
DT 23-OCT-2001 (first entry)
XX
DE Neisseria gonorrhoeae antigenic protein.
XX
KW Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.
XX
OS Neisseria gonorrhoeae.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "Mature N. gonorrhoeae antigen"
XX
PN WO200138350-A2.
XX
PD 31-MAY-2001.
XX
PF 28-NOV-2000; 2000WO-IB001851.
PR 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX
PA (CHIR-) CHIRON SPA.
PA (STAT-) STATENS INST FOLKEHELSE.
XX
PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX
DR WPI; 2001-381289/40.
DR N-PSDB; AAS07279.
XX
PT Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX
PS Claim 1; Page 37-39; 92pp; English.
XX
CC The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.
CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the
CC pharynx, causing meningitis and, occasionally, septicaemia in the absence
CC of meningitis. This antigenic protein is useful in the manufacture of a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria, such as meningitis and septicaemia. It is also useful as a
CC diagnostic reagent for detecting the presence of Neisseria bacteria or
CC antibodies raised against Neisseria, and as a reagent for raising the
CC antibodies. The Neisserial nucleotide sequences can be expressed in a
CC variety of different expression systems, for example, mammalian cells,
CC baculoviruses, plants, bacteria and yeast
XX

CC displayed in the specification (see AAU03958)
XX
SQ Sequence 797 AA;

Query Match 98.9%; Score 875; DB 4; Length 797;
Best Local Similarity 98.9%; Pred. No. 3e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMWLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLVATGFDDVRVETADGQLLLTVIERPTTGSNLITGAKMLQNDAIKKNLSEFGLAQ 120
DB 61 IIKSLVATGFDDVRVETADGQLLLTVIERPTTGSNLITGAKMLQNDAIKKNLSEFGLAQ 120

QY 121 SQYFNOATLNOAVAGLKEEVLGRGKLNIOITPKVTKLARNRVDDITIDSGKSAKITD 178
DB 121 SQYFNOATLNOAVAGLKEEVLGRGKLNIOITPKVTKLARNRVDDITIDSGKSAKITD 178

RESULT 13
AAB23788
ID AAB23788 standard; protein; 797 AA.
XX
XX AAB23788;
DT 12-JAN-2001 (first entry)
XX
XX Neisseria meningitidis serogroup A amino acid sequence.
DE
XX
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX
XX Neisseria meningitidis.
OS
XX WO2000050075-A2.
PN
XX
XX 31-AUG-2000.
PD
XX
XX 09-FEB-2000; 2000WO-IB000176.
PF
XX
XX 26-FEB-1999; 99US-0121792P.
PR
XX
XX (CHIR-) CHIRON SPA.
PA
XX
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
PI
XX
XX WPI; 2001-015529/02.
DR
XX
XX
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
XX Claim 22; Page 33; 39pp; English.
PS
XX
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup A amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
XX invention
XX

SQ Sequence 797 AA;

Query Match 98.9%; Score 875; DB 4; Length 797;
 Best Local Similarity 98.9%; Pred. No. 3e-84;
 Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKQIASALMVLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLKQIASALMVLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITD 178
 DB 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITD 178

RESULT 14
 AAB84746
 ID AAB84746 standard; protein; 797 AA.
 XX
 AC AAB84746;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Amino acid sequence of a Neisseria serogroup A protein.
 XX
 KW Serogroup A protein; outer membrane protein; Neisserial infection;
 KW vaccine.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein /note= "signal peptide"
 FT Protein /note= "mature protein"
 XX
 XX WO200152885-A1.
 XX
 PD 26-JUL-2001.
 XX
 XX 17-JAN-2001; 2001WO-IB000166.
 XX
 XX 17-JAN-2000; 2000GB-00001067.
 PR 09-MAR-2000; 2000GB-00005699.
 XX
 XX (CHIR-) CHIRON SPA.
 XX
 XX Pizza M, Rappuoli R, Giuliani M;
 XX
 DR WPI; 2001-451895/48.
 DR N-PSDB; AAH42130.
 XX
 XX Composition for treating or preventing infection to, detecting, or for
 PT raising antibodies against Neisserial bacteria, comprises an N.
 PT meningitidis serogroup B outer membrane preparation and an immunogenic
 PT component.
 XX
 XX Disclosure; Page 71-74; 83pp; English.
 XX
 XX The present sequence represents a Neisseria serogroup A protein. The
 CC protein is used to produce the compositions of the invention. The
 CC specification describes a composition, comprising a Neisseria
 CC meningitidis serogroup B outer membrane preparation and an immunogenic
 CC component. The immunogenic component is protein disclosed in WO99/57280,
 CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
 CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
 CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
 CC medicament for treating or preventing infection due to Neisserial
 CC bacteria; a diagnostic reagent for detecting the presence of Neisserial

CC bacteria or of antibodies raised against Neisserial bacteria; and/or a
 CC reagent which can raise antibodies against Neisserial bacteria. It may
 CC also be used as a vaccine
 XX
 SQ Sequence 797 AA;

Query Match 98.9%; Score 875; DB 4; Length 797;
 Best Local Similarity 98.9%; Pred. No. 3e-84;
 Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKQIASALMVLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLKQIASALMVLGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITD 178
 DB 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITD 178

RESULT 15
 AAY84946
 ID AAY84946 standard; protein; 792 AA.
 XX
 AC AAY84946;
 XX
 DT 12-SEP-2003 (revised)
 DT 21-AUG-2000 (first entry)
 XX
 DE Amino acid sequence of outer membrane protein (omp) 85.
 XX
 KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
 KW meningococcal infection; protective immune response; vaccine.
 XX
 OS Neisseria gonorrhoeae.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Peptide /note= "signal peptide"
 XX
 XX WO200023595-A1.
 XX
 XX 27-APR-2000.
 XX
 XX 22-OCT-1998; 98WO-US022352.
 XX
 XX 22-OCT-1998; 98WO-US022352.
 XX
 XX (UYMO-) UNIV MONTANA.
 XX
 XX Judd RC, Manning SD;
 PI
 XX WPI; 2000-339694/29.
 DR N-PSDB; AAA15155.
 XX
 XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
 PT meningitidis useful for vaccine, therapeutic and diagnostic compositions
 PT for gonococcal or meningococcal infections.
 XX
 XX Claim 1; Fig 2; 98pp; English.
 PS
 XX The present sequence represents an outer membrane protein (omp) 85 of
 CC Neisseria gonorrhoeae. The omp polypeptides and polynucleotides are
 CC useful in compositions for use in the prevention, treatment and diagnosis
 CC of non-symptomatic gonococcal infection or meningococcal infection and
 CC symptomatic disease. They are also useful for the detection of
 CC hybridisation complexes. Antigens and antibodies specific omp proteins
 CC also provide diagnostic, therapeutic and prophylactic compositions for
 CC the treatment or prevention of the infections described above. The
 CC antibodies are useful for inducing a protective immune response in humans

CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC species. The proteins, antibodies and polynucleotide sequences of the
CC present invention may also be used in the screening and development of
CC chemical compounds such as drugs or vaccines. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
SQ

Sequence 792 AA;

Query Match	97.5%;	Score 863;	DB 3;	Length 792;
Best Local Similarity	98.3%;	Pred. No. 5.8e-83;		
Matches 175;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	MKLKQIASALMLGISPLAFADFTI	QIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA	60
Db	1	MKLKQIASALMLGISPLAFADFTI	QIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA	60
QY	61	IIKSLYATGFFDDRVRETADGQLLT	VIERTTIGSLNITGAKMLONDAIKKNLESFGLAQ	120
Db	61	IIKSLYATGFFDDRVRETADGQLLT	VIERTTIGSLNITGAKMLONDAIKKNLESFGLAQ	120
QY	121	SOYFNOATLNQAVAGLKEEYVLRGKLN	IQITPKVTKLARNRVDITIDEGKSAKITD	178
Db	121	SOYFNOATLNQAVAGLKEEYVLRGKLN	IQITPKVTKLARNRVDITIDEGKSAKITD	178

Search completed: July 6, 2005, 15:13:14
Job time : 53.6354 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:05:39 ; Search time 13.6923 Seconds
(without alignments)
970.438 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178
Perfect score: 885
Sequence: 1 MKLKQIASALMMLGISPLAF.....RNRVDITIDEGKSAKID 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	797	4	US-09-994-192-4
2	863	97.5	792	4	US-09-994-192-2
3	296.5	33.5	827	4	US-09-543-681A-6425
4	295.5	33.4	821	4	US-09-352-991A-21013
5	292	33.0	815	4	US-09-489-039A-12469
6	289	32.7	813	4	US-09-540-236-3472
7	286	32.3	813	4	US-09-701-711-2
8	286	32.3	813	4	US-09-328-352-7498
9	282	31.9	865	4	US-09-489-039A-8469
10	276	31.2	825	4	US-08-433-522A-2
11	236.5	26.7	797	3	US-08-942-046-2
12	236.5	26.7	797	3	US-08-942-046-4
13	236.5	26.7	797	3	US-08-433-522A-6
14	236.5	26.7	797	3	US-09-135-166-2
15	236.5	26.7	797	3	US-09-135-166-4
16	236.5	26.7	797	3	US-09-135-166-6
17	236.5	26.7	797	3	US-08-942-046-2
18	236.5	26.7	797	3	US-08-942-046-4
19	236.5	26.7	797	3	US-08-942-046-6
20	234.5	26.5	792	3	US-08-433-522A-8
21	234.5	26.5	792	3	US-09-135-166-8
22	234.5	26.5	792	3	US-08-942-046-8
23	234.5	26.5	793	3	US-08-433-522A-10
24	234.5	26.5	793	3	US-09-135-166-10
25	234.5	26.5	793	3	US-08-942-046-10
26	151	17.1	896	4	US-09-689-065B-5
27	93.5	10.6	795	4	US-09-198-452A-314

28 93.5 10.6 795 4 US-09-438-185A-302 Sequence 302, App
29 92 10.4 865 4 US-09-711-164-354 Sequence 354, App
30 89.5 10.1 944 4 US-09-328-352-4401 Sequence 4401, App
31 86.5 9.8 465 4 US-09-489-039A-8591 Sequence 8591, App
32 84 9.5 365 4 US-10-101-464A-510 Sequence 510, App
33 83.5 9.4 313 3 US-08-480-640A-192 Sequence 192, App
34 83.5 9.4 313 3 US-08-686-968C-192 Sequence 192, App
35 83.5 9.4 313 3 US-08-488-237A-192 Sequence 192, App
36 83.5 9.4 313 3 US-08-375-992A-192 Sequence 192, App
37 83.5 9.4 313 4 US-08-472-679H-192 Sequence 192, App
38 83 9.4 850 4 US-09-489-039A-13490 Sequence 13490, A
39 82.5 9.3 424 4 US-09-543-681A-5349 Sequence 5349, App
40 80 9.0 257 4 US-09-328-352-6621 Sequence 6621, App
41 78 8.8 267 4 US-09-252-991A-17521 Sequence 17521, A
42 77 8.7 838 4 US-09-489-039A-9864 Sequence 9864, App
43 76 8.6 192 4 US-09-302-540-9869 Sequence 9869, App
44 76 8.6 1132 4 US-09-198-452A-466 Sequence 466, App
45 76 8.6 1414 4 US-09-438-185A-446 Sequence 446, App

ALIGNMENTS

RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UM85C147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match 100.0%; Score 885; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 1.7e-93;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKLKQIASALMMLGISPLAFADFTTQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTTQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLTVERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTVERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDIDEGKSAKID 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDIDEGKSAKID 178

RESULT 2
US-09-994-192-2
; Sequence 2, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UM85C147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192

; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2

Query Match 97.5%; Score 863; DB 4; Length 792;
Best Local Similarity 98.3%; Pred. No. 5.9e-91;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIVCTPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITD 178
DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITD 178

RESULT 3
US-09-543-681A-6425
; Sequence 6425, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6425
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6425

Query Match 33.5%; Score 296.5; DB 4; Length 827;
Best Local Similarity 38.4%; Pred. No. 2.9e-25;
Matches 68; Conservative 34; Mismatches 74; Indels 1; Gaps 1;
QY 1 MKLKQIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGS 59
DB 27 MAMKKLLIASLLGSAATGSDGVVDIQIEGLQRVAVGAALLNMPVRVGVSDVSDDDIS 86
QY 60 AIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLA 119
DB 87 RTIRSLFATGNFDDVRVLRDGNVLIQVQKERTPIASITFSGNKAIKEDMLKQNLDAASNIR 146
QY 120 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKIT 176
DB 147 IGETLDRMTLANIEKGLDFYFSGKYNATKVVVVTPLPNRRVDLKLVPAGVGSATI 203

RESULT 4
US-09-252-991A-21013
; Sequence 21013, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21013
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21013

Query Match 33.4%; Score 295.5; DB 4; Length 821;
Best Local Similarity 37.7%; Pred. No. 3.8e-25;
Matches 66; Conservative 36; Mismatches 70; Indels 3; Gaps 1;
QY 3 LKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAII 62
DB 33 LPALLSALM---IAEVHAESFTVSDIRVNGLQKVSAGSVFAALPLNVGETIDDDQALVQAT 89
QY 63 KSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQ 122
DB 90 RSLFKTGFDDIQLGDRGNLVTVVVERPSISIEGNAISKEDLLKGLQSGLAEG 149
QY 123 YFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKIT 177
DB 150 IFQRTATLEGVRNELQRYVQAQGRYSNAEIVPQPRNRVALKININEGTVAIS 204

RESULT 5
US-09-489-039A-12469
; Sequence 12469, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12469
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12469

Query Match 33.0%; Score 292; DB 4; Length 815;
Best Local Similarity 38.0%; Pred. No. 9.5e-25;
Matches 68; Conservative 31; Mismatches 72; Indels 8; Gaps 1;
QY 6 IASALMMLGISPLAFAD-----FTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTH 57
DB 5 ITWAMKKLLIASLLFSATVYGAEGFVKDHFEGQLRVAVGAALLSMPVRPGDVTDDDD 64
QY 58 GSAIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFG 117
DB 65 ISNTIRALPATGNFDDVRVLRDGTLLVQVKERTPIASITFSGNKSVDKMLKQNLASG 124
QY 118 LAQSQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKI 176
DB 125 VRVGESLDRITTIADIEKGLDFYFSGKYSASVKAIVTLPNRRVDLKLVPFQEGVSAKI 183

RESULT 6
US-09-540-236-3472
; Sequence 3472, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

QY 122 QYFNQATLNOAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEKSAKI 176
Db 121 DVLIREKLNFAKSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKL 175

RESULT 13

US-08-433-522A-6
; Sequence 6, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,522A
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-522A-6

Query Match 26.7%; Score 236.5; DB 3; Length 797;
Best Local Similarity 30.3%; Pred. No. 2.5e-18;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;
QY 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDTYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGVQDLEQQIRASLPVRAGQRTDNDVANI 60
QY 62 IKSLYATGFFDDVRVETADGQLLTIVERTPTIGSLNITGAKMLQNDIAKKNLESFGLAQS 121
Db 61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVPTTEALKQNLDANGFKVG 120
QY 122 QYFNQATLNOAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEKSAKI 176
Db 121 DVLIREKLNFAKSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKL 175

RESULT 14

US-09-135-166-2
; Sequence 2, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele

; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-135-166-2

Query Match 26.7%; Score 236.5; DB 3; Length 797;
Best Local Similarity 30.3%; Pred. No. 2.5e-18;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;
QY 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGDTYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGVQDLEQQIRASLPVRAGQRTDNDVANI 60
QY 62 IKSLYATGFFDDVRVETADGQLLTIVERTPTIGSLNITGAKMLQNDIAKKNLESFGLAQS 121
Db 61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVPTTEALKQNLDANGFKVG 120
QY 122 QYFNQATLNOAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEKSAKI 176
Db 121 DVLIREKLNFAKSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKL 175

RESULT 15

US-09-135-166-4
; Sequence 4, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/135,166
APPLICATION NUMBER: US/09/135,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-135-166-4

Query Match 26.78; Score 236.5; DB 3; Length 797;
Best Local Similarity 30.3%; Pred. No. 2.5e-18;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;
Qy 3 LKQIASALMLGIGSLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGVQGDLEQQIRASLPVRAGORVTDNDVANI 60
Qy 62 IKSLEYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
Db 61 VRSILFVSGREDDVKAHQEGDVLVVSVVAKSIIISDVKIKGNSVIPTTEALKQNLDAANGFKVG 120
Qy 122 QYFNQATLNOAVAGLKEEYLGKLNITQITPKYTKLARNRVDIDITIDECKSAKI 176
Db 121 DVLIREKLINEFAKSVKEHYASVGRYNATVEPIVNTLPNNRABILIQINEDDKAKL 175

Search completed: July 6, 2005, 15:20:40
Job time : 14.6923 secs